

From single-cell RNA-seq to spatial resolution

Bulk transcriptomics



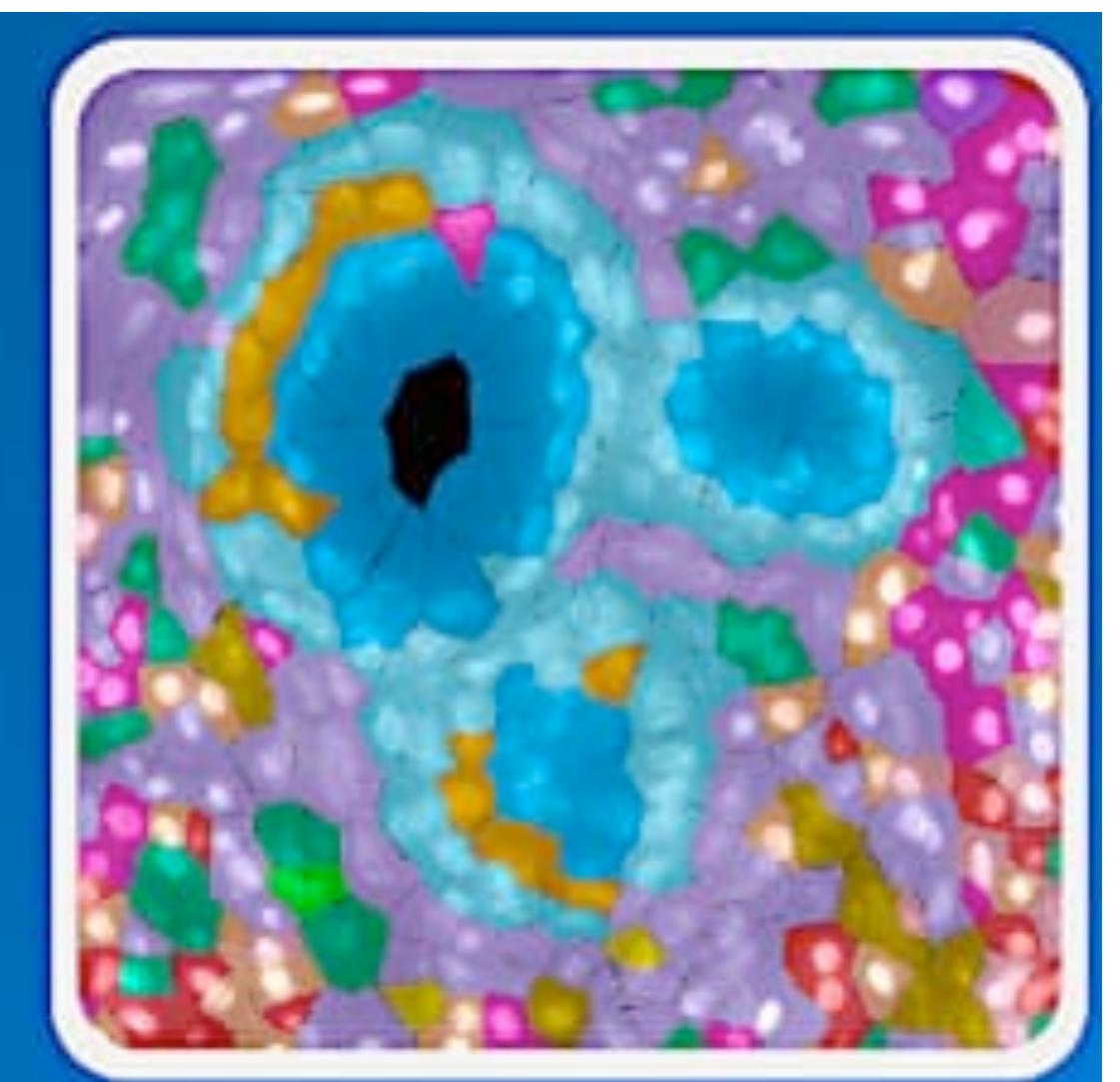
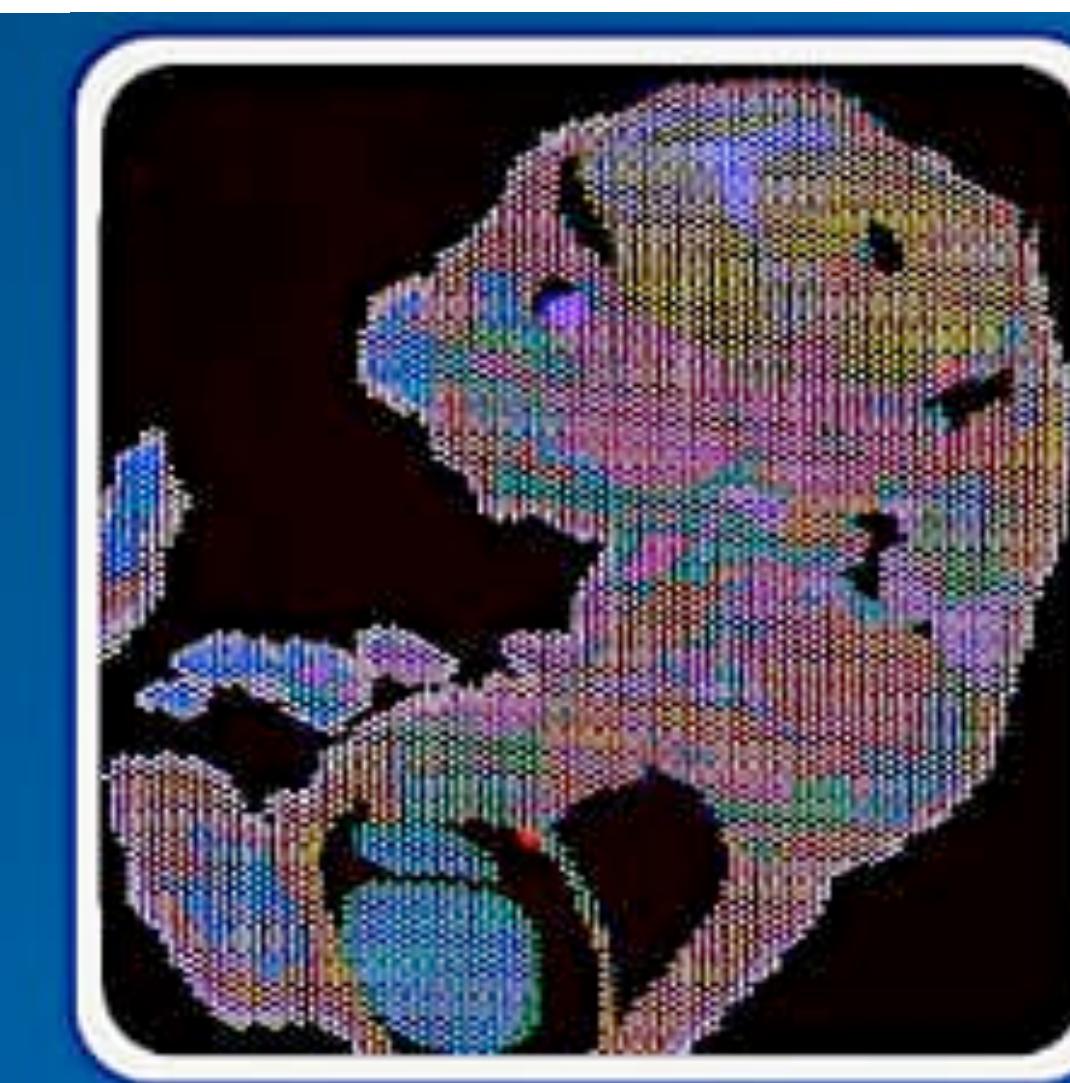
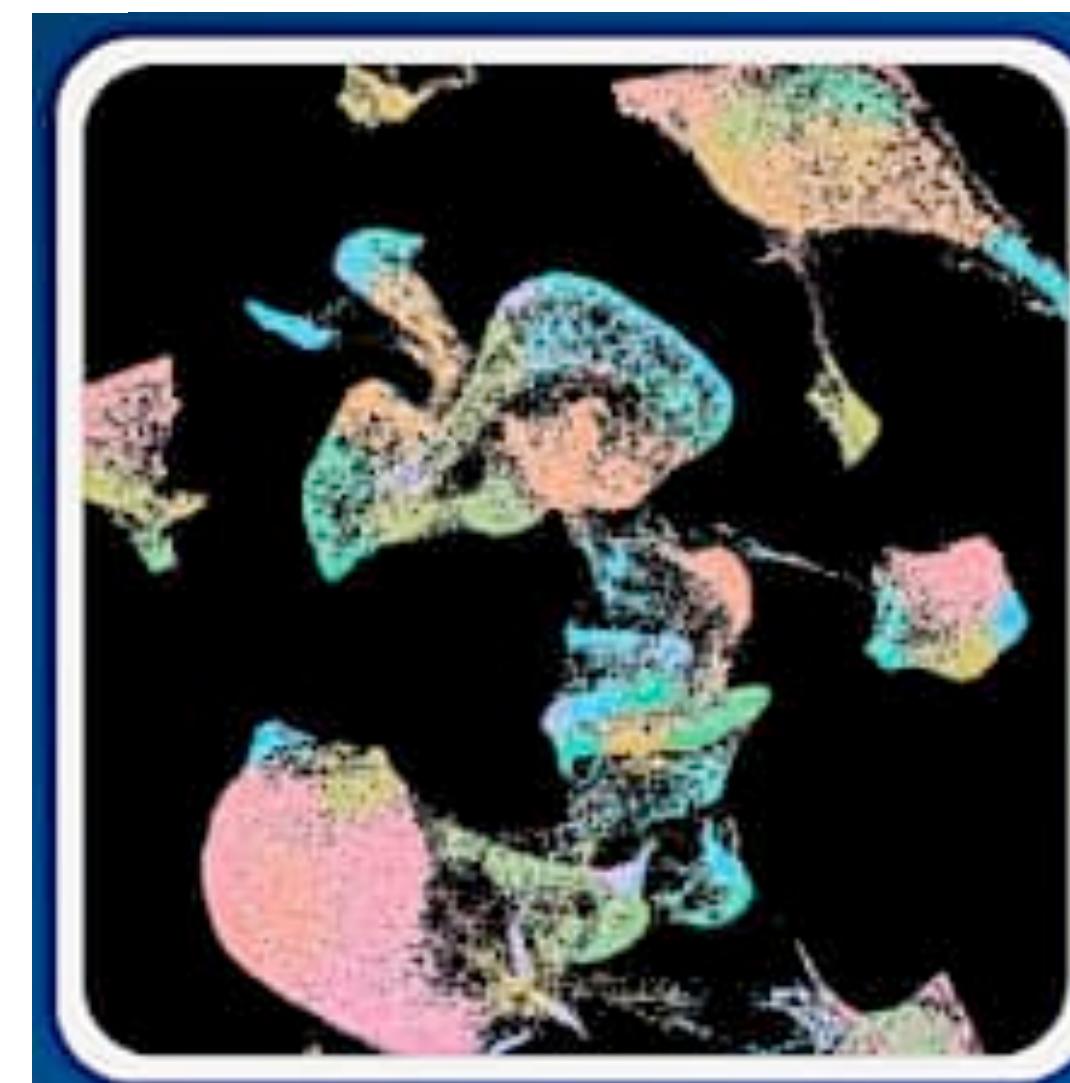
