

Single cell transcriptomics

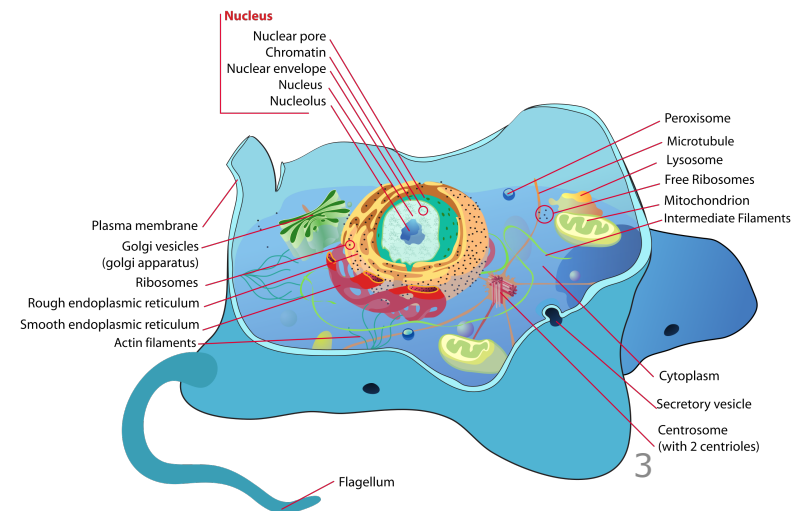
Introduction to single cell RNA-seq



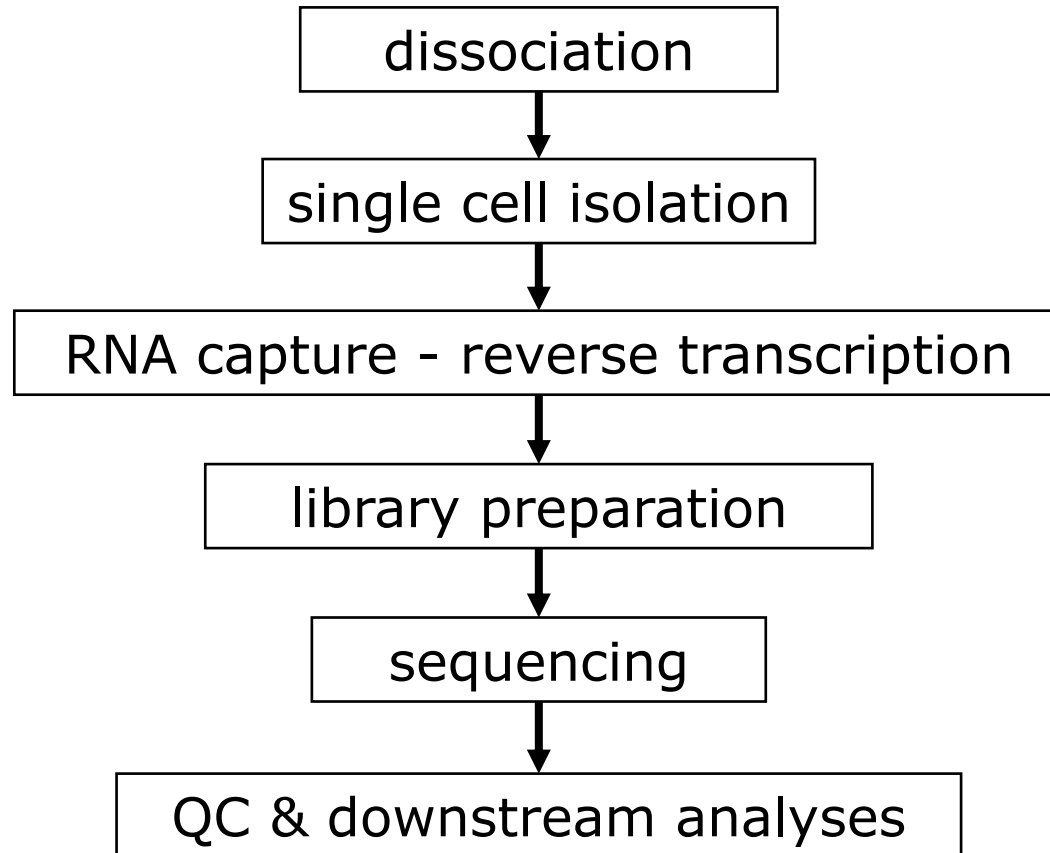
Ralf Kabelitz, CC BY 3.0

Why single cell RNAseq?

