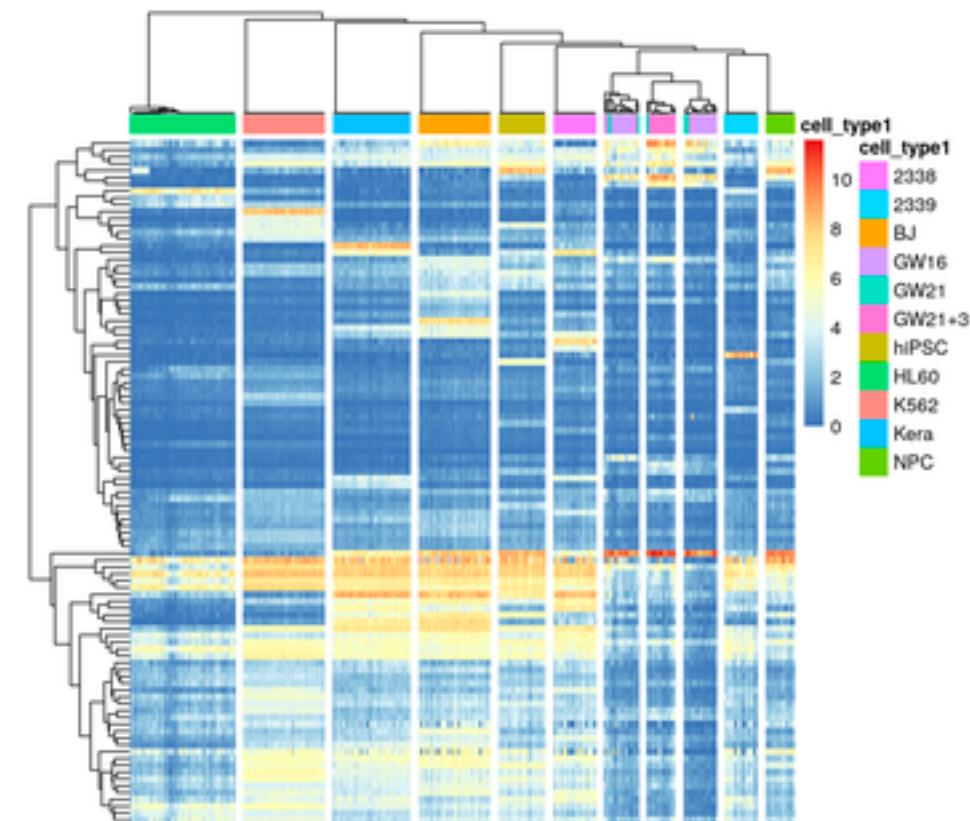
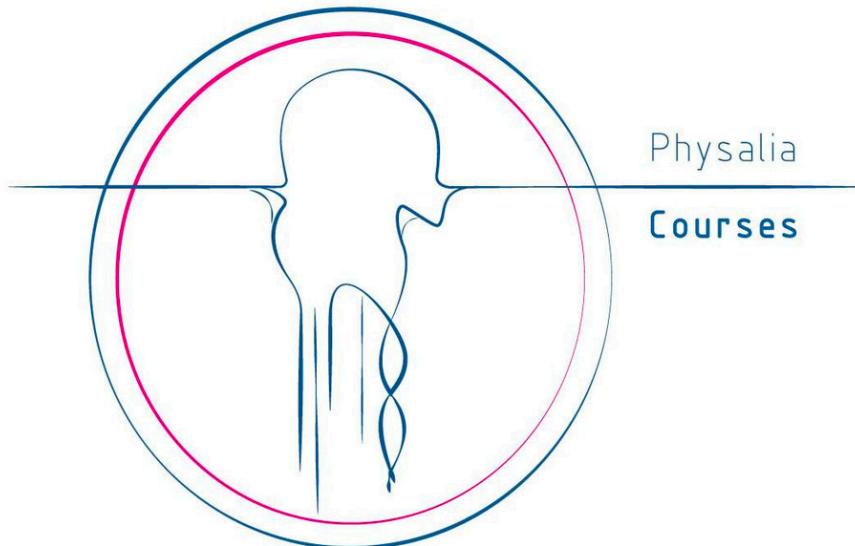


Analysis of Single Cell RNA-Seq Data: Batch Effects and Data Integration

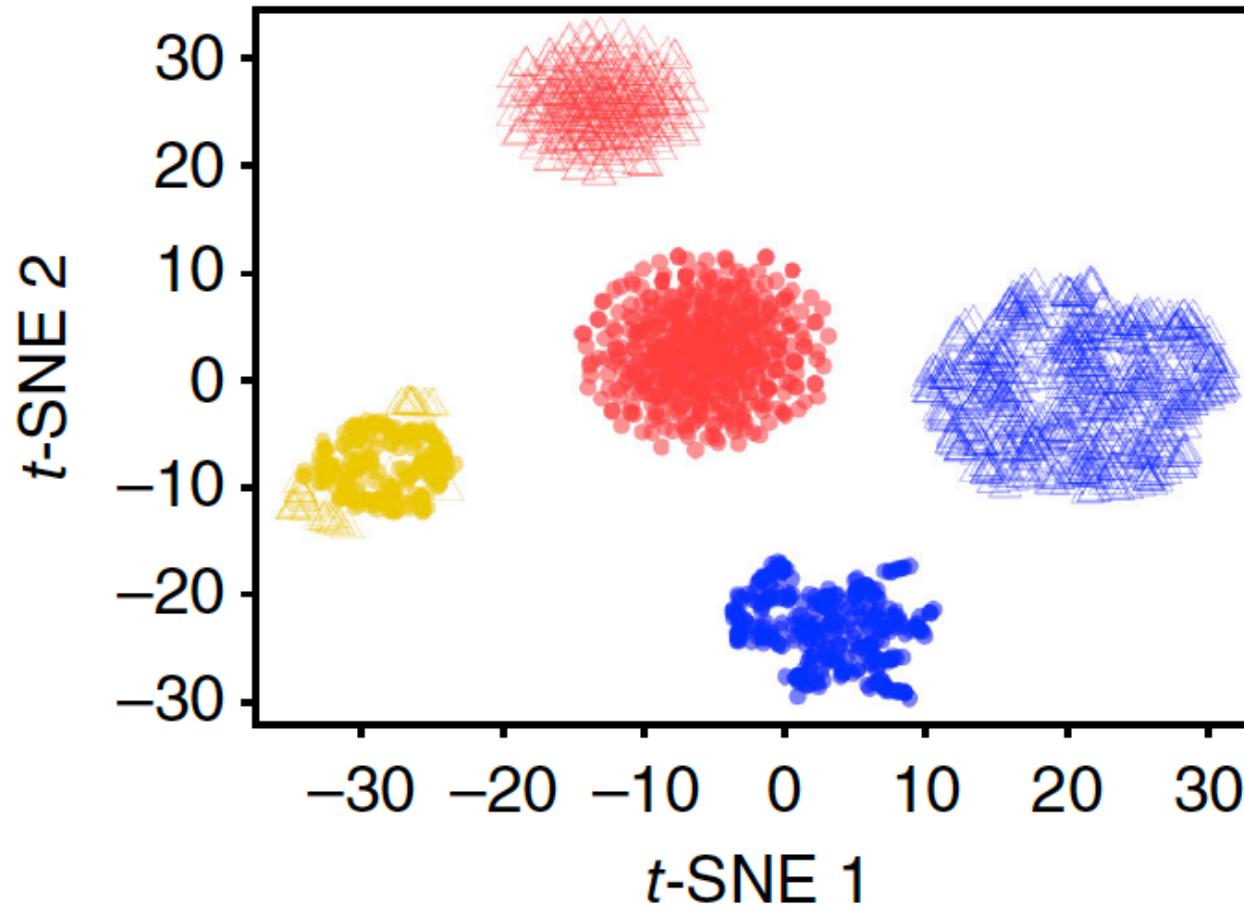
Orr Ashenberg, Jacques Serizay
June 2021



Batch Effects Outline

- Sources of batch effects
- Computational approaches to correct for batch effects and integrate data
- Assessing batch effect corrections and the assumptions of these methods

Distinguishing biological effects and technical, batch effects is a difficult problem



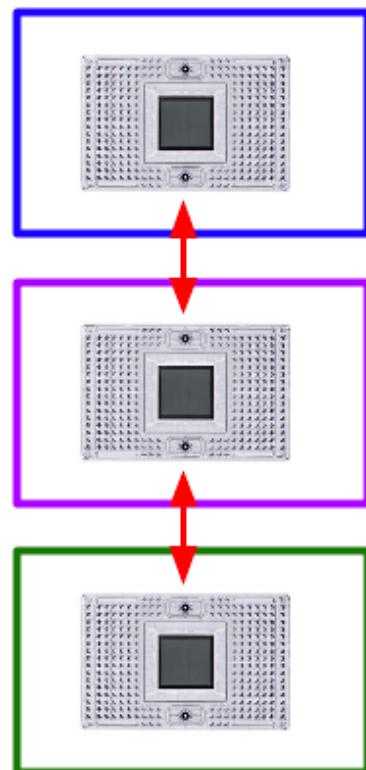
Cells are colored by cell type.

Symbols represent different batches.