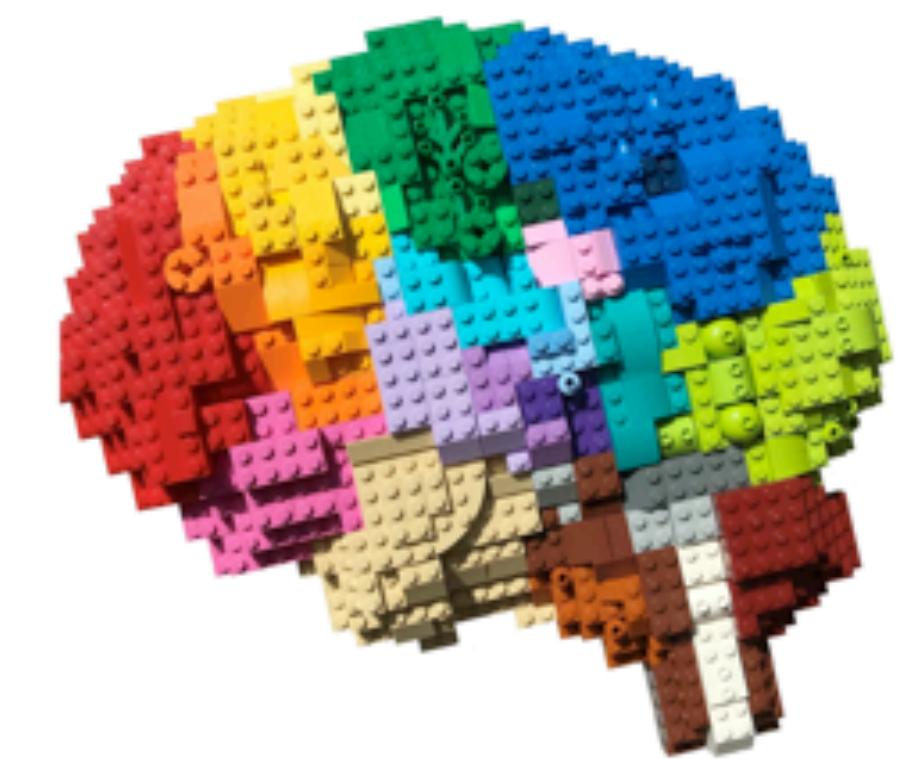
Single-cell transcriptomics