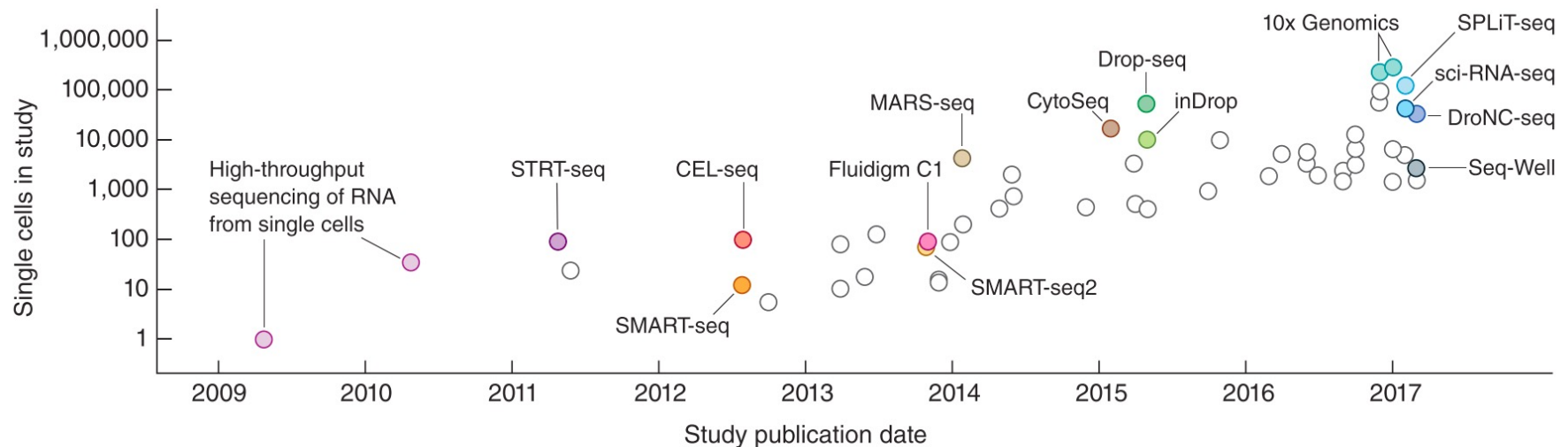
- **Cell:** basic structural and functional unit of life
- Annotation of cell type and/or state
- Differential gene expression between and within cell types



scRNA-seq workflow



Technologies

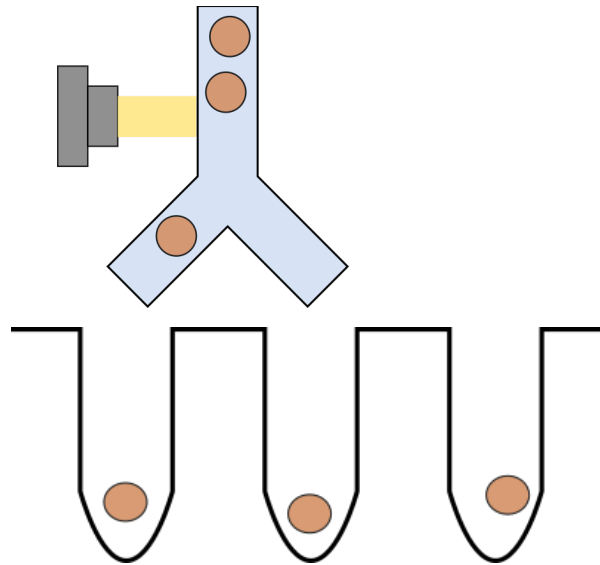


1. Physical separation: e.g. SMART-seq
2. Droplet-based: e.g. 10x genomics (3' kit)
3. Combinatorial indexing: e.g. SPLiT-seq

Svensson V et al., Exponential scaling of single-cell RNA-seq in the past decade. Nat Protoc. 2018;13:599–604.