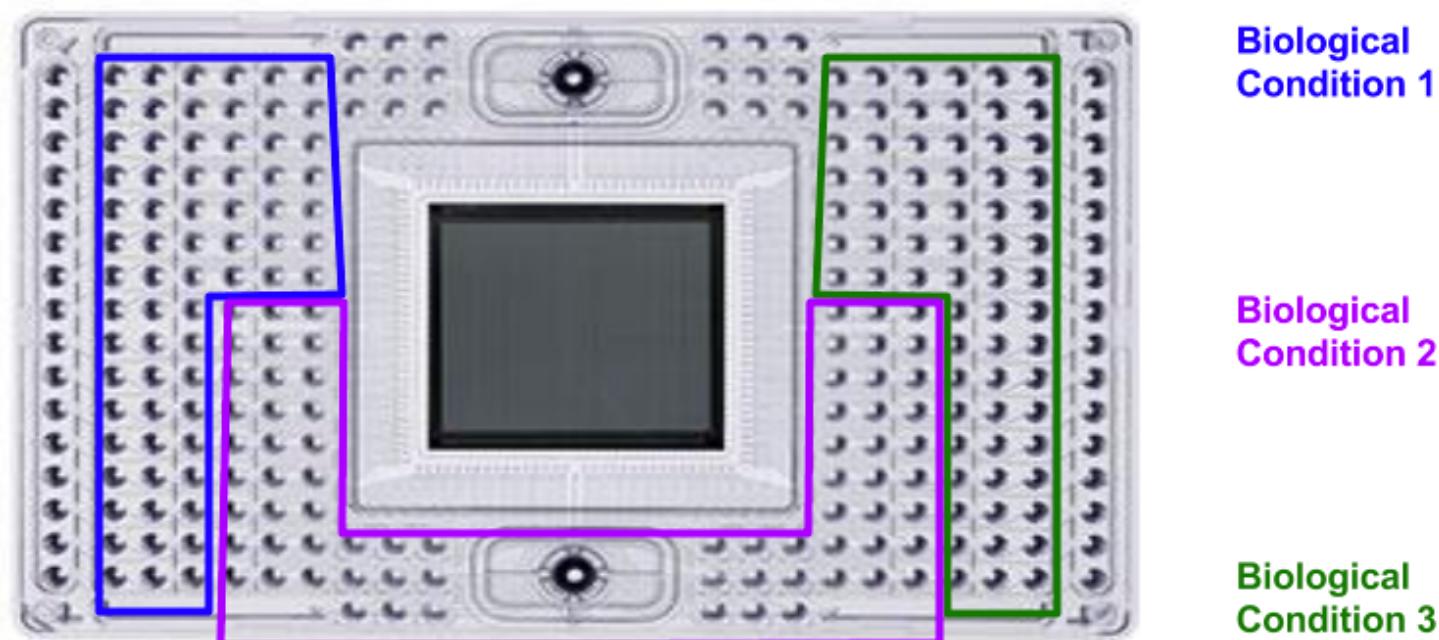
Correcting for batch effects allows us to combine datasets and boost biological signal, while reducing technical confounders

The most powerful way to control batch effects is with careful experimental design

Completely Confounded



Unconfounded



Sound experimental design : Replication, Randomization and Blocking
- R. A. Fisher, 1935

Batch effects: technical sources

- Differences in how samples are sequenced
 - sequencing depth and saturation
 - sequencing instrument



Miseq

~ 20M reads total



Nextseq

~ 500M reads total

HiSeq 4000

4 billion reads

Batch effects: technical sources

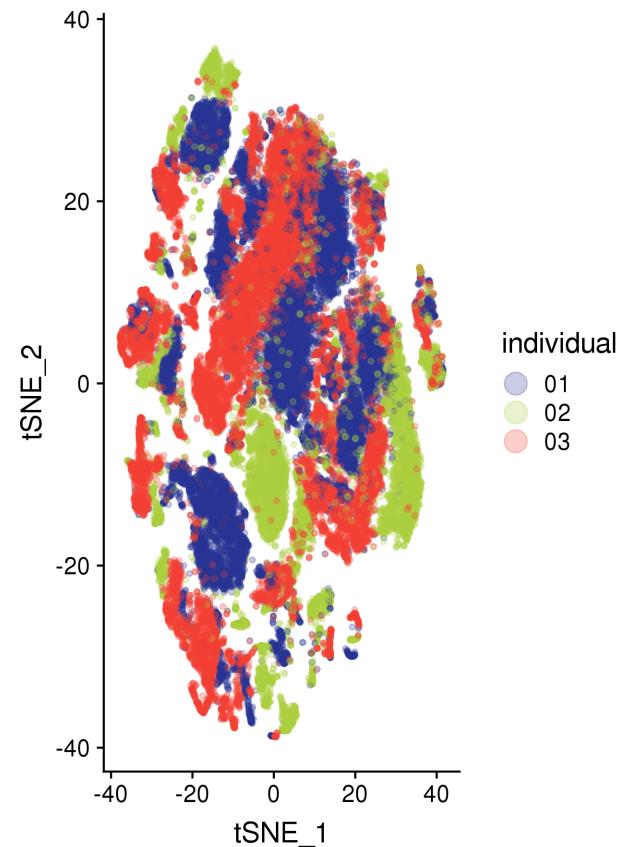
	SMART-seq2	CEL-seq2	STRT-seq	Quartz-seq2	MARS-seq	Drop-seq	inDrop	Chromium	Seq-Well	sci-RNA-seq	SPLiT-seq
Single-cell isolation	FACS, microfluidics	FACS, microfluidics	FACS, microfluidics, nanowells	FACS	FACS	Droplet	Droplet	Droplet	Nanowells	Not needed	Not needed
Second strand synthesis	TSO	RNase H and DNA pol I	TSO	PolyA tailing and primer ligation	RNase H and DNA pol I	TSO	RNase H and DNA pol I	TSO	TSO	RNase H and DNA pol I	TSO
Full-length cDNA synthesis?	Yes	No	Yes	Yes	No	Yes	No	Yes	Yes	No	Yes
Barcode addition	Library PCR with barcoded primers	Barcoded RT primers	Barcoded TSOs	Barcoded RT primers	Barcoded RT primers	Barcoded RT primers	Barcoded RT primers	Barcoded RT primers	Barcoded RT primers	Barcoded RT primers and library PCR with barcoded primers	Ligation of barcoded RT primers
Pooling before library?	No	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
Library amplification	PCR	In vitro transcription	PCR	PCR	In vitro transcription	PCR	In vitro transcription	PCR	PCR	PCR	PCR
Gene coverage	Full-length	3'	5'	3'	3'	3'	3'	3'	3'	3'	3'
Number of cells per assay											

A few basic approaches to batch correction

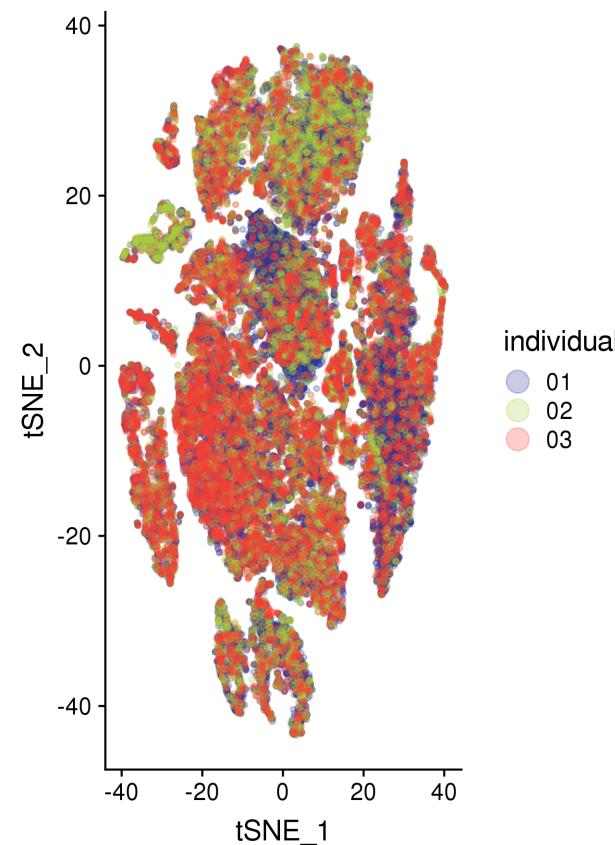
- Down sampling of sequencing reads
- Normalization
- Using variable genes common to multiple samples
- Removing genes correlated with batch
- Regression of residuals with technical covariates
 - batch id
 - number of UMI per cell
 - number of genes per cell
 - % mitochondrial reads
- ComBat (developed for microarray experiments)

Batch correction and data modality integration

Batch effects often arise when patient samples are analyzed together



batch correction
→

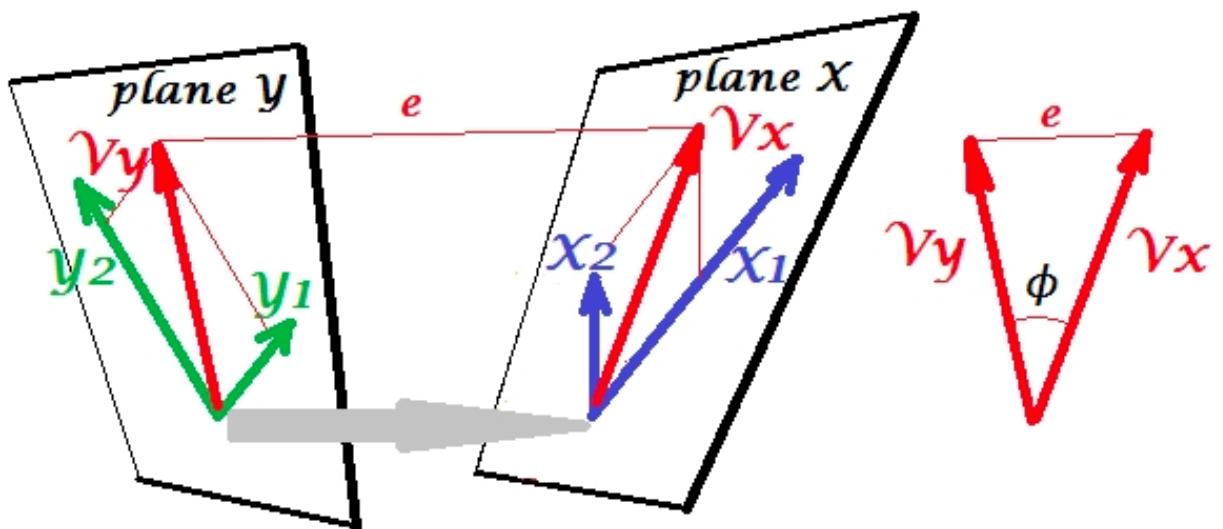


Batch correction and data modality integration

- Seurat v3
- LIGER (Linked Inference of Genomic Experimental Relationships)
- Conos (Clustering on Network of Samples)