Spatial transcriptomics



Spatial single-cell transcriptomics



Overview

Introduction: Why Spatial resolution?

Part 3: Spatial transcriptomics

- Visium Technology
- Pipeline for Spatial transcriptomics
- Hands-on analysis

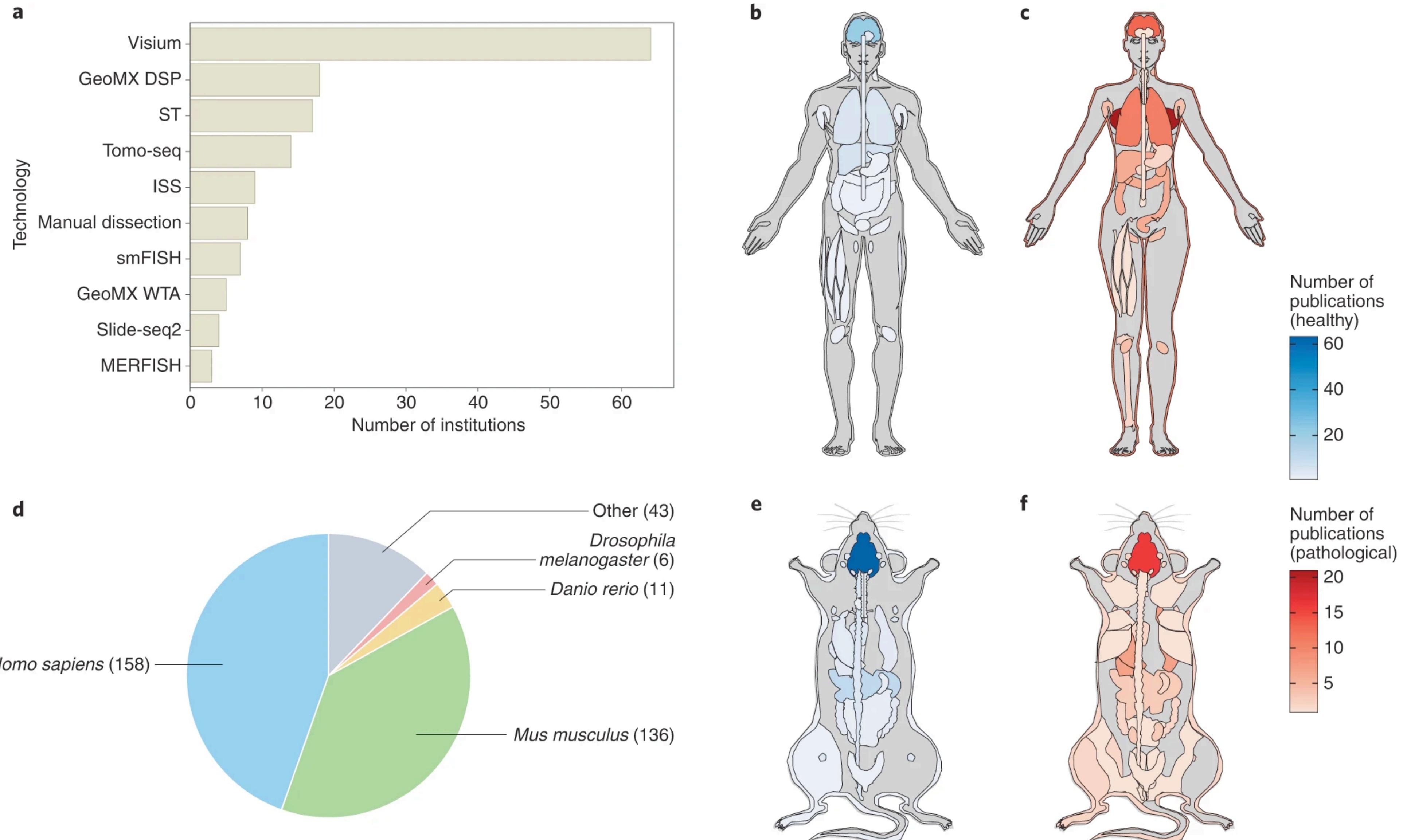
Part 4: Single-cell Spatial transcriptomics