SMART-seq

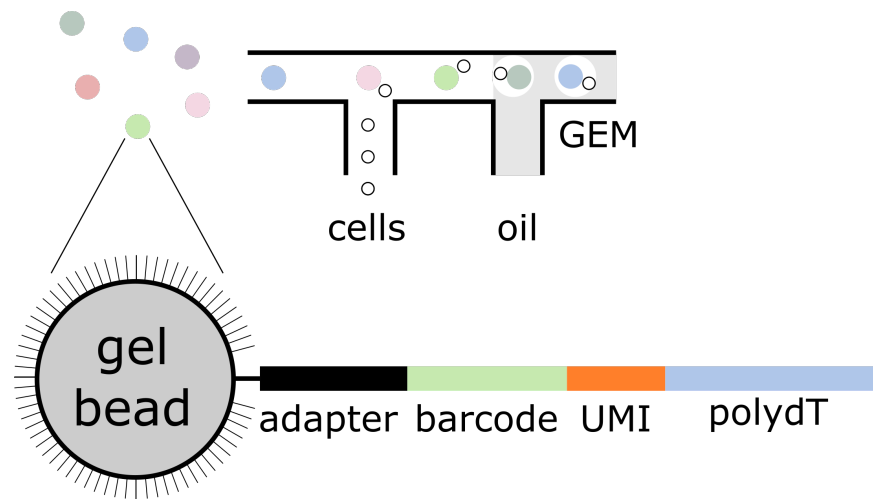
- Use FACS for: 1 well = 1 cell
- Library preparation per cell
- Whole gene can be sequenced

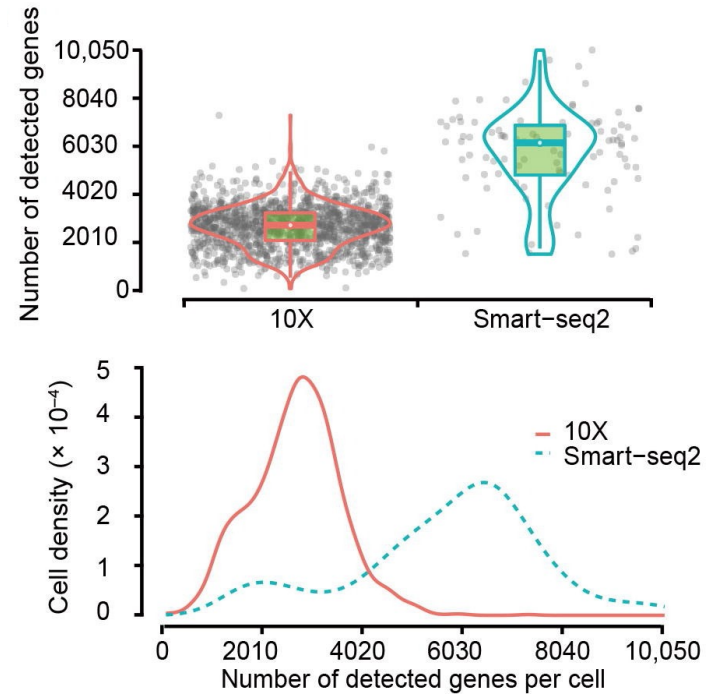
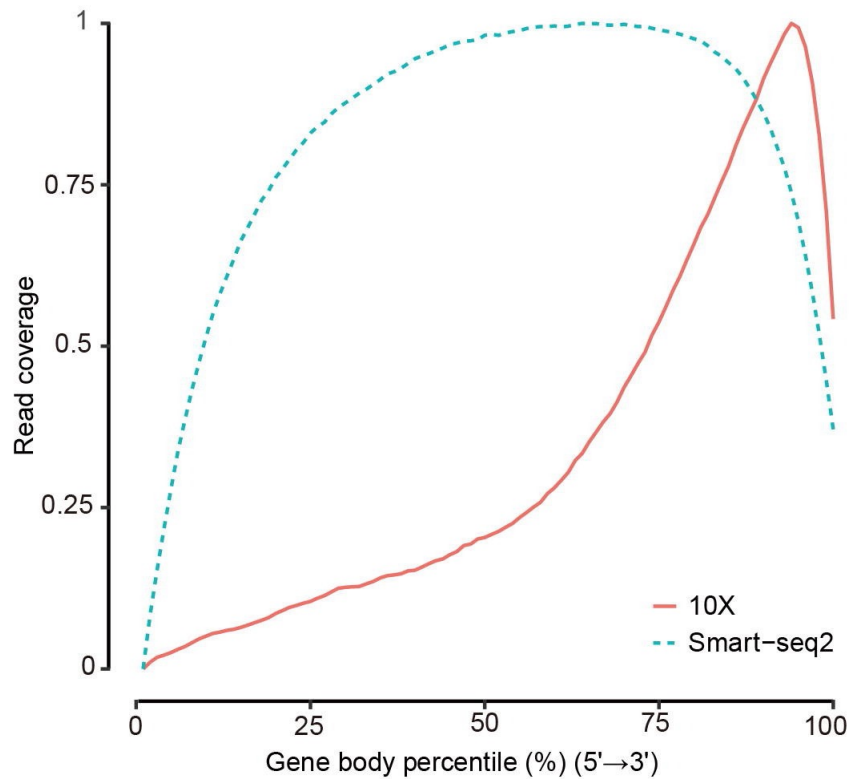


Hagemann-Jensen M et al. Single-cell RNA counting at allele and isoform resolution using Smart-seq3. Nat Biotechnol. 2020;38:708–14.