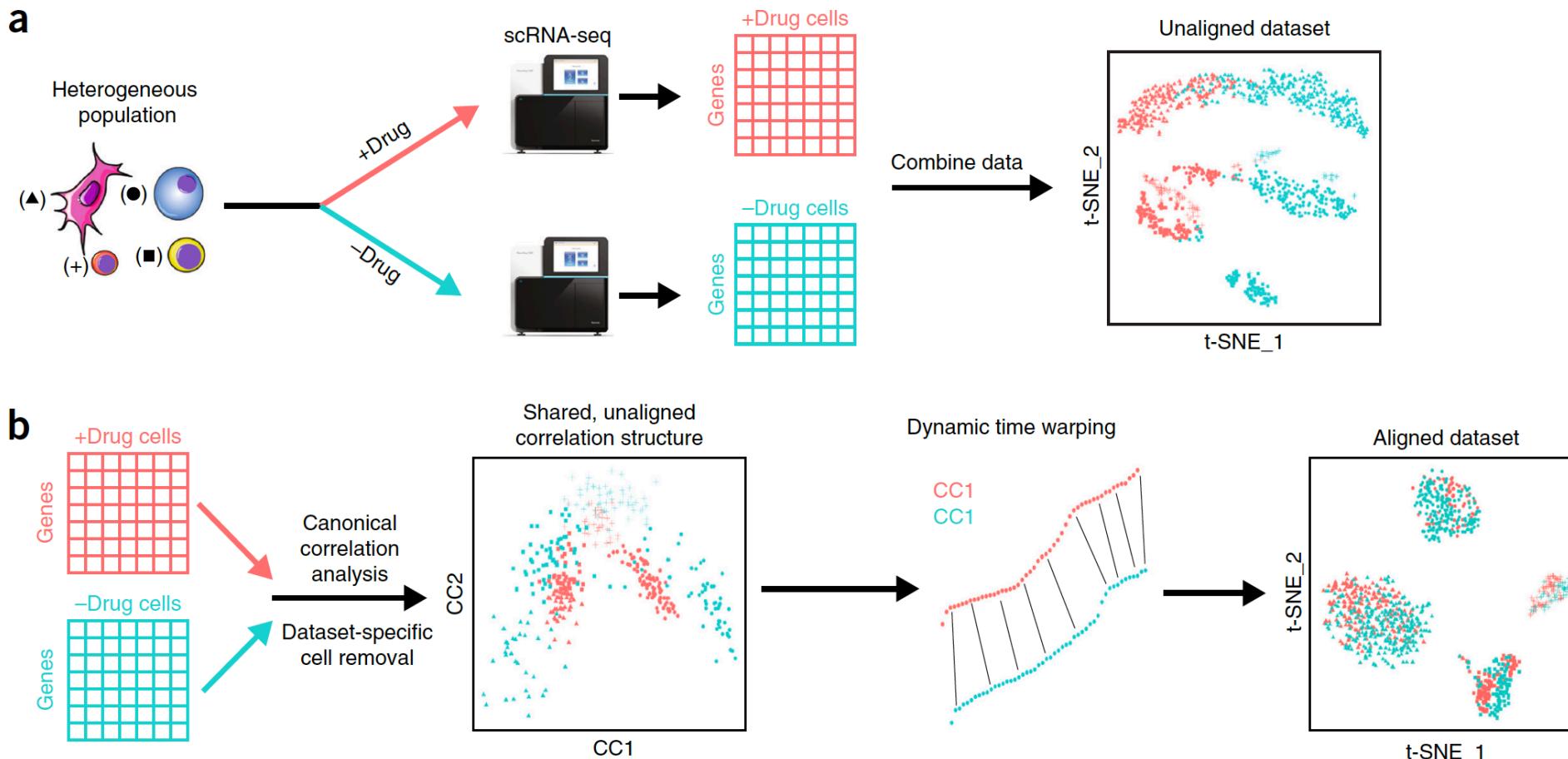
Canonical Correlation Analysis (CCA)

- CCA finds the linear combinations of variables across two datasets that are maximally correlated with one another.
 - The first pair of canonical variables maximizes the correlation across datasets.
 - The second pair of canonical variables maximizes the correlation subject to the constraint of not being correlated with the first pair, and so on.



- Goals of CCA
 - Similar to Principle Components Analysis (PCA)
 - Dimensional reduction: explain covariation between datasets with a small number of linear combinations of variables

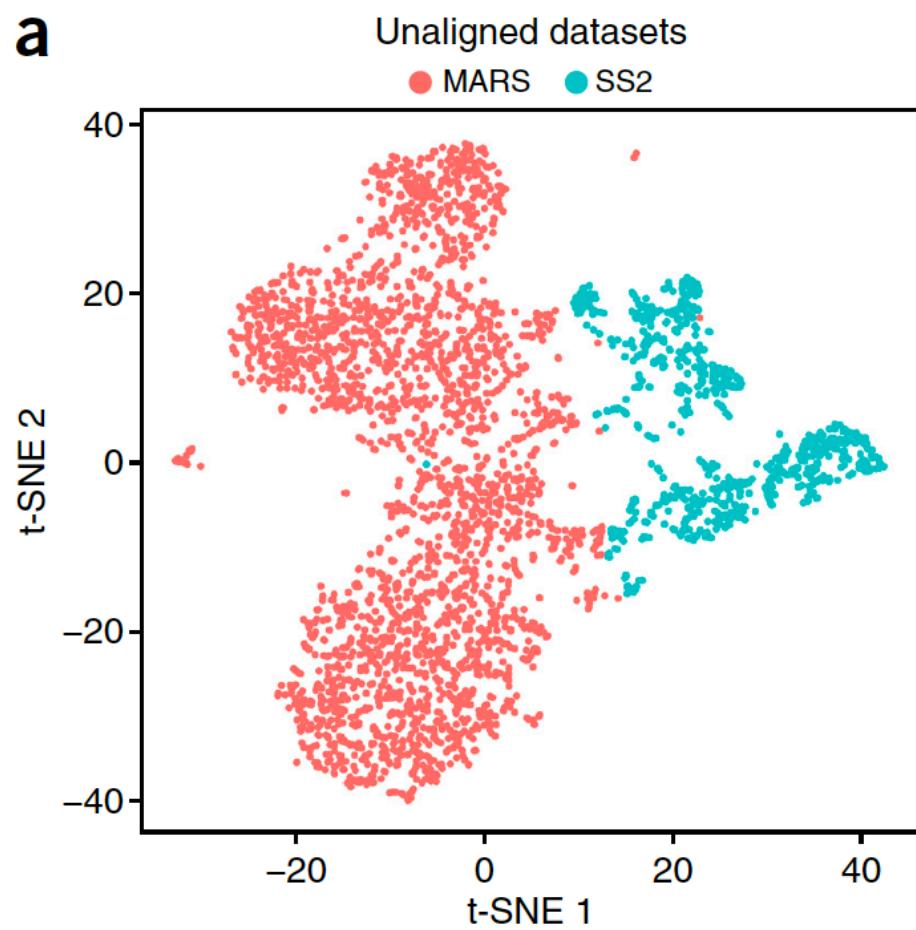
Canonical Correlation Analysis (CCA)



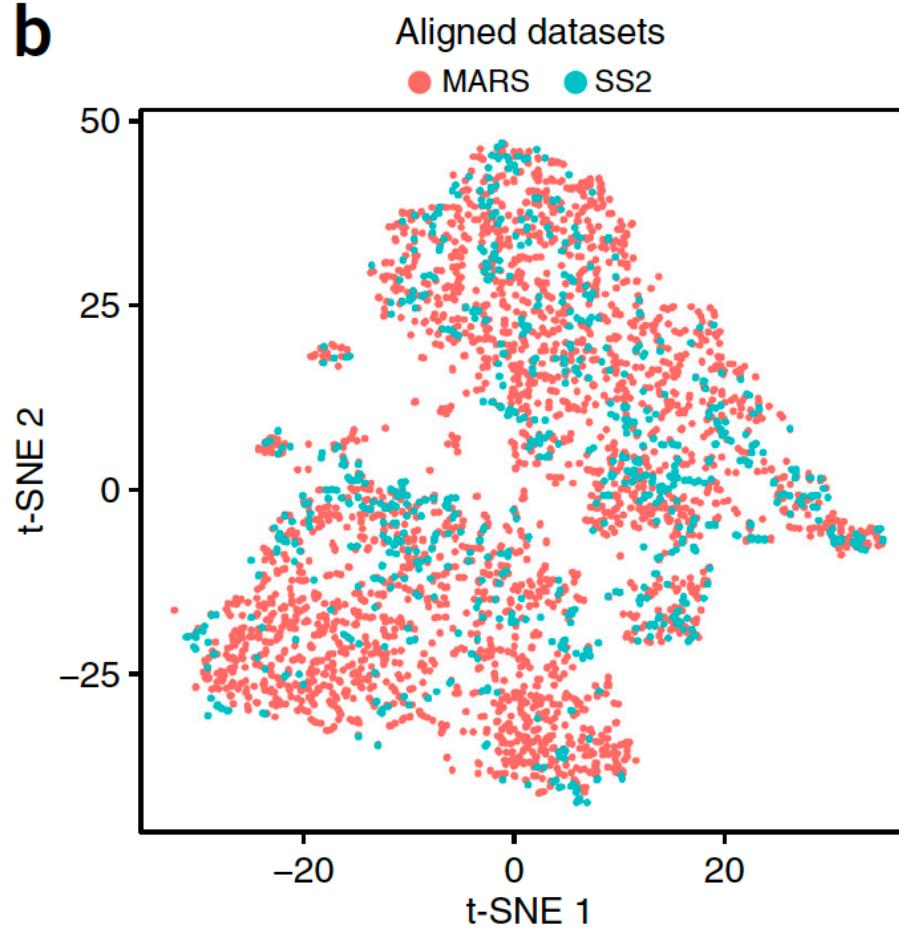
"Effectively, we treat the data sets as multiple measurements of a gene–gene covariance structure, and search for patterns that are common to the data sets."

Canonical Correlation Analysis (CCA)