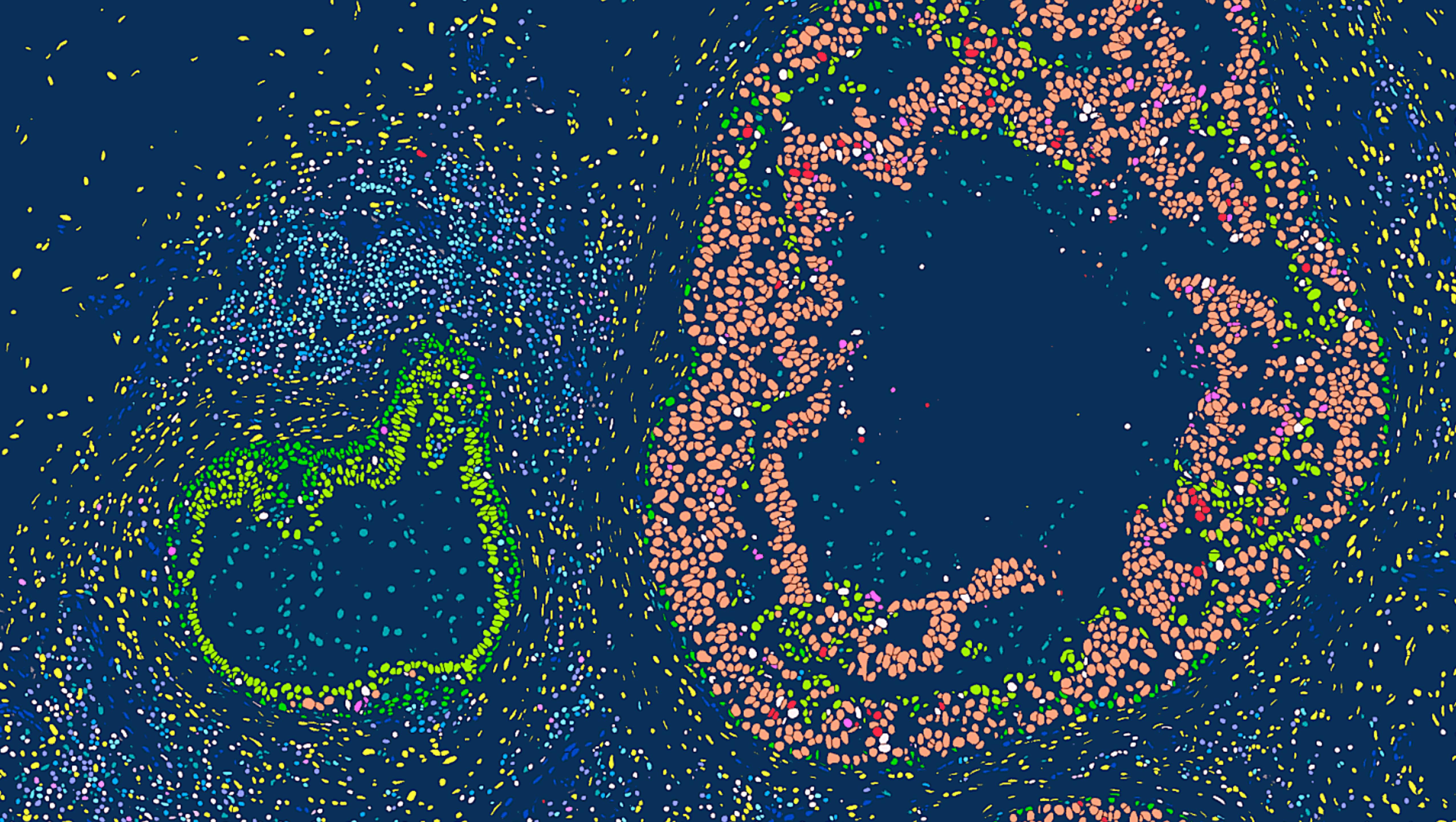
- Different technologies
- Pipeline for Single-cell Spatial transcriptomics
- Hands-on analysis

Optional:

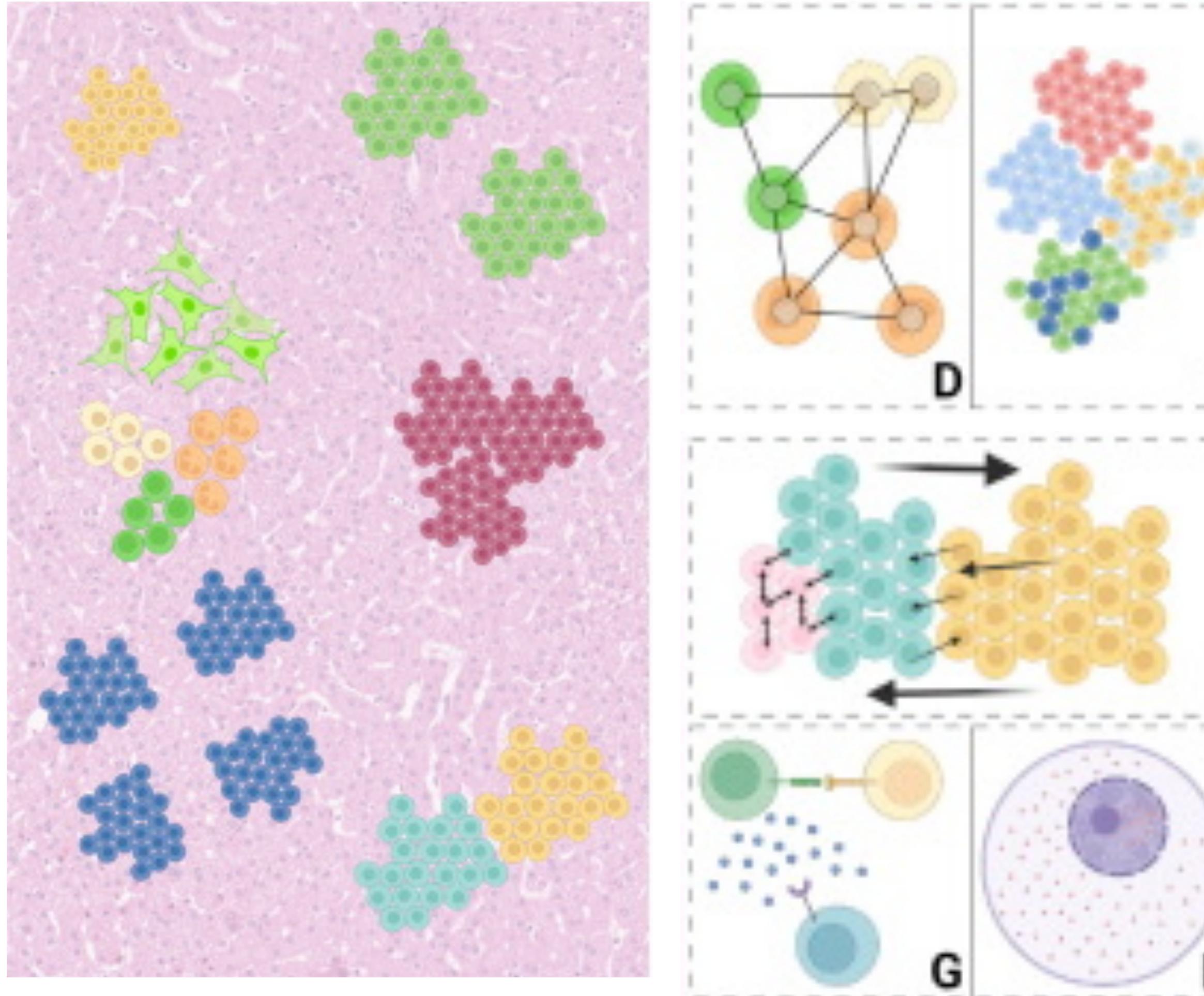
- Team-work

Introduction - Spatial





Introduction - Computational analysis spatial transcriptomics



a Cell-cell interactions

- 1: Sender cell produces ligand



- 2: Receiver cell binds to ligand



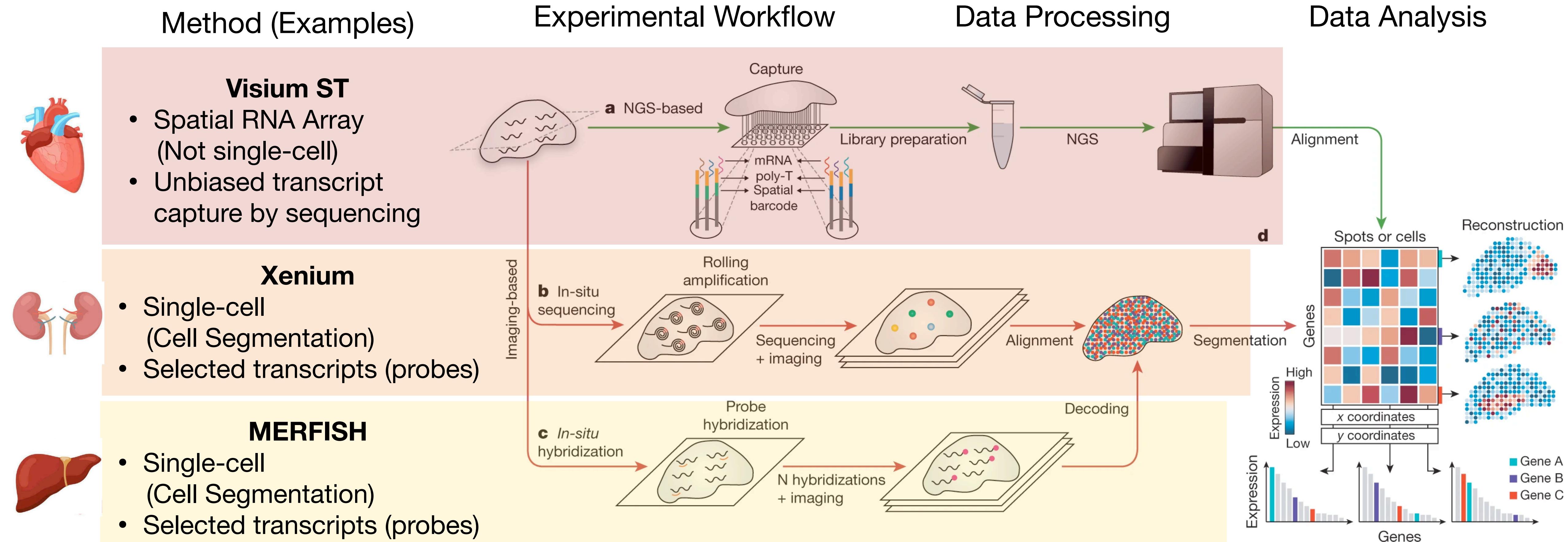
Interaction With Without



- 4: Altered Gene Expression

Walker *et al.* (2022): Deciphering tissue structure and function using spatial transcriptomics. *Commun Biologie*.
<https://doi.org/10.1038/s42003-022-03175-5>

Spatial Transcriptomics technologies - Overview



Tissue that will be analyzed in the hands-on for each spatial method

Rao *et al.* (2021): Exploring tissue architecture using spatial transcriptomics. *Nature*. <https://doi.org/10.1038/s41586-021-03634-9>

Part 3

Introduction: Why Spatial resolution?

Part 3: Spatial transcriptomics

- Visium Technology
- Pipeline for Spatial transcriptomics
- Hands-on analysis

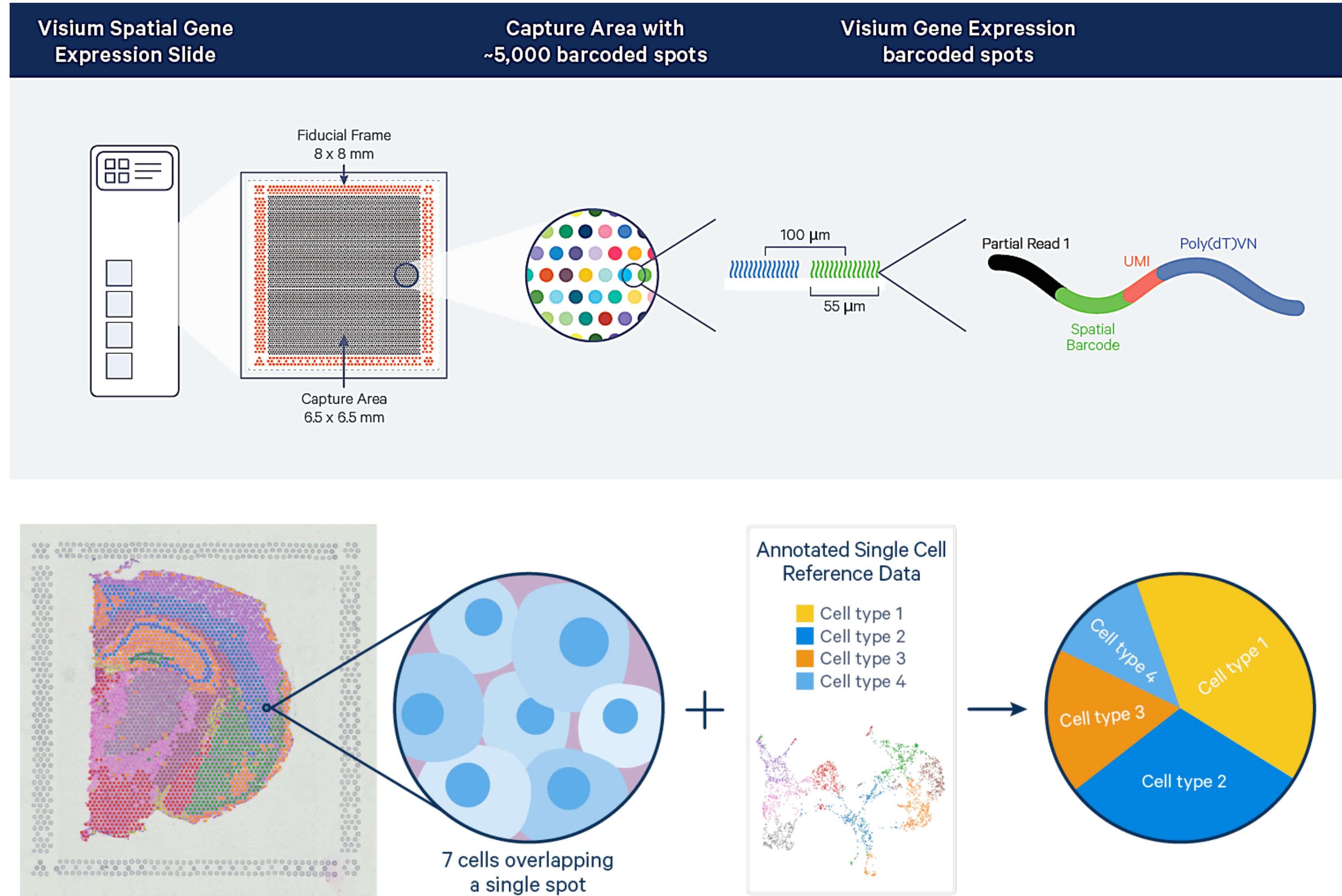
Part 4: Single-cell Spatial transcriptomics