10x genomics (3' kit)

- Cell isolation within oil droplet
- RNA capture with 1 bead/cell
- Sequencing from 3' end
- Only expression



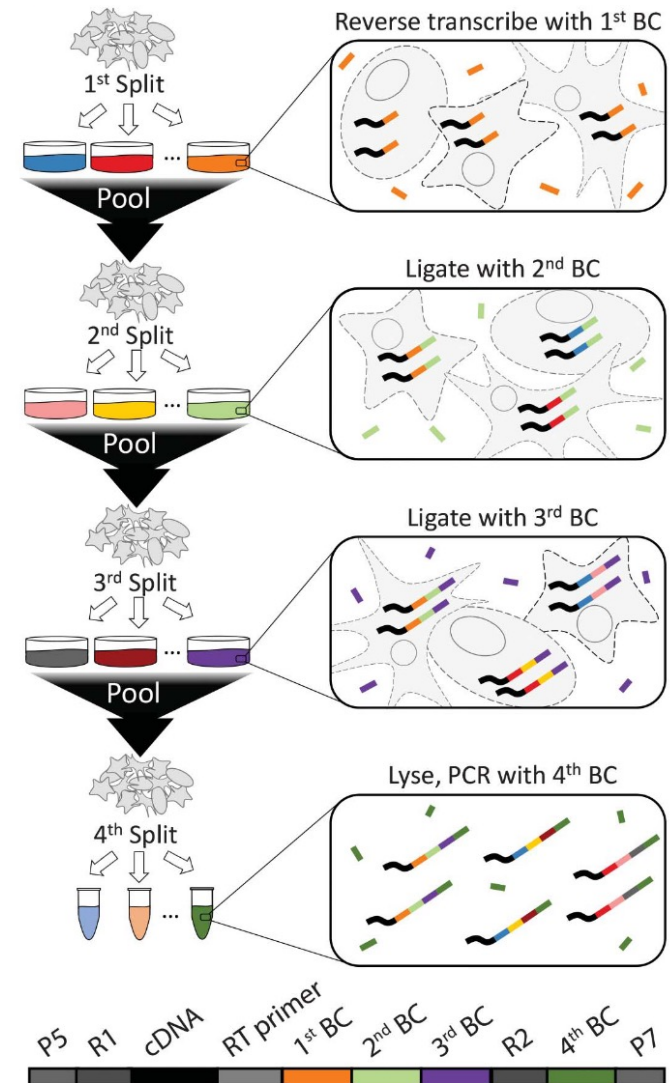


Wang X, et al. Direct Comparative Analyses of 10X Genomics Chromium and Smart-seq2. Genomics Proteomics Bioinformatics; 2021

Droplet (10x genomics)	SMART-seq
3' poly-A bead capture	polydT reverse transcription
Strong bias 3' end	Whole transcript coverage
Expression analysis	Expression + isoform analysis
Low # transcripts/cell	High # transcripts/cell
Investment (cell sorter)	Only FACS needed
10-100k cells	up to 1k cells
1 sample \approx 1 library	1 cell = 1 library
Isolation by droplets - doublets	Isolation by FACS – bias to large cells
Low cost/cell	High cost/cell

SPLiT-seq (Parse biosci)

- Based on:
 - formaldehyde fixation
 - in-cell RT + ligation
- 4 rounds of pooling-splitting and barcoding
- Characteristics:
 - Flexible (fixation + no devices needed)
 - Laborious



Rosenberg AB, et al. Single-cell profiling of the developing mouse brain and spinal cord with split-pool barcoding. *Science*. 2018;360:176–82.