a



b

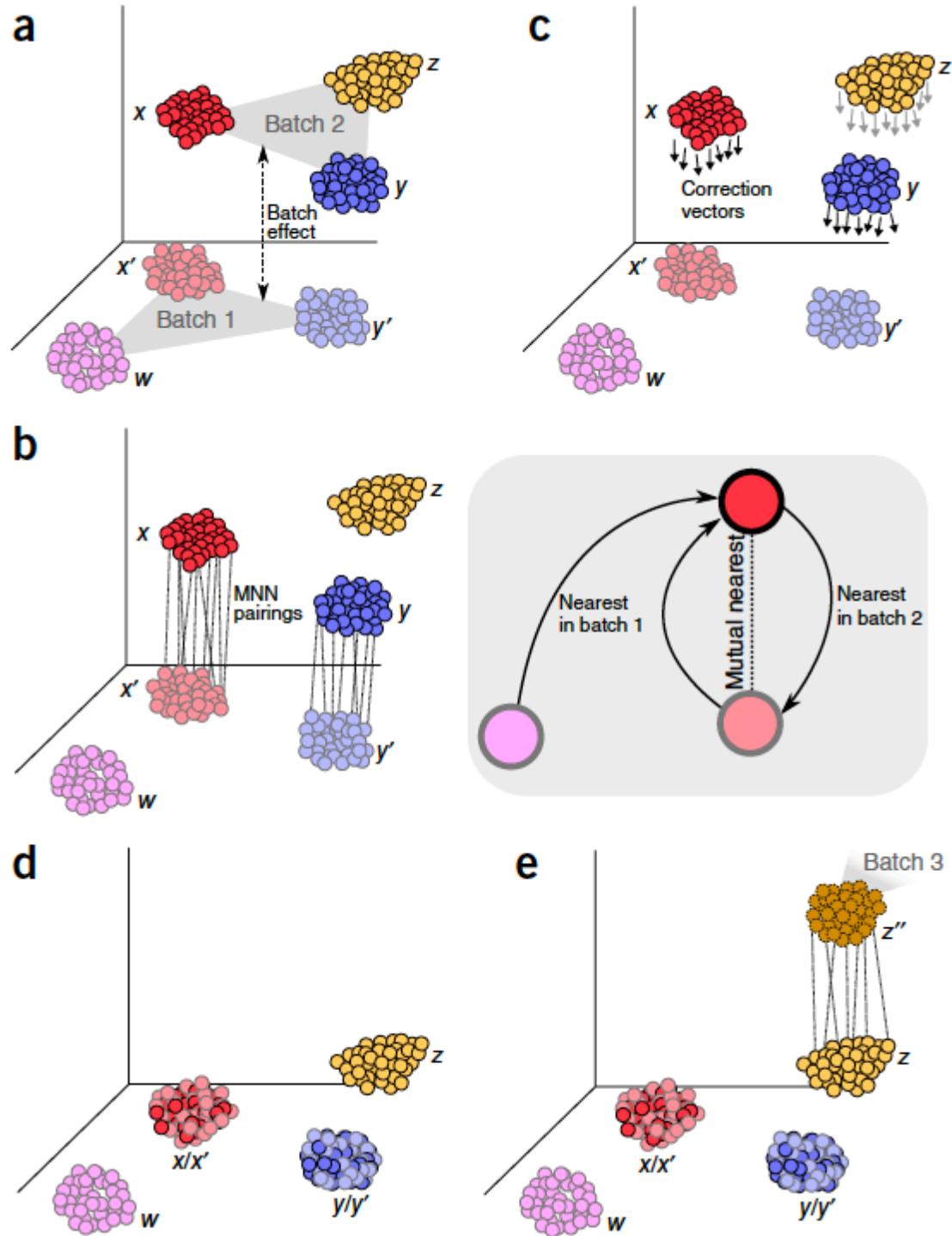


Assessing the performance of batch correction

"For every cell, we calculate how many of its k nearest-neighbors belong to the same data set and average this over all cells. If the data sets are well-aligned, we would expect that each cells' nearest neighbors would be evenly shared across all data sets."

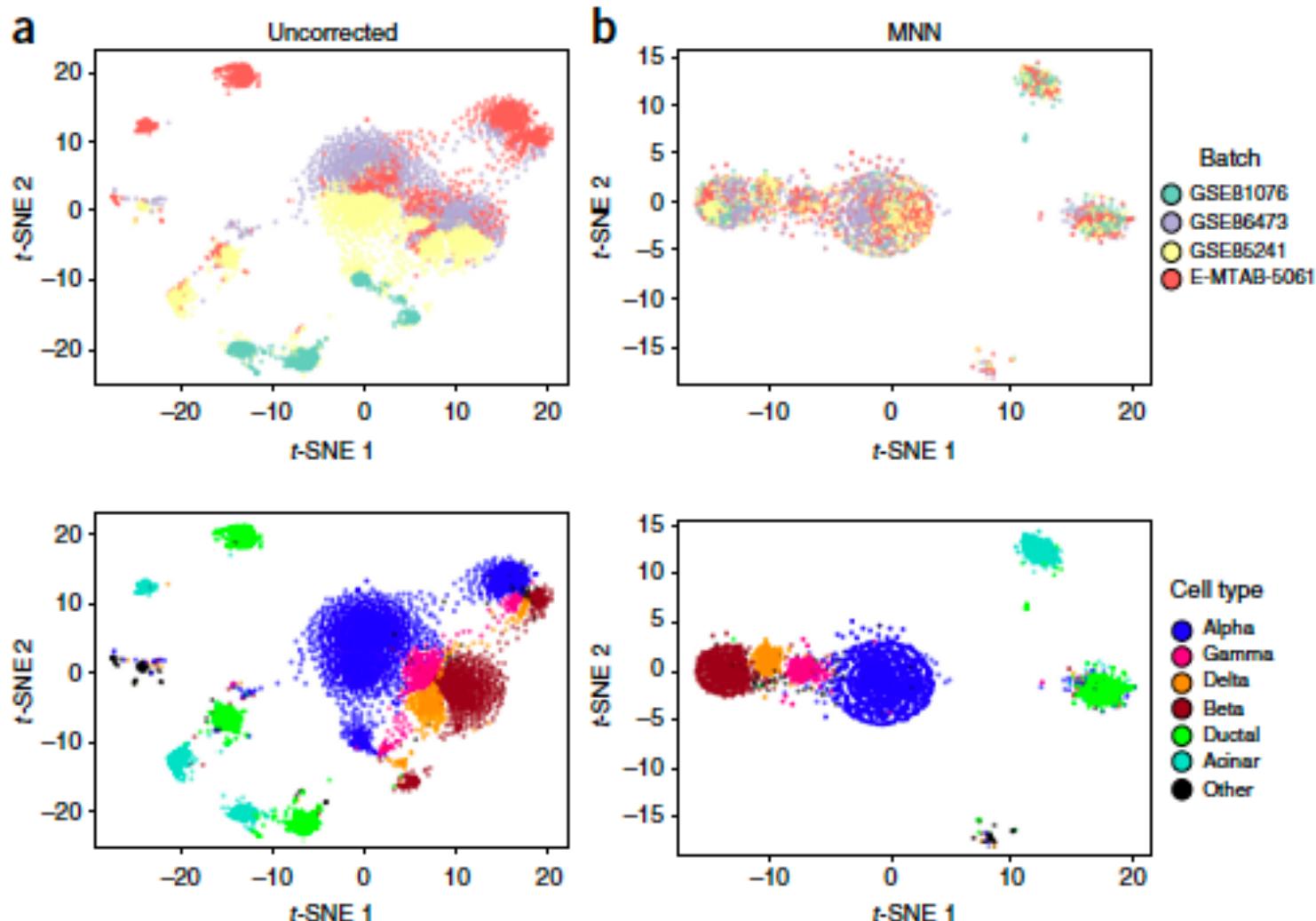
Mutual Nearest Neighbors

"If a pair of cells from each batch is contained in each other's set of nearest neighbors, those cells are considered to be mutual nearest neighbors. We interpret these pairs as containing cells that belong to the same cell type or state despite being generated in different batches. Thus, any systematic differences in expression level between cells in MNN pairs should represent the batch effect."