- Different technologies
- Pipeline for Single-cell Spatial transcriptomics
- Hands-on analysis

Optional:

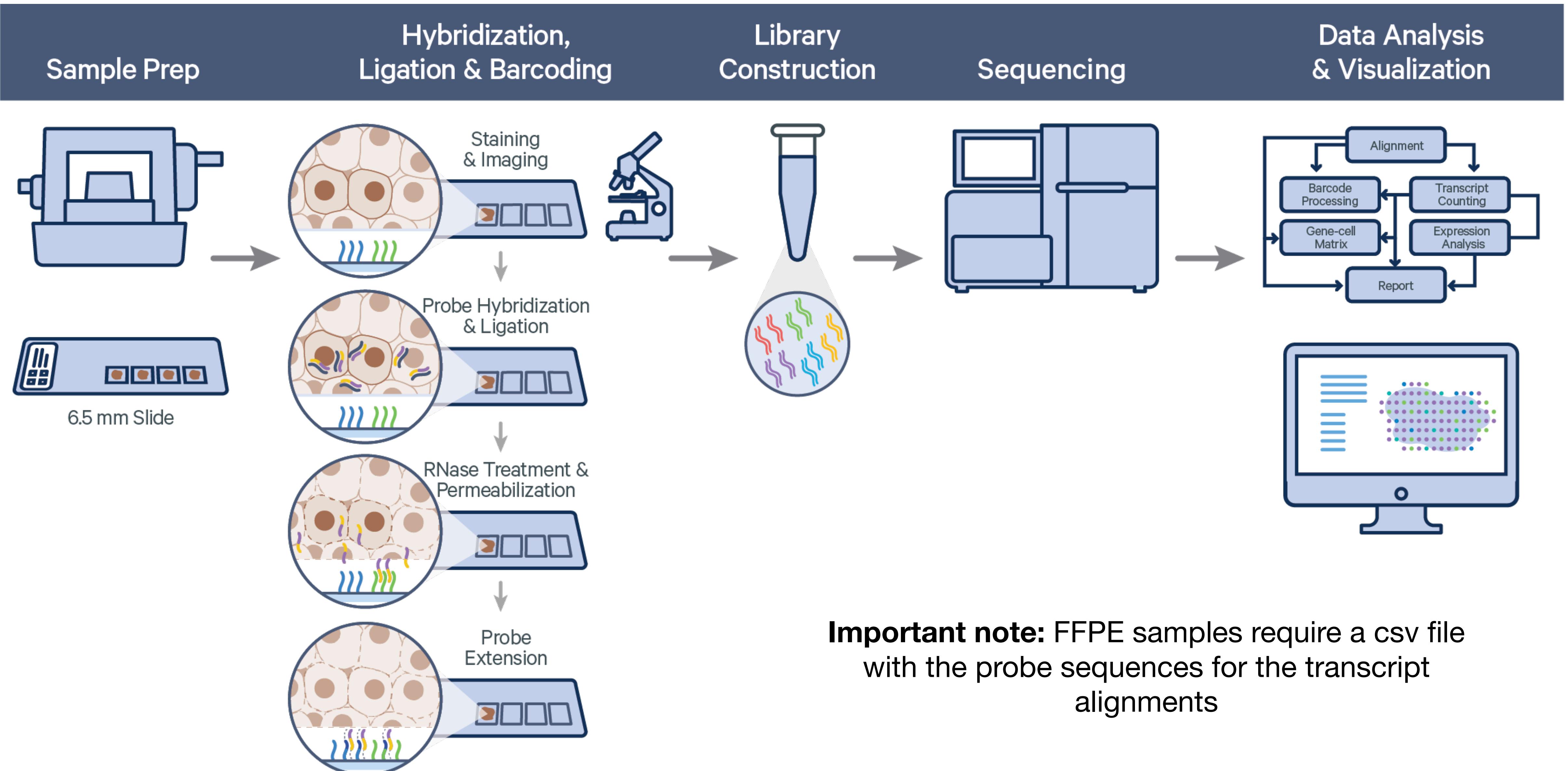
- Team-work

Visium - 10X Genomics