Quiz Question 2

Experimental design

- Replication, randomization and blocking
- Be aware of confounding factors, e.g.:
 - Person performing handling
 - Reagents
 - Sequencing lane/library
- Record any factor for downstream correction

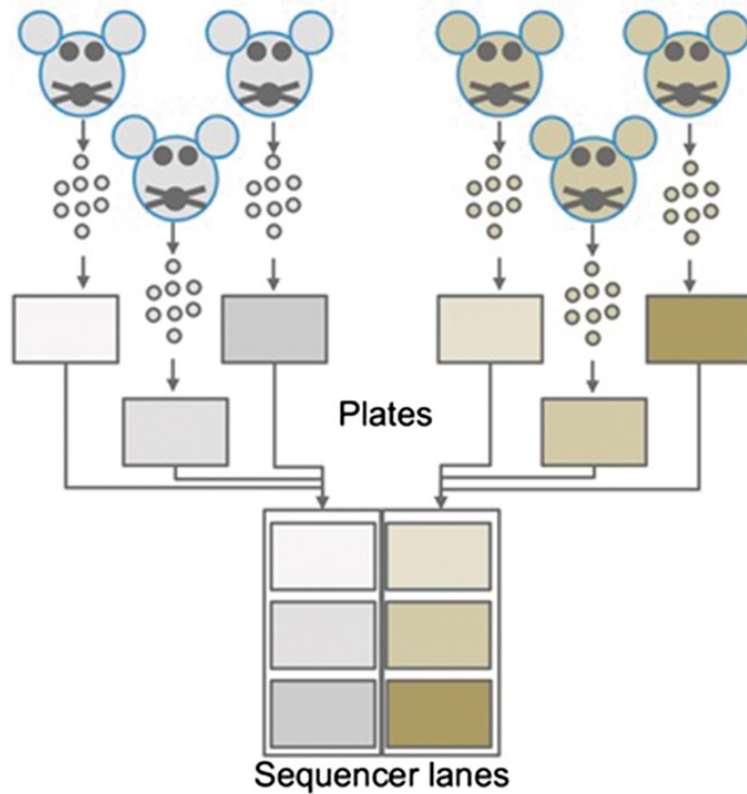


Further reading:

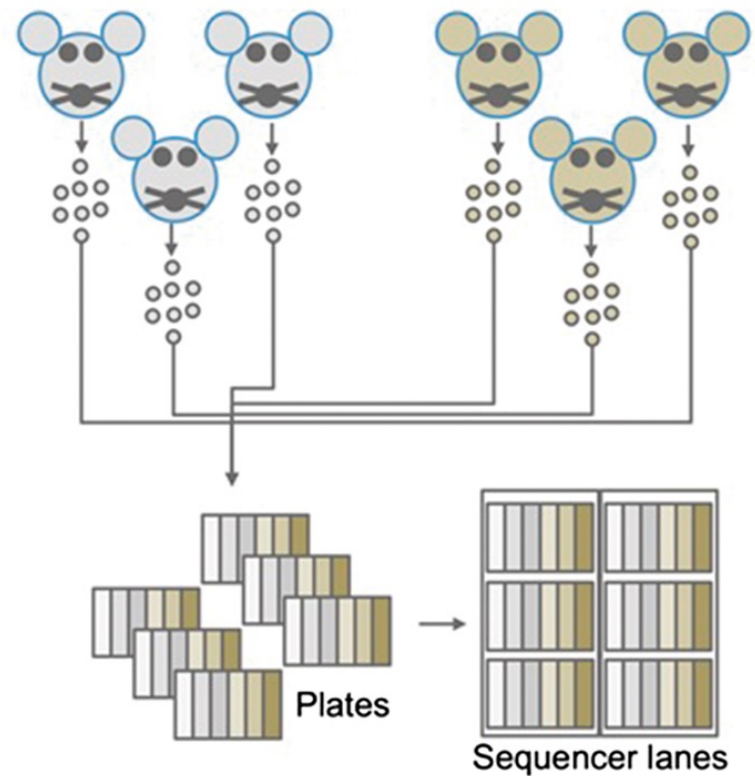
- <https://doi.org/10.3389/fcell.2018.00108>
- <https://doi.org/10.1093/bib/bby007>
- <https://doi.org/10.1093/bfqp/elx035>