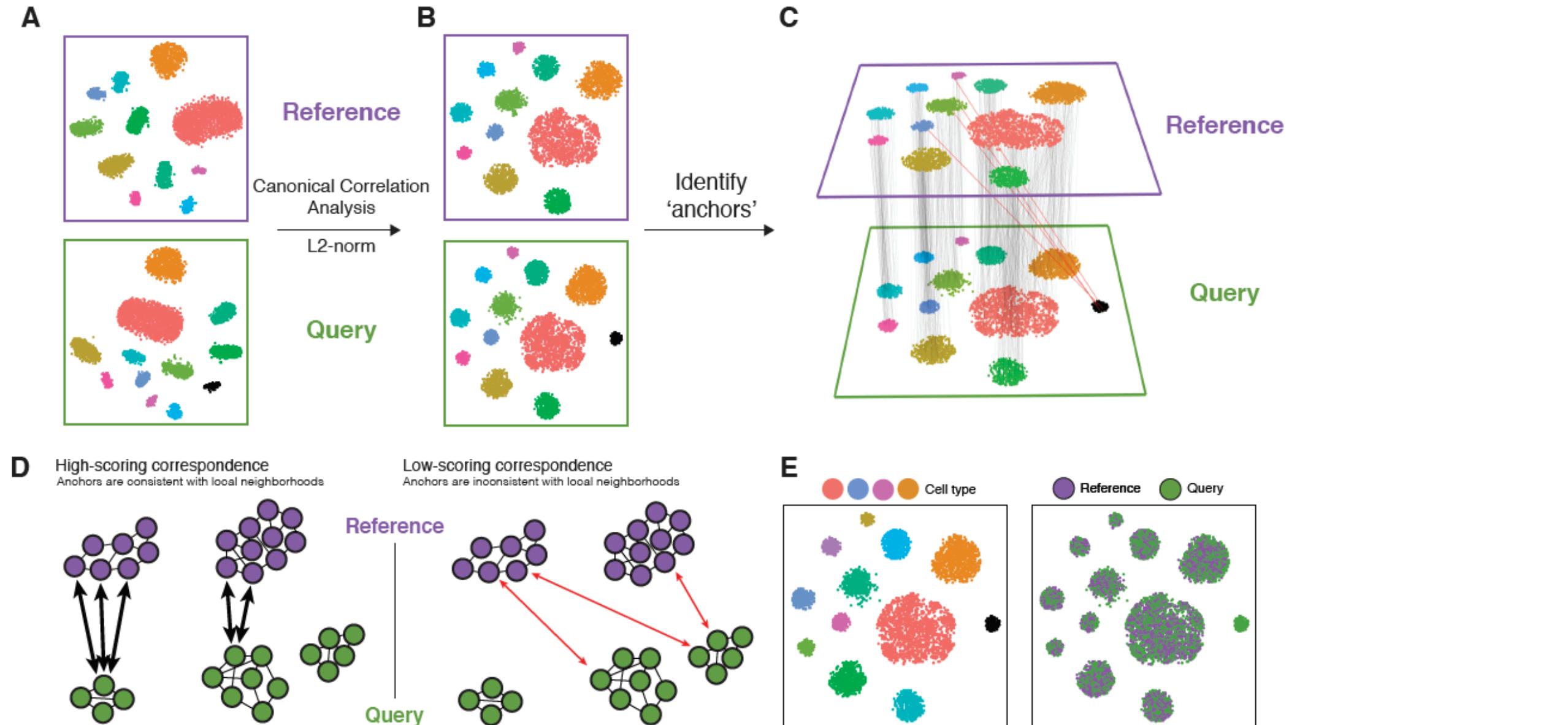


Mutual Nearest Neighbors

4 pancreas datasets



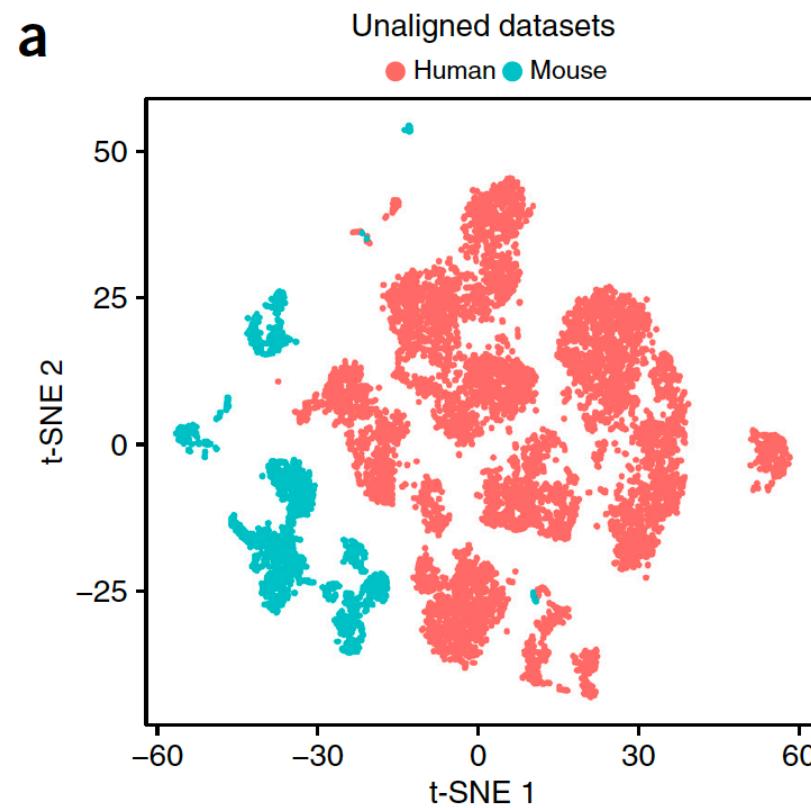
Combining CCA and Mutual Nearest Neighbors (Seurat v3)



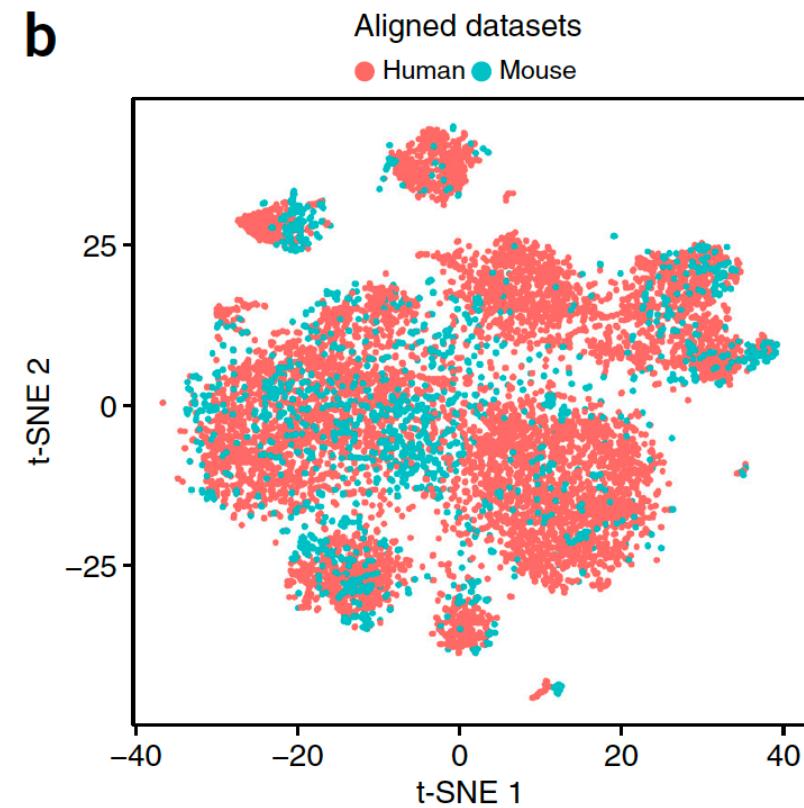
Combining CCA and Mutual Nearest Neighbors (Seurat v3)

Human and mouse pancreas datasets

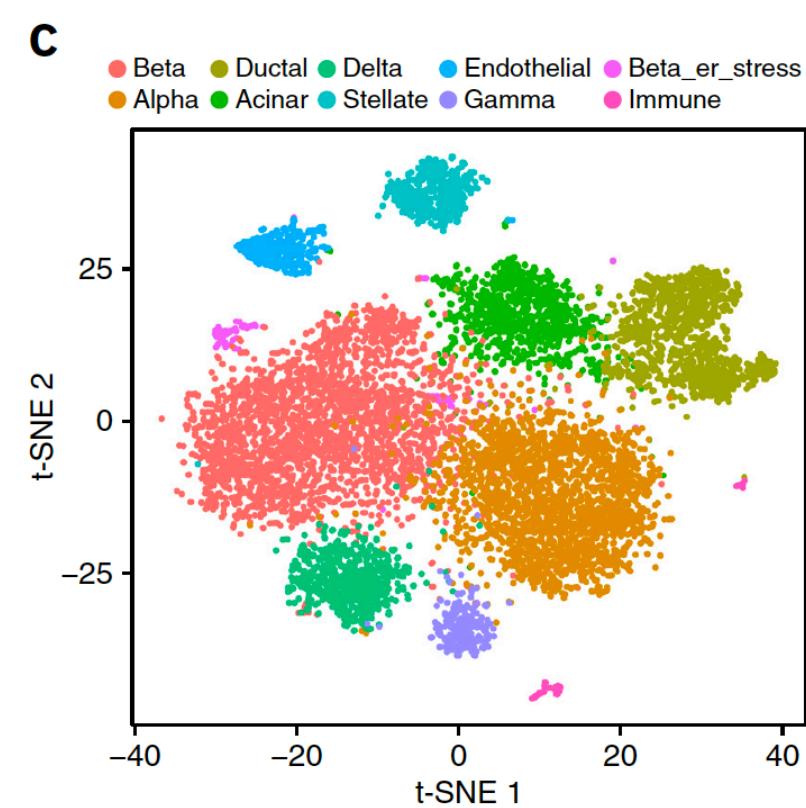
a



b



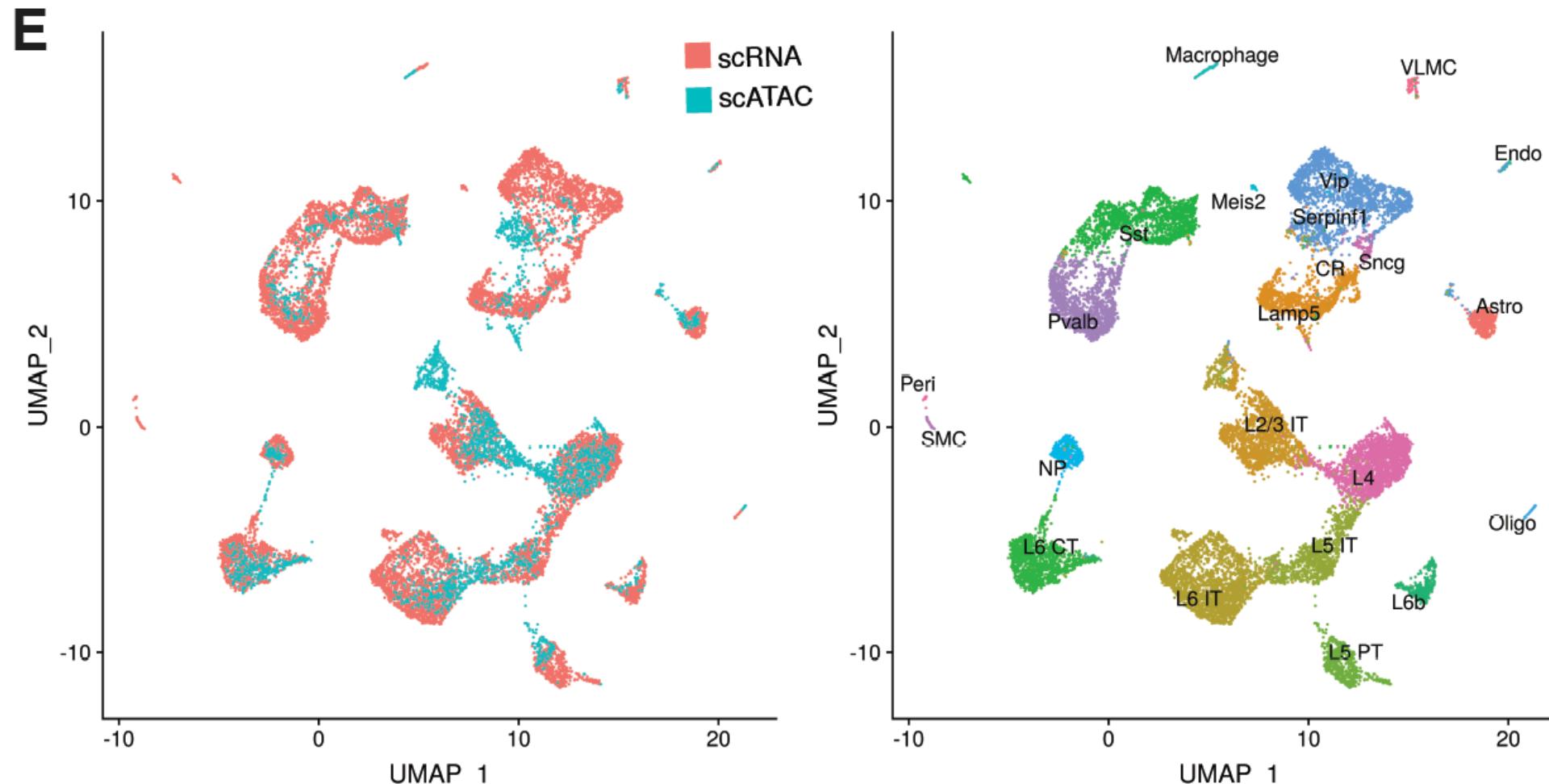
c



Classifying nuclei from a single cell ATAC-seq experiment using single cell RNA-seq data as a reference

