

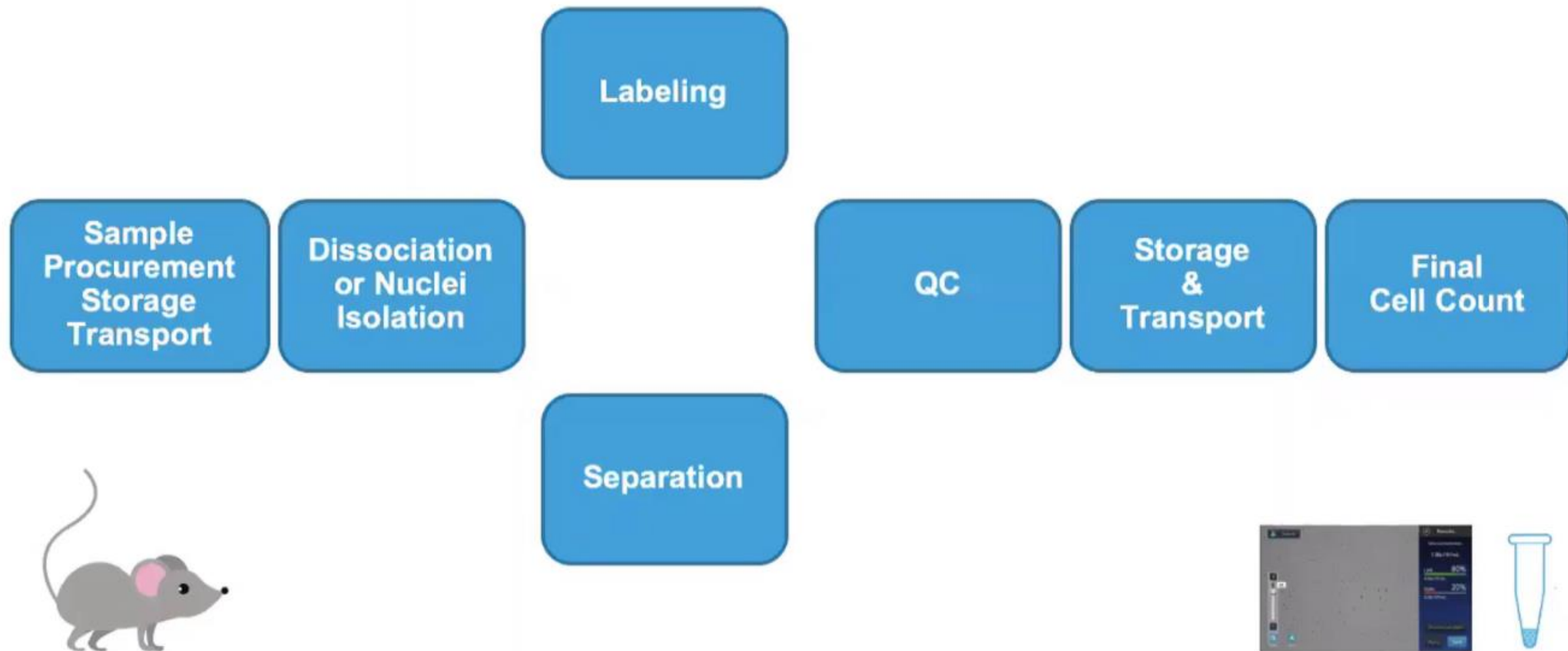
Sample Prep and Experimental Design

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20 October 2020


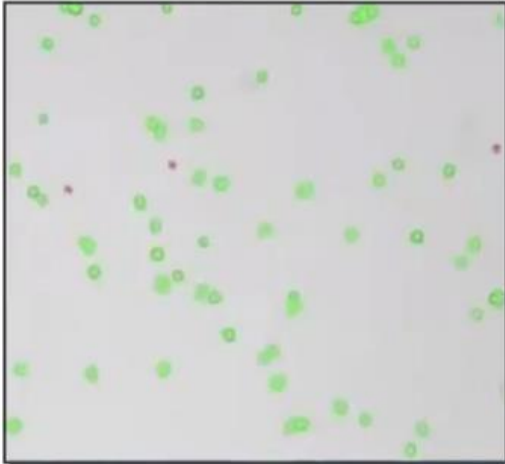
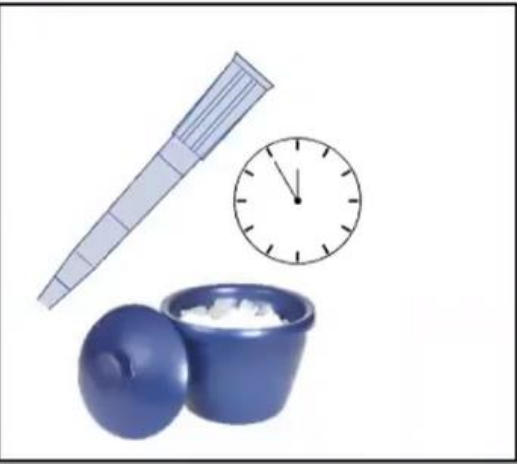
What is sample prep?



Know what you are working with

Cells Tested	Species	Cell Source	Total RNA (pg/cell)	Cell Size (μm)
PBMC	Human	Extracted from blood	~0.75	~5-10
E18 neuron	Mouse	Brain tissue	~2-3	~9
Jurkat	Human	Suspension	5.5	~12
Raji	Human	Suspension	7.3	~12
293T	Human	Adherent	14.2	~18
3T3	Mouse	Adherent	16.1	~18
HCC1954	Human	Adherent	15.7	~18
HCC38	Human	Adherent	21.6	~30

Quality is critical

Goal is to minimize	Clean	Healthy	Gentle
			
	<ul style="list-style-type: none">• Aggregates/clumps• Subcellular debris• Free-floating RNA/DNA	<ul style="list-style-type: none">• RNA leakage• RNA degradation	<ul style="list-style-type: none">• Physical decomposition