Experimental design

Confounded design

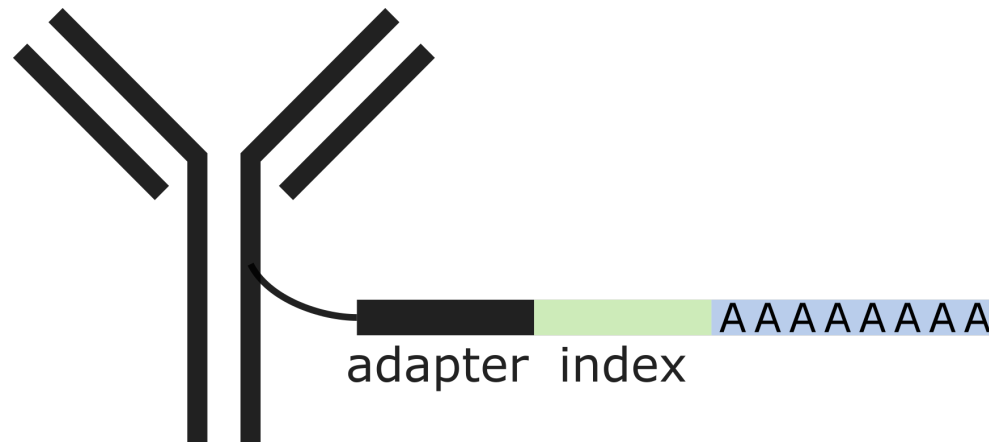


Balanced design



Question 3

Quantify proteins

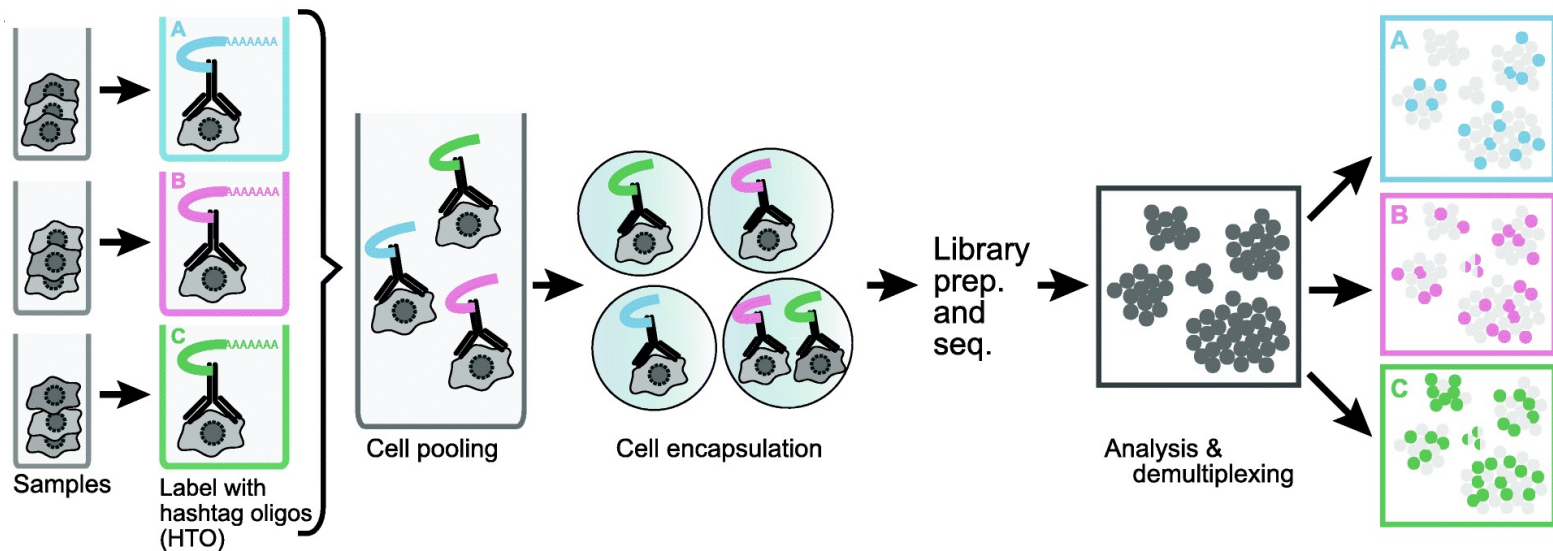


- Quantification of (cell-surface) proteins
- Together with transcriptome

Stoeckius M et al. Simultaneous epitope and transcriptome measurement in single cells. Nat Methods. 2017;14:865–8.

Cell hashing

Solution to 1 sample = 1 library



Stoeckius M et al. Cell Hashing with barcoded antibodies enables multiplexing and doublet detection for single cell genomics. *Genome Biol. Genome Biology*; 2018;19:1–12.

Question 4

single-nucleus RNA-seq

- Alternative to scRNA-seq
- For tissues difficult to dissociate
- No ribosomes -> no translation of transcription factors during processing
- Lower representation of immune cells + surface proteins