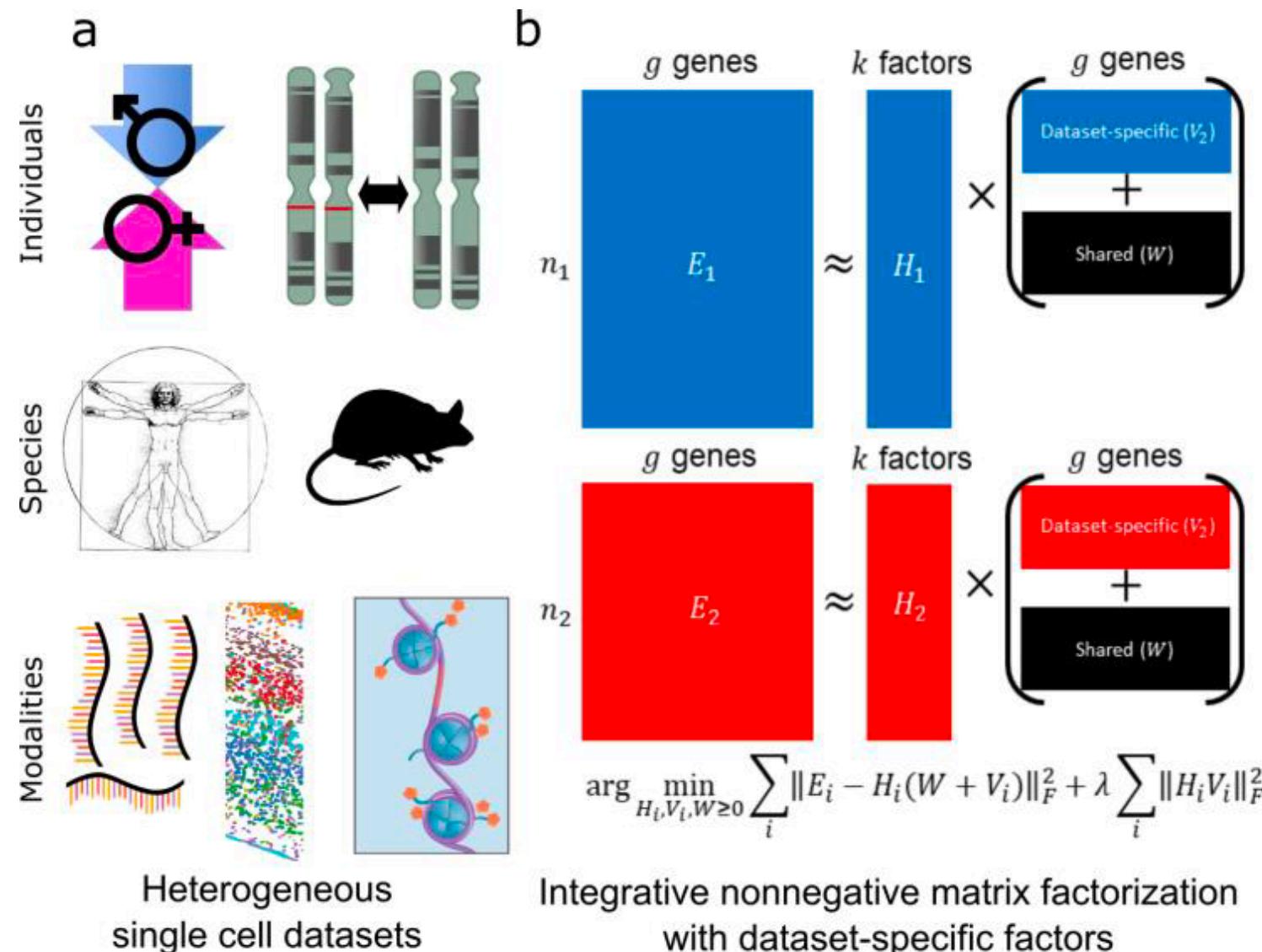
Integrating data modalities

14,249 cells from scRNA-seq and 2,548 cells from scATAC-seq



Batch correction and data modality integration using LIGER

LIGER implements
non-negative
matrix factorization



Batch correction and data modality integration using LIGER

LIGER implements
non-negative
matrix factorization

b

$$\begin{array}{ccc} g \text{ genes} & k \text{ factors} & \\ n_1 & \approx & H_1 \\ E_1 & & \end{array}$$
$$\times$$

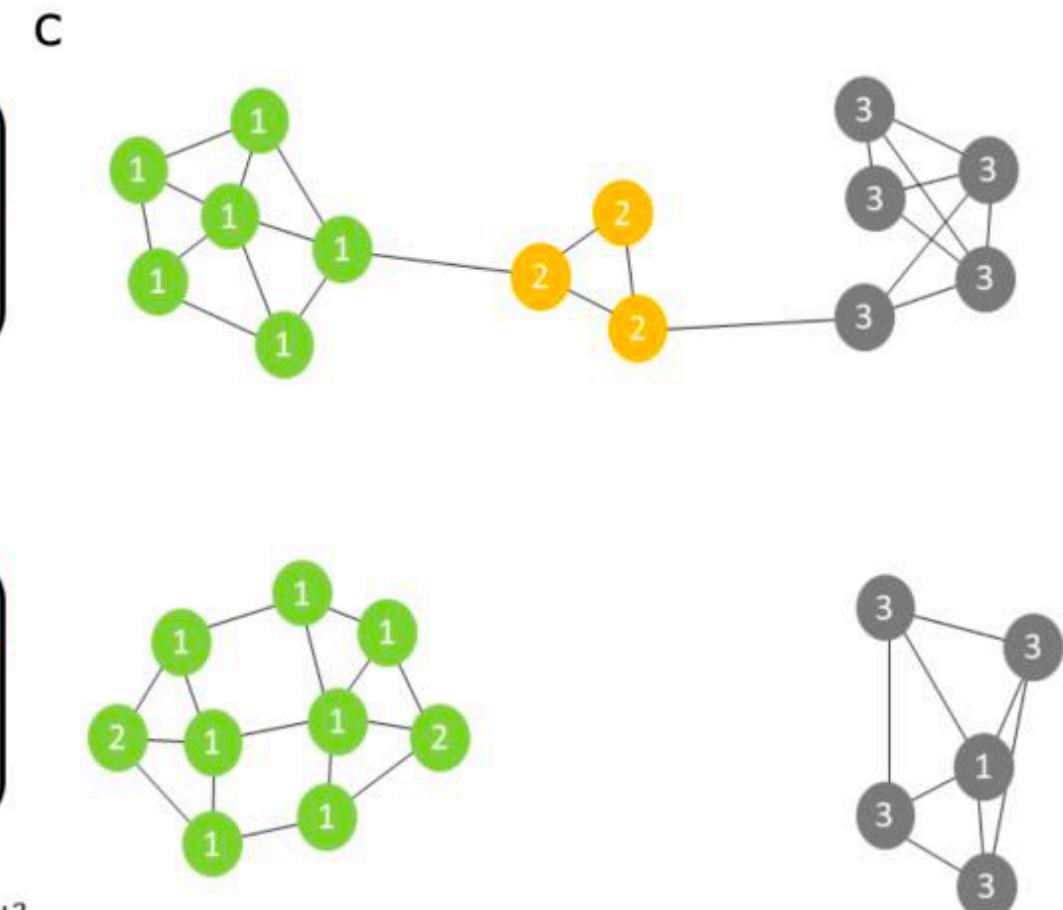
$\begin{array}{c} g \text{ genes} \\ \text{Dataset-specific } (V_2) \\ + \\ \text{Shared } (W) \end{array}$

$$\begin{array}{ccc} g \text{ genes} & k \text{ factors} & \\ n_2 & \approx & H_2 \\ E_2 & & \end{array}$$
$$\times$$

$\begin{array}{c} g \text{ genes} \\ \text{Dataset-specific } (V_2) \\ + \\ \text{Shared } (W) \end{array}$

$$\arg \min_{H_i, V_i, W \geq 0} \sum_i \|E_i - H_i(W + V_i)\|_F^2 + \lambda \sum_i \|H_i V_i\|_F^2$$

Integrative nonnegative matrix factorization
with dataset-specific factors

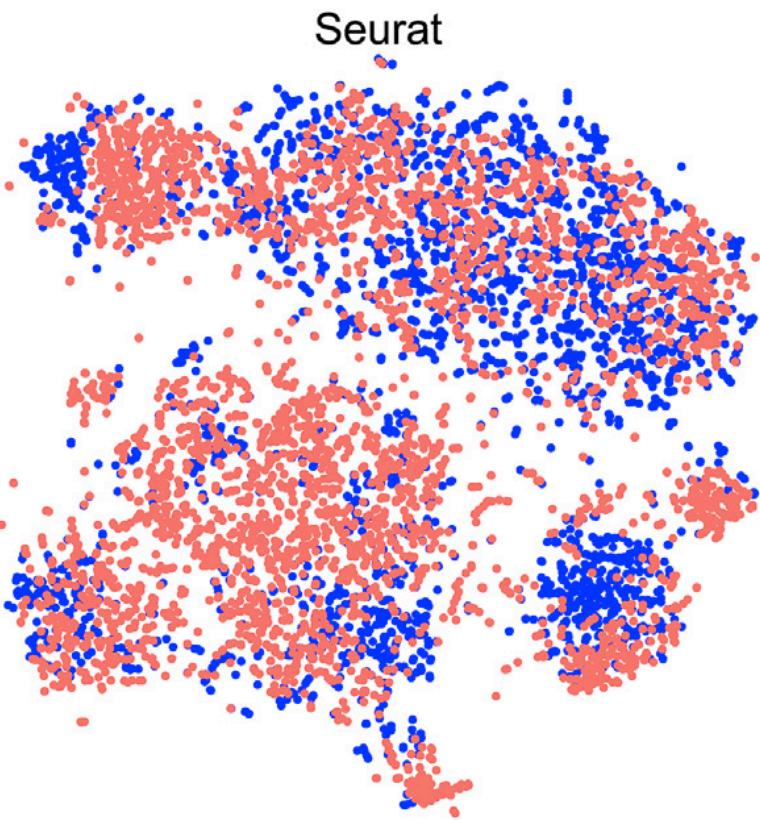


Joint clustering using
shared factor neighborhood graph

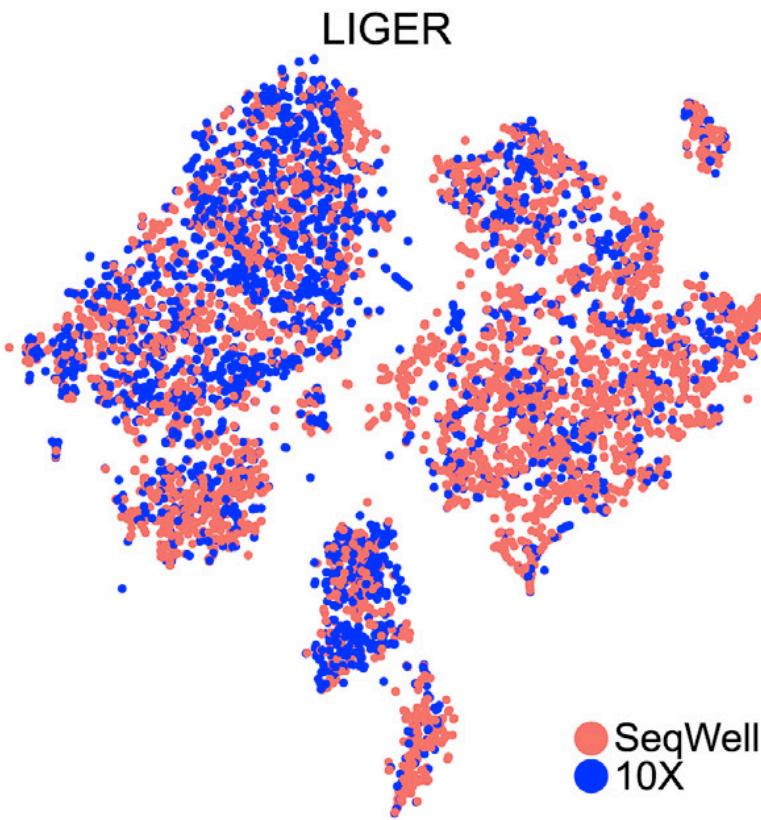
Integrating blood cell datasets using LIGER