Handle with care

Minimize handling, both pipetting and centrifugation

Metric	Control	Wide Bore (Rough)	Narrow Bore (Rough)	Vortex 5s
Number of Cells	1,118	846	1,012	983
Reads per Cell	50,000	50,000	50,000	50,000
Valid Barcodes	95.40%	95.50%	95.30%	95.50%
Fraction Reads in Cells	79.40%	72.80%	54.00%	63.10%
Reads Mapped Confidently to Transcriptome	70.50%	71.40%	71.80%	71.00%
Valid UMIs	99.40%	99.40%	99.40%	99.40%
Median Genes per Cell	3,137	3,180	2,833	2,934

Sample procurement, storage, transport

CNV

Cultured cells, PBMCs
*Fresh and cryopreserved
*10x protocols work as-is

Fresh tissue
*Minimal optimization

Snap-frozen tissue
*Minimal optimization

Fixation?
*Not tested but likely
(ethanol or methanol)

ATAC

Cultured cells, PBMC
*Fresh and cryopreserved
*10x protocols work as-is

Fresh tissue
*Optimization

Snap-frozen tissue
*Optimization

Fixation?
*Not tested

GEX

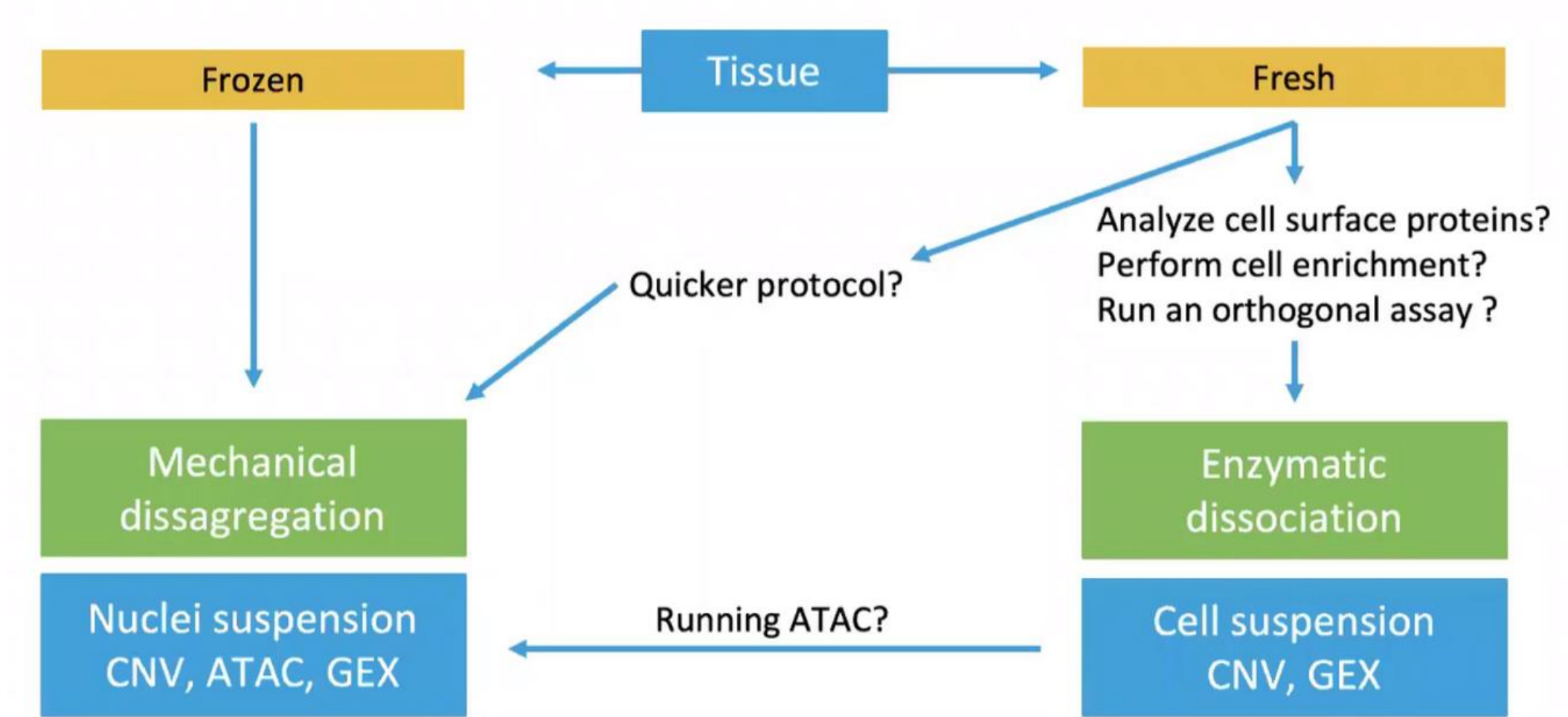
Cultured cells, PBMC
*Fresh and cryopreserved
*10x protocols work as-is

Fresh tissue
*Significant optimization

Snap-frozen tissue
*Nuclei (no cell surface proteins)
*Technically challenging
*Significant optimization

Fixation?
*Methanol (but we prefer
cryopreservation)

How to choose a dissociation method



Separation

Separate intact cells and nuclei from

- Aggregates/clumps
- Debris
- Free-floating mRNA
- Dead cells
- Enrichment/depletion

Challenges with separation

- Samples are fragile
- Physical stress
- Buffers
- Time
- Yield

Want the minimum handling necessary. Maintain sample integrity.

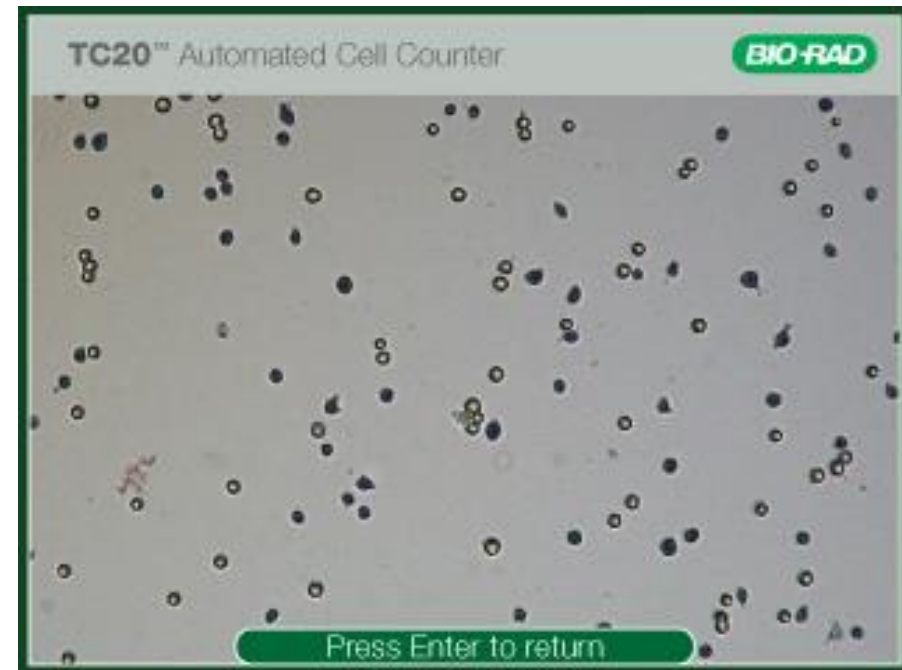
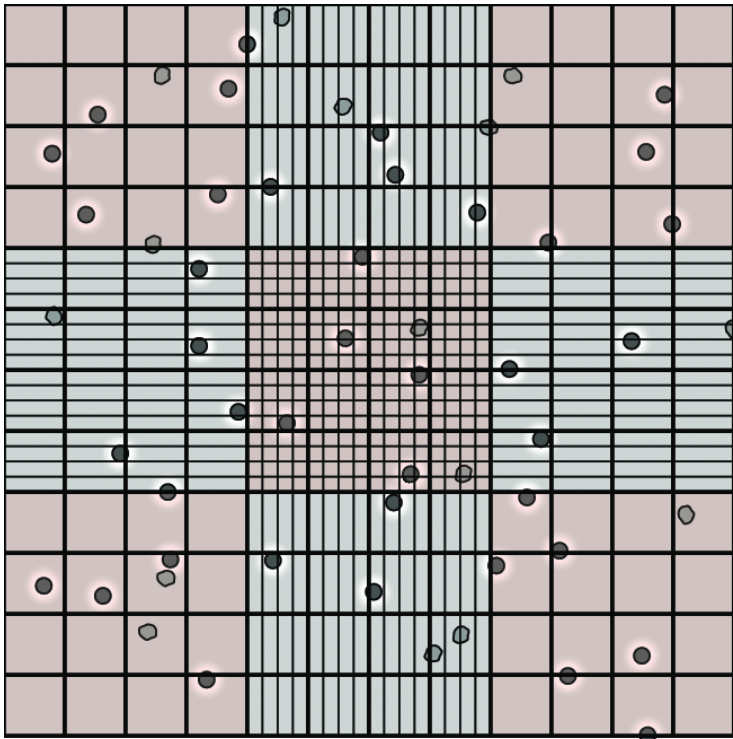
There are many separation methods

Method	Thorough c'fuge (e.g. 3x in PBS + 0.04% BSA)	Gentle c'fuge (e.g. 1x in media)	Magnetic beads	Density Gradient	FACS
10x Protocol Example	PBMC (CG000039)	Cell Prep Guide (CG000053)	Dead cell removal (CG000093)	Nuclei isolation (CG000124)	Customer Developed Protocol (Martelotto)
Can be used with	Abundant	Limited	Abundant	Abundant	Limited
Benefit	Clean	Gentle	Specific, easily accessible, scalable	Removes Debris	Versatile, quick
Challenges	Lossy, can be harsh	Less thorough	Lossy	Lossy, harsh	Expensive, can be harsh

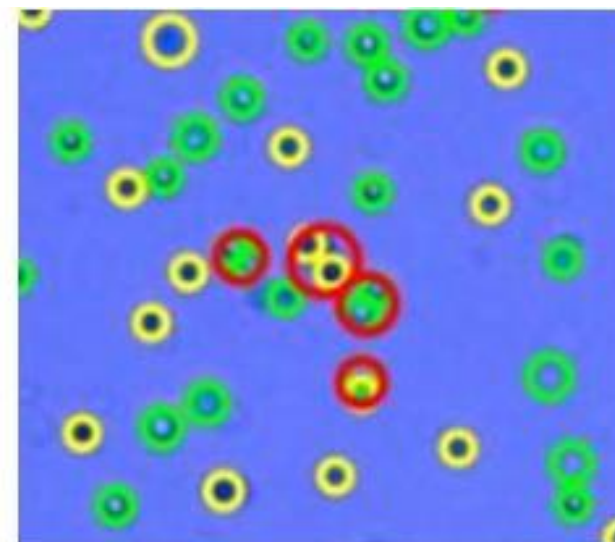
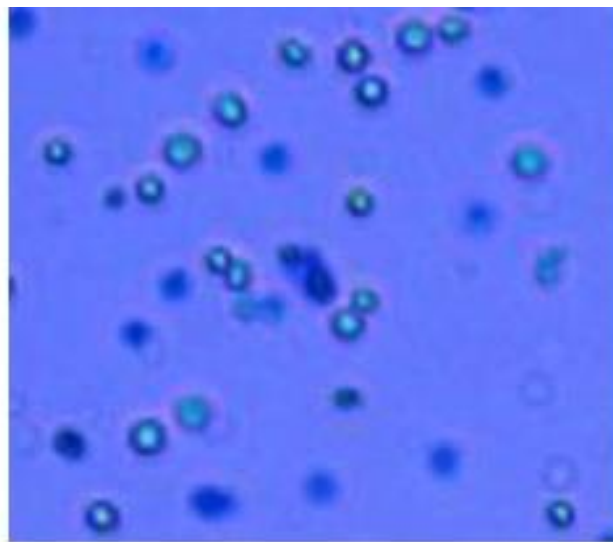
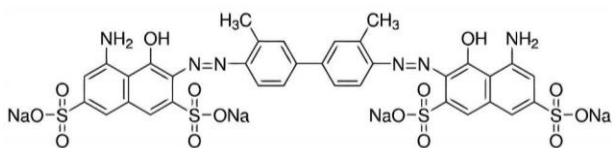
Washing / straining

- 3 washes in PBS + 0.04% BSA before loading
- Use a relatively large volume for washes relative to cell number
 - Concentrated cells can clump
- Large cell aggregates or debris can increase the risk of clogs
 - => Use a cell strainer, 30 to 40 μm
 - BUT – this will result in sample loss, volume loss, and possible cell loss

Counting and viability assessment



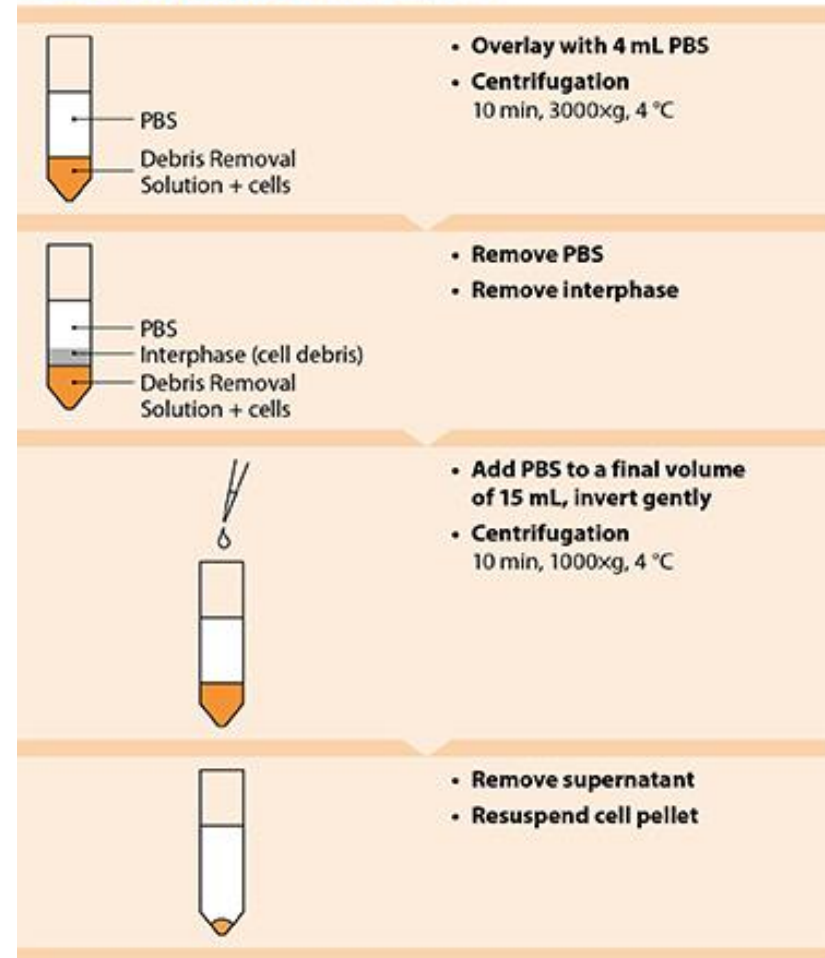
Counting and viability assessment – live/dead



- Alive
- Dead
- Aggregation

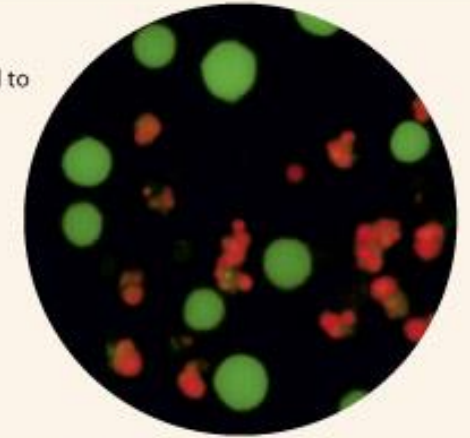
Dead cell and debris removal

Debris removal protocol overview, steps 6–13

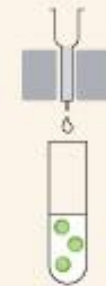


Source:
Miltenyi

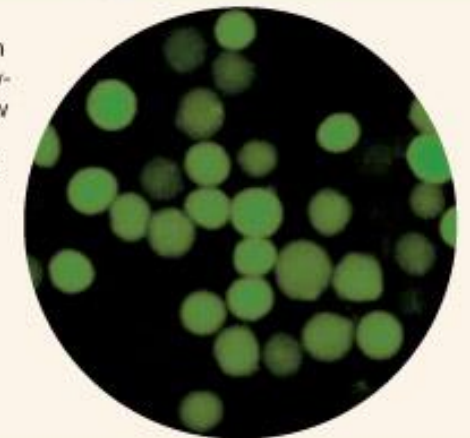
1. The ready-to-use MicroBeads are added to the cell preparation.



2. The sample is separated over a MACS[®] Column in the magnetic field of a MACS[®] Separator. Cell debris, dead, and dying cells are retained in the column.



3. The viable cell fraction is collected in the flow-through. Cells can now be used directly for culture and functional experiments.



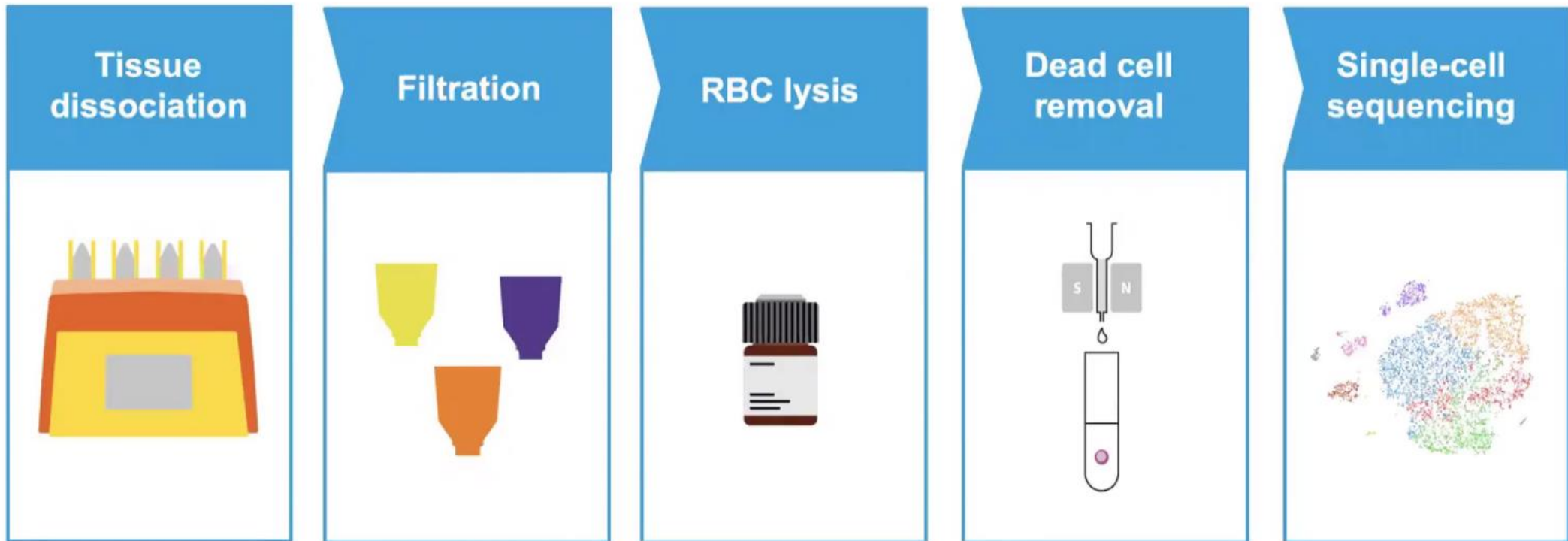
Storage after preparation?

- [Cryopreservation](#) (DMSO)
 - No quantifiable difference between fresh and cryopreserved scRNA-seq samples
- [Methanol fixation](#)

****NOTE:** both approaches have shown a potential bias in cell-type composition, and it is strongly recommended to thoroughly evaluate preservation methods for new cell types that have not been tested.

- iCell8 and Rhapsody microwells – freeze plate after single cell sorting

Example: tumor processing workflow



Summary of key sample prep lessons

- Treat cells gently and keep them happy
 - Try gentle(r) lysis conditions
 - Reduce washing steps
 - Use a swinging bucket centrifuge
 - Keep cells in media + FBS instead of PBS
- Work quickly
 - Consider sorting
 - Minimize handling steps
- *Consider the benefits and drawbacks of different techniques*

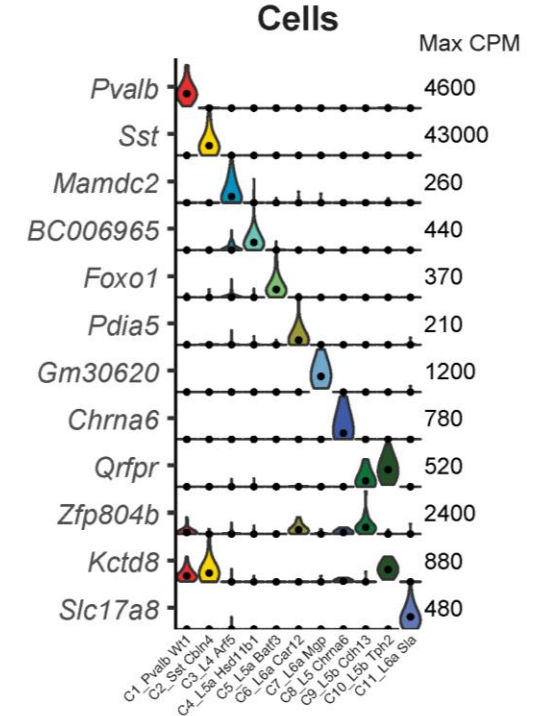
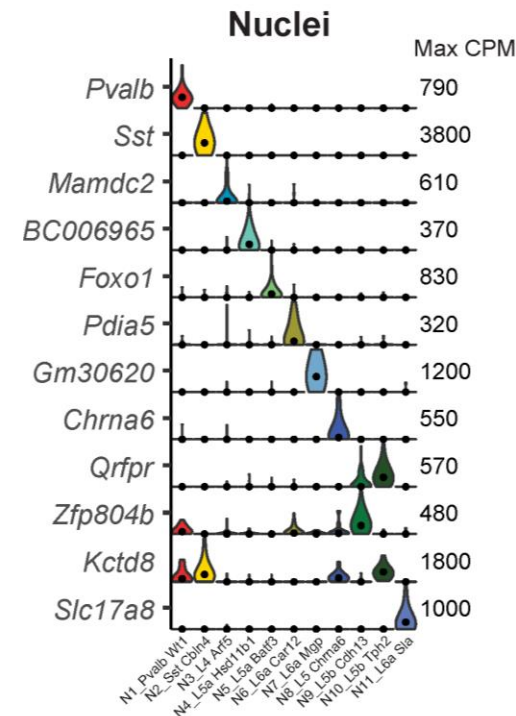
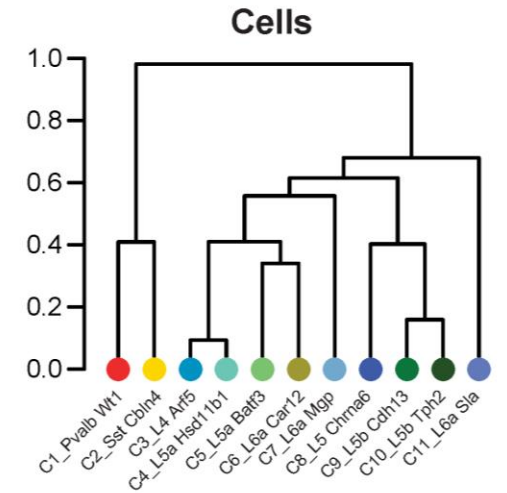
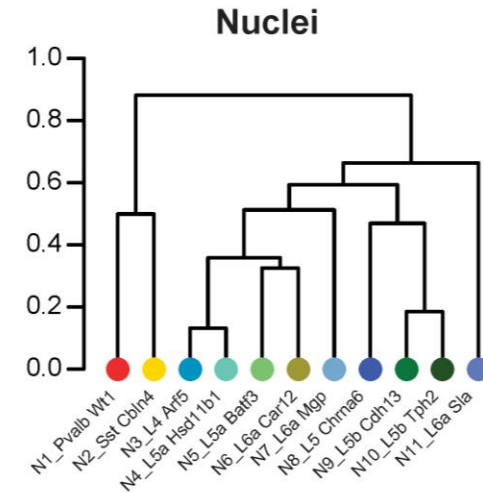
Nuclei vs whole cell

What if cells are not an option?

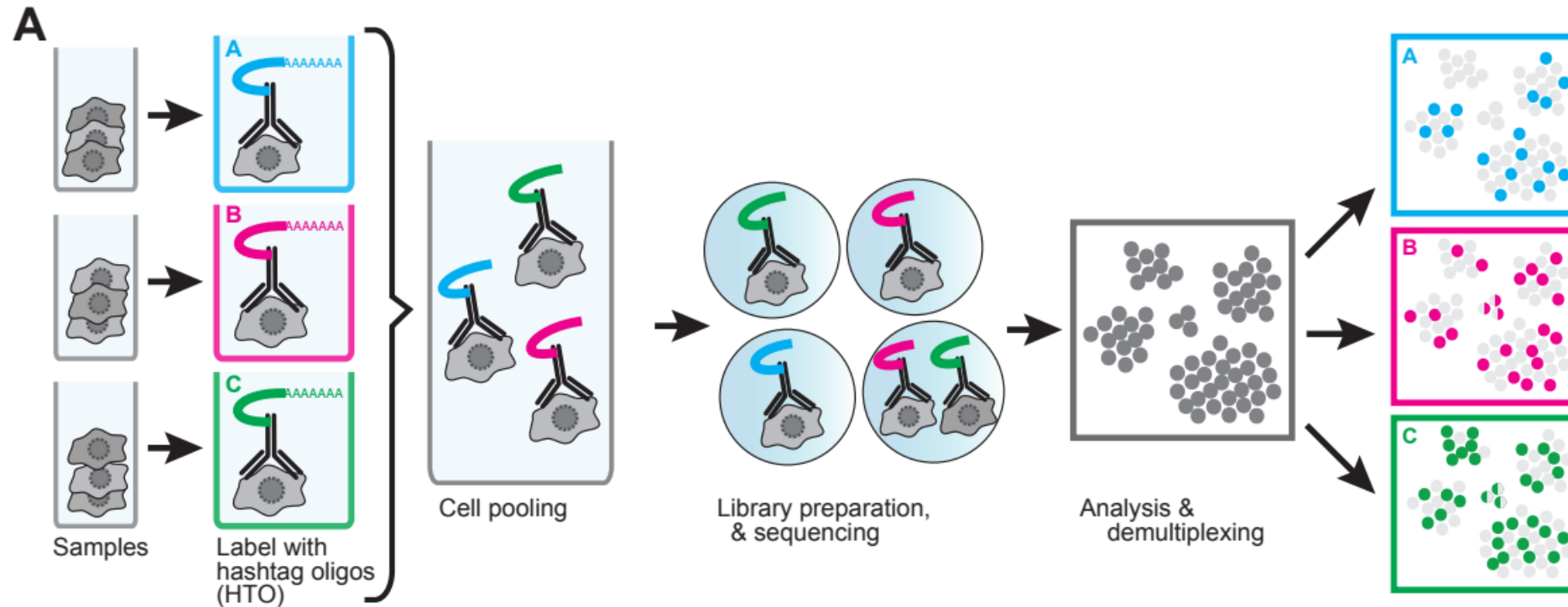
- Neurons
- Snap-frozen
- FFPE

snRNA-seq is nearly identical to scRNA-seq

- Fewer unique transcripts
- More variability in per-nucleus content



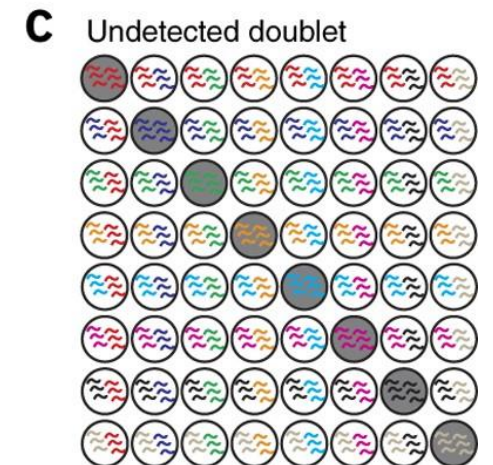
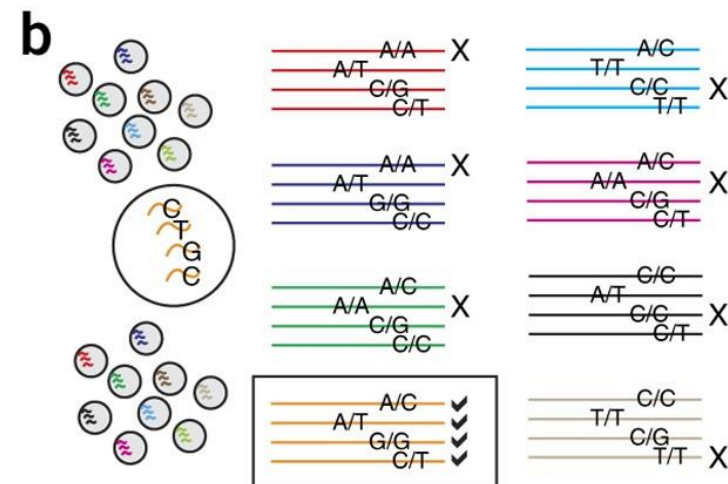
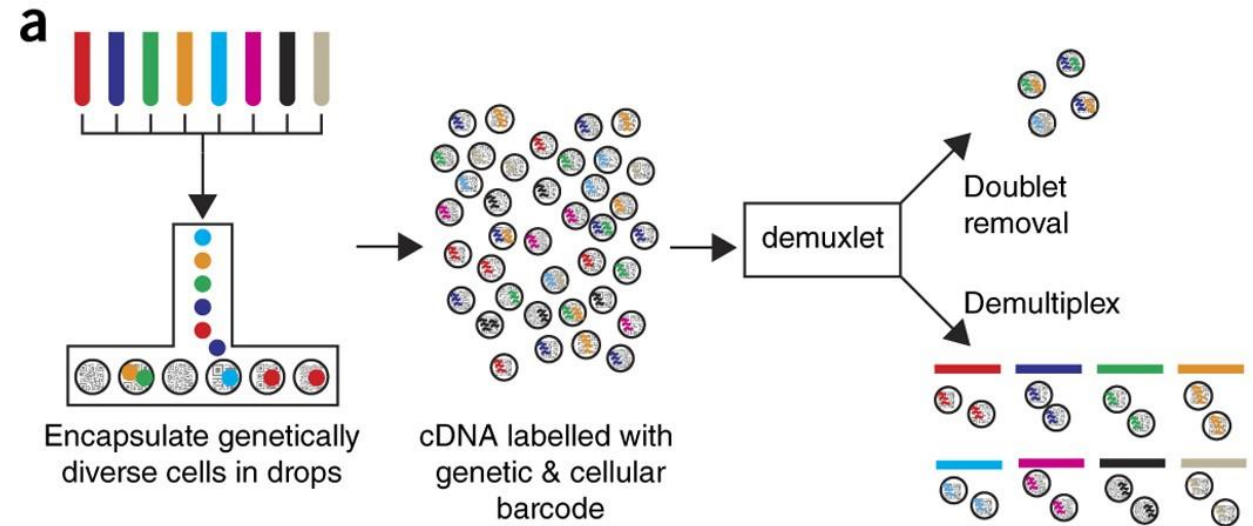
Cell hashing / multiplexing option 1



Pooled 8 PBMC samples in 1 reaction, “super-loading” 20k cells per reaction (5k multiplet)

Cell hashing / multiplexing option 2

Demuxlet
Demultiplex samples using natural genetic variation



How many cells?

Consider sample heterogeneity and subpopulation frequency

General rule of thumb:

- Heterogenous populations require MORE cells
 - Here, a larger number of cells will provide greater statistical power
 - Heterogeneity can be reduced through experimental design (sorting, transgenics)
- Identification of rare cells requires MORE cells

How many samples?

Power calculations + group size estimates

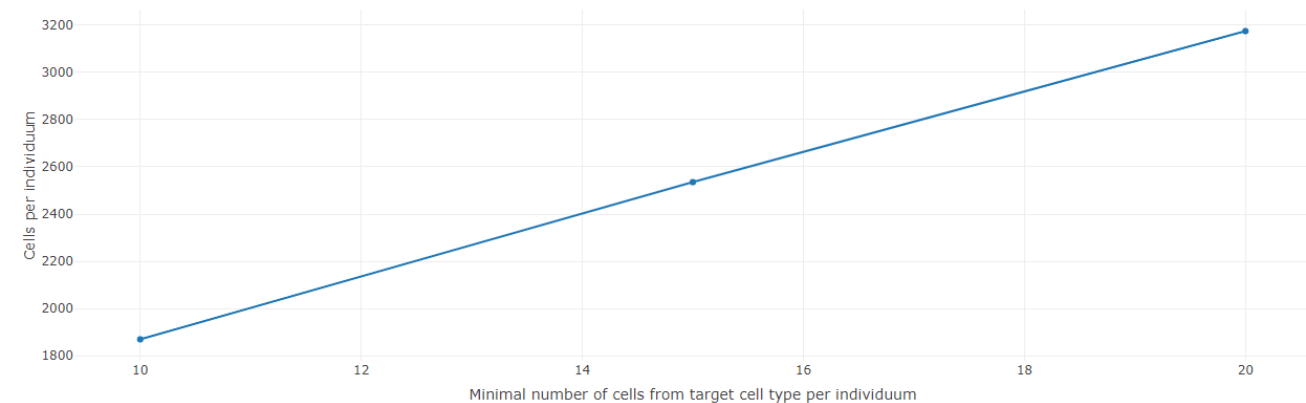
- Is other single-cell data is available (flow- or mass-cytometric data)?
- Computational tools available:
 - [How many cells?](#) – Satija lab
 - [SCOPIT](#) – Navin lab
 - [scPower](#) – Theis and Hening labs

Study parameters

Samples	5
Cell type frequency	0.01
Detection power	0.95
Minimal number of cells	<input type="range" value="10 22"/>

1 11 21 31 41 51 61 71 81 91 100

Required cells per person to detect rare cell types with a certain power



The figure shows the required number of cells per individual (y-axis, log scale) to detect the minimal number of cells from a target cell type per individual (x-axis) with a certain probability. The power depends on the total number of individuals and the frequency of the target cell type. Note that the required number of cells per sample only counts correctly measured cells (no doublets etc), so the number is a lower bound for the required cells to be sequenced.

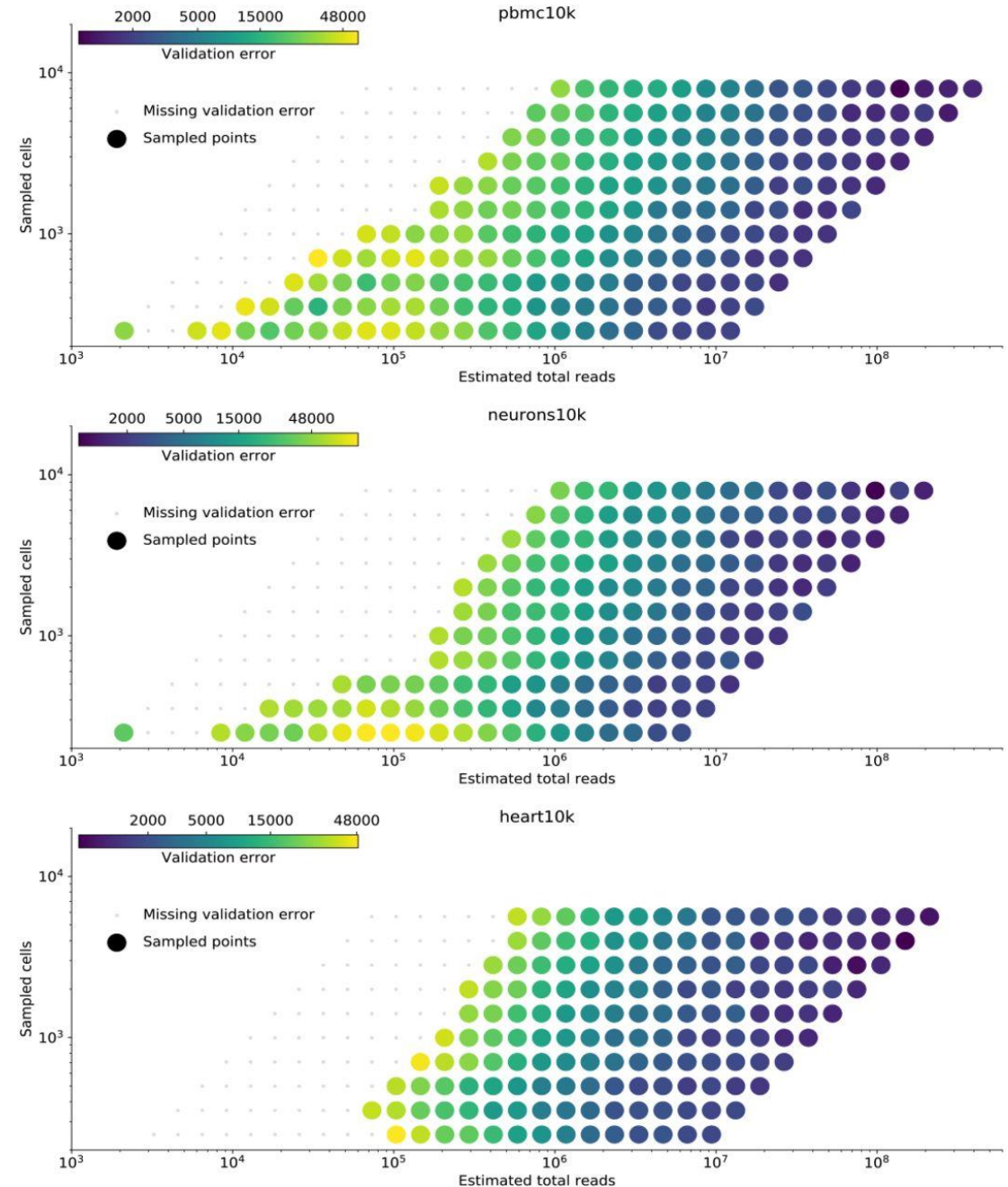
Pilot experiment recommended before large-scale data production

How deep?

For 3' counting approaches:

<15k reads/cell, doubling reads reduces error by 30-40%

>15k reads/cell, doubling reads or cells has little effect (1-3%)



How deep?

For 3' counting approaches:

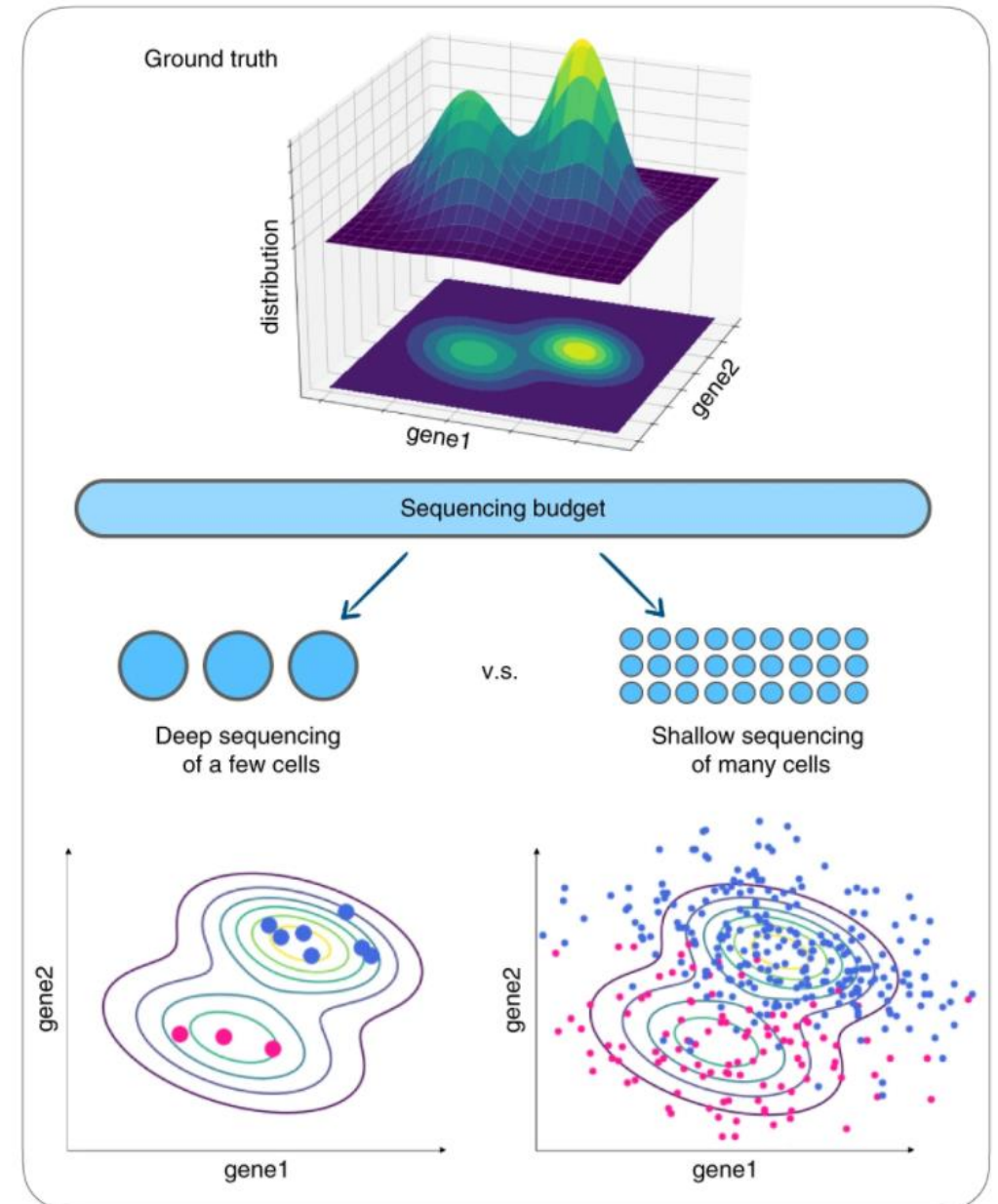
One read per cell per gene

[sceb \(single-cell empirical Bayes\) estimator \(Python package\)](#)

Zhang, Ntranos and Tse Nat Comm 2020

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Sequencing budget allocation problem



How deep?

- BUT... not all cells will have the same depth of sequencing