Higher alignment score =
better data integration

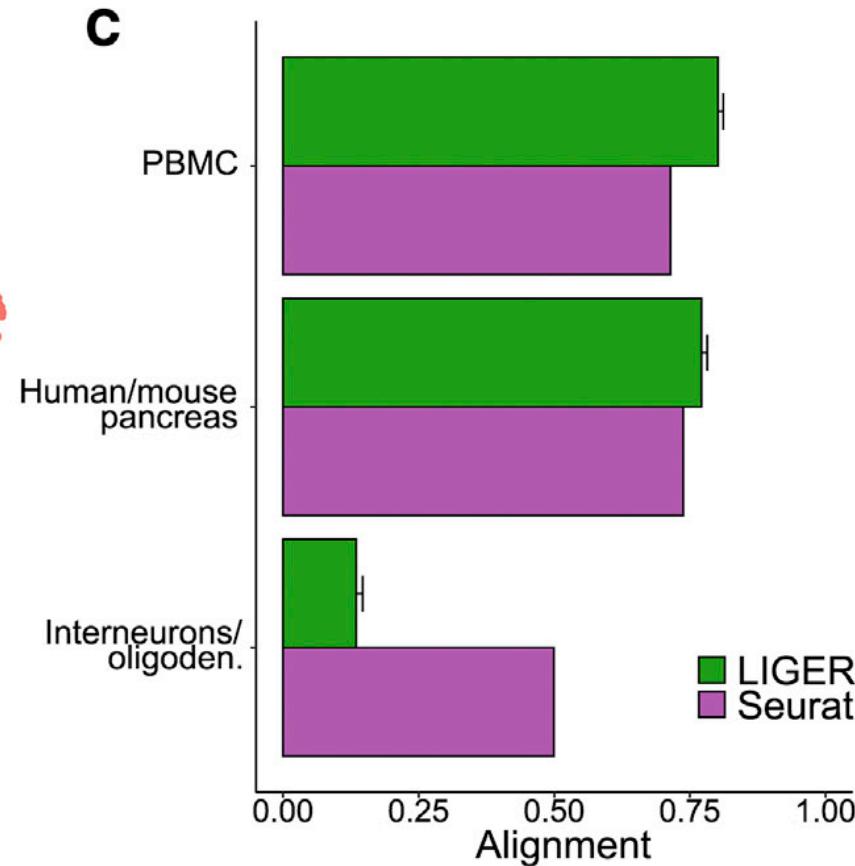
A



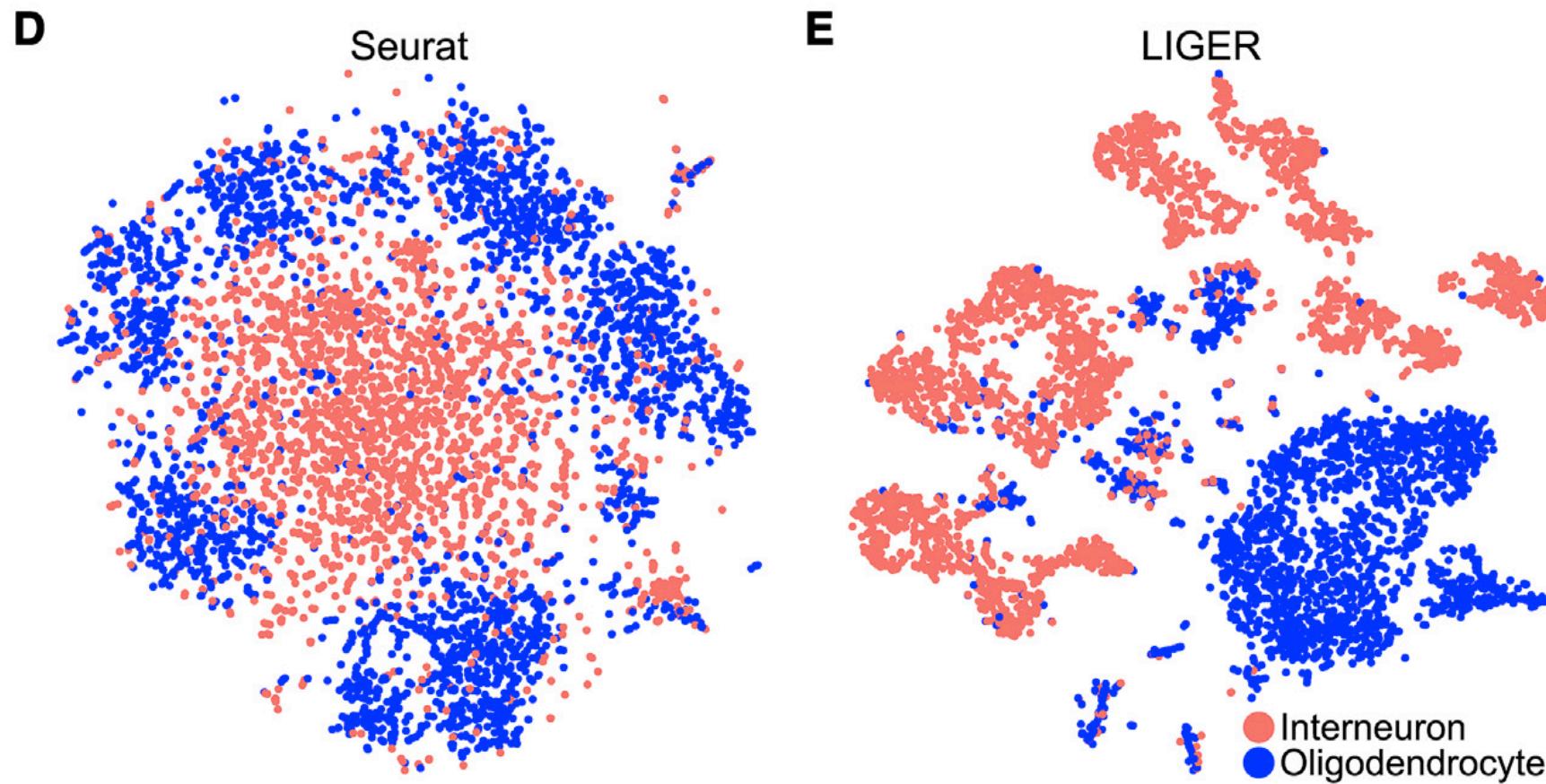
B



C

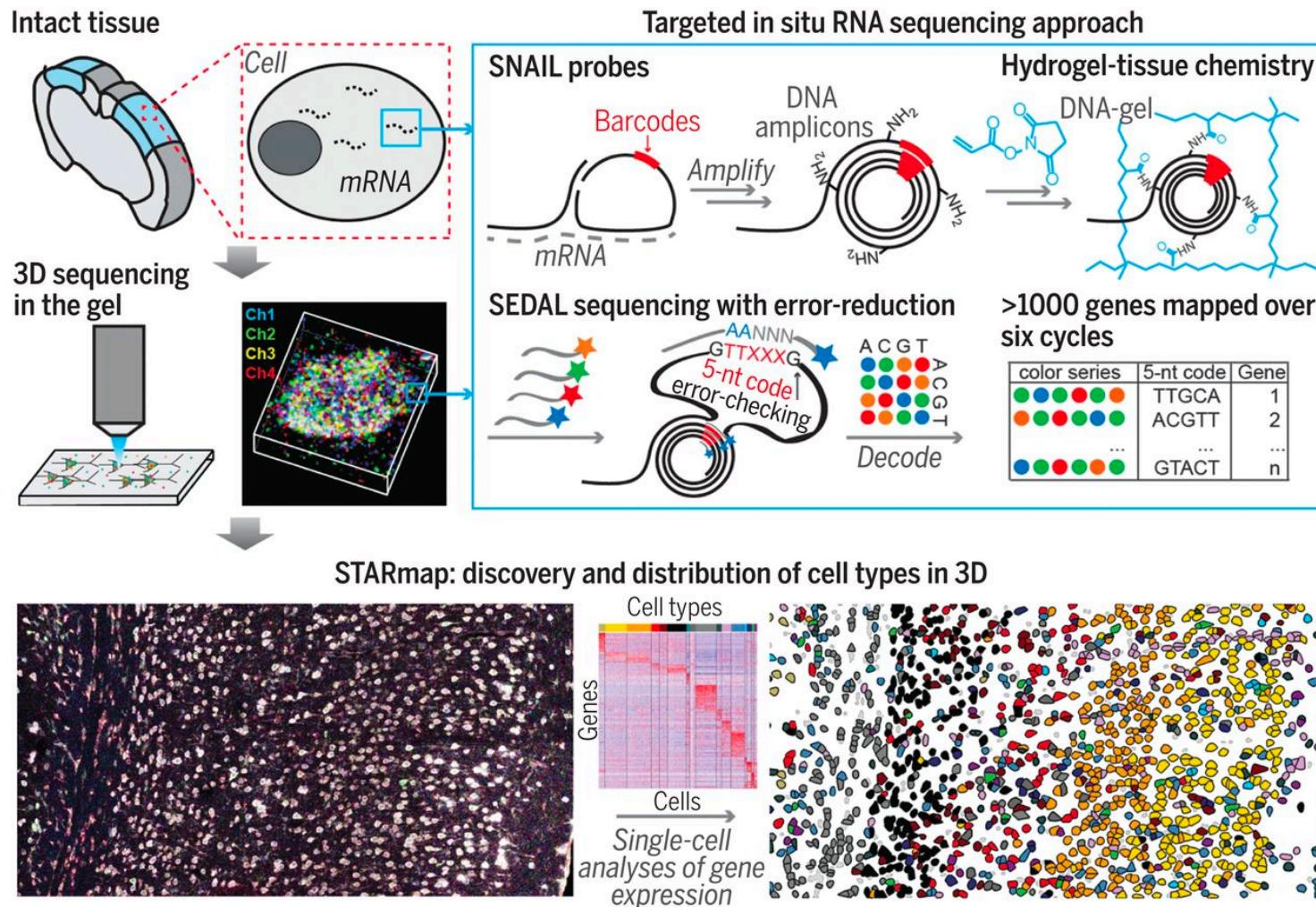


Integrating blood cell datasets using LIGER

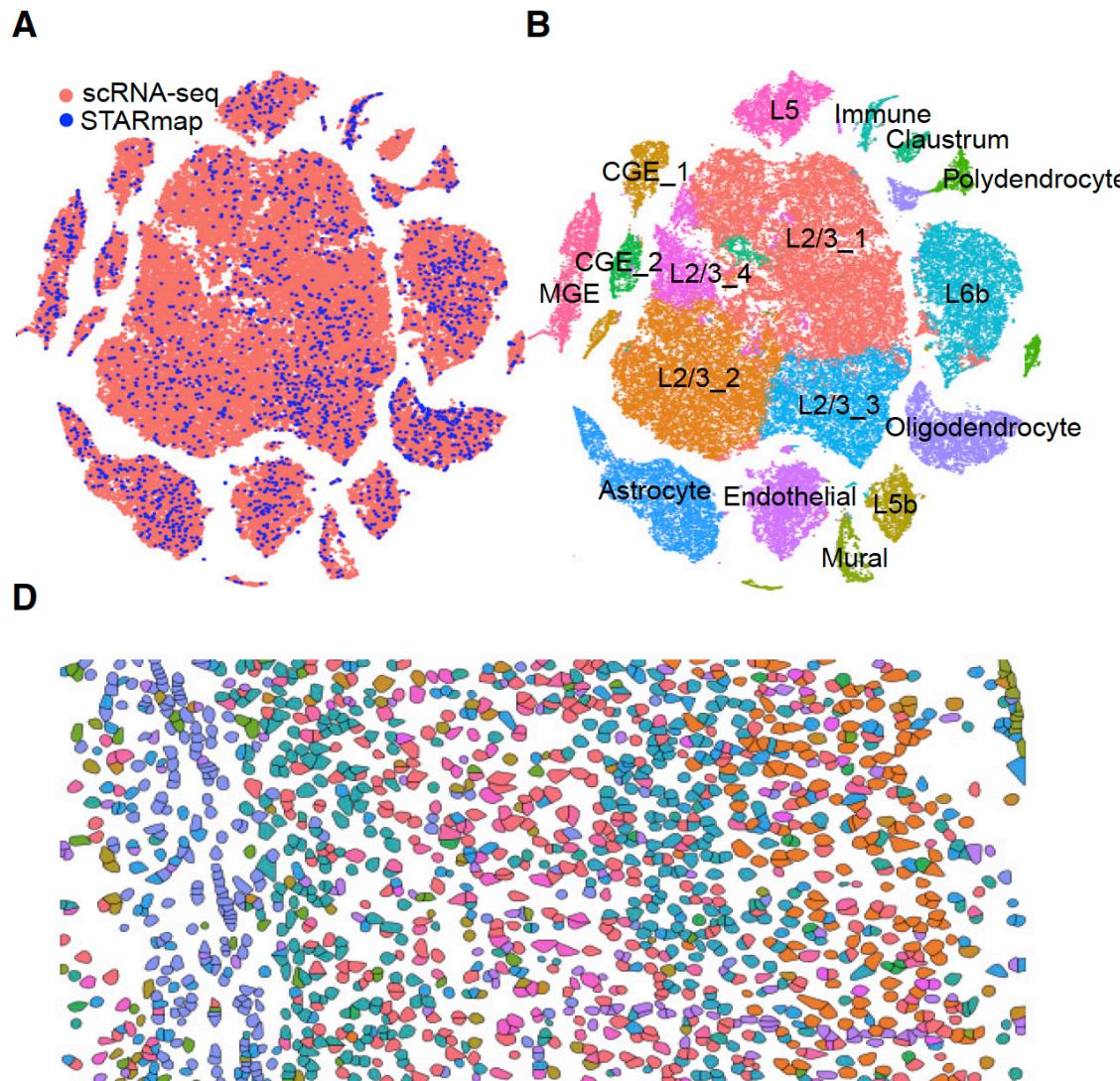


Ideally, divergent cell types should not cluster together after batch correction.

In situ spatial transcriptomic data in mouse frontal cortex STARmap



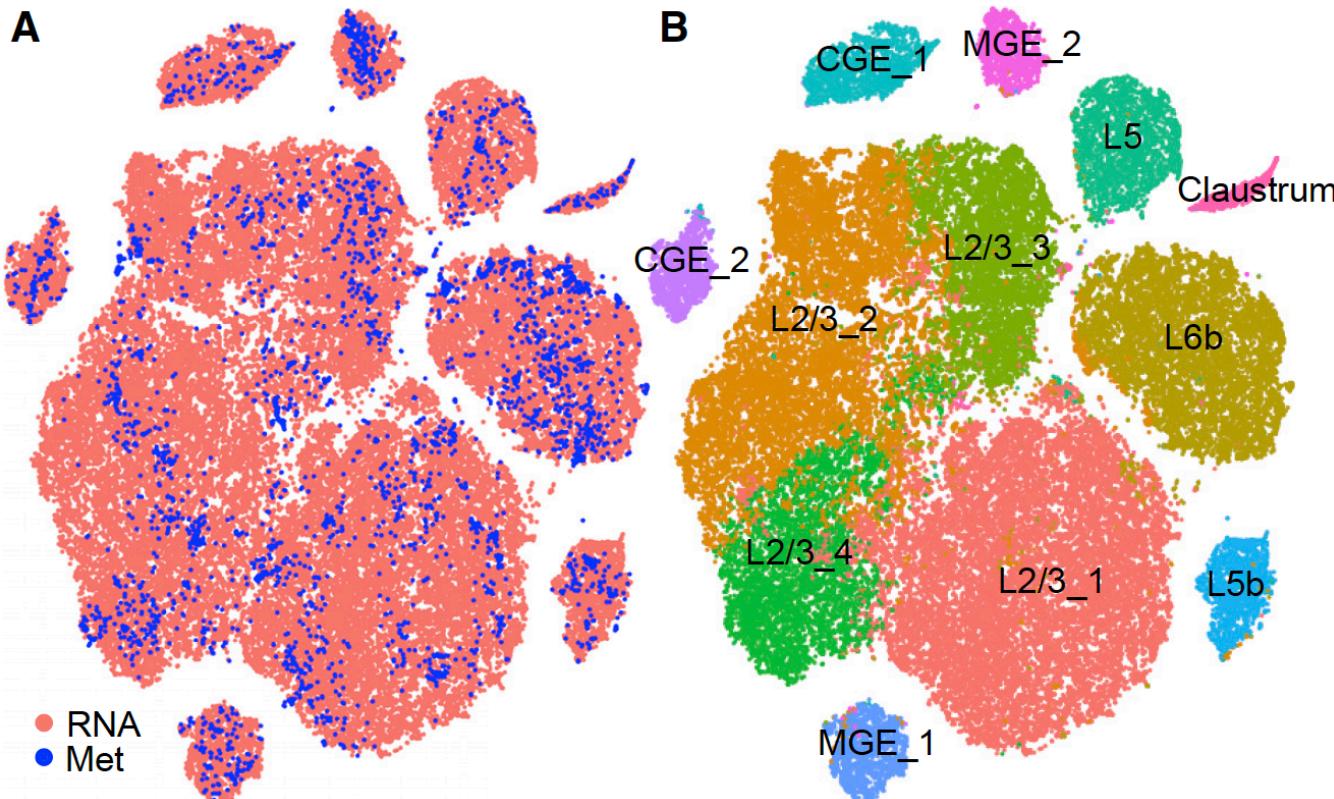
Using LIGER to integrate single-cell transcriptomic and *in situ* spatial transcriptomic data



71,000 cells from scRNA-seq
2,500 cells from STARmap

What are advantages of integrated analysis of these 2 datasets?

Using LIGER to integrate single-cell transcriptomic and single-cell DNA methylation data

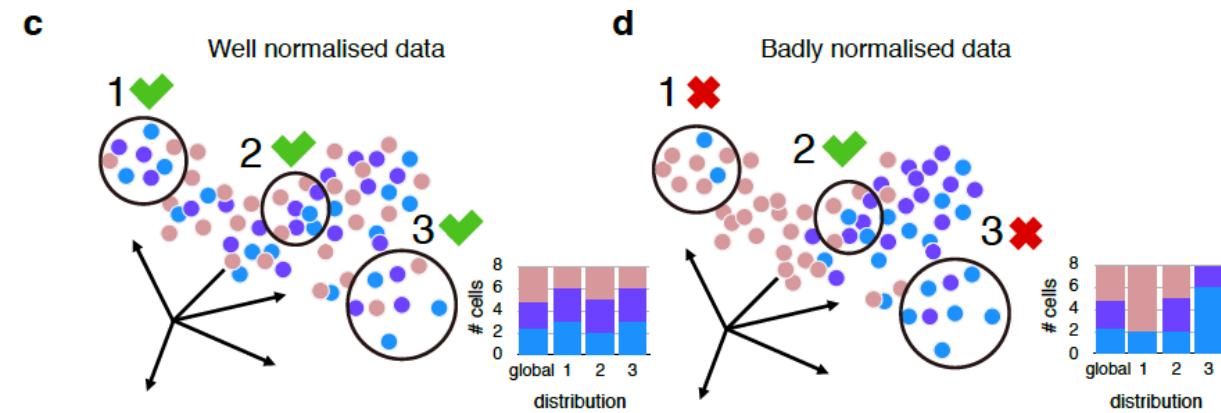


56,000 cells from scRNA-seq
3,000 cells from DNA methylation

"We reasoned that, because gene body methylation is generally anticorrelated with gene expression, reversing the direction of the methylation signal would allow joint analysis."

Methods to assess performance of batch correction

- Entropy of batch mixing
- kBET - k-nearest neighbor batch effect test



- Silhouette coefficient
 - cells of the same cell type are close together and far from other cells of a different type
- Adjusted rand index
 - do batch labels and cluster labels agree with one another?
- Biological significance

Common assumptions during batch correction

- At least one cell population is found shared in both datasets
- The batch effect and the biological differences do not overlap with one another (ie orthogonal)
- The magnitude and variation of the biological effect you care about is greater than that of the batch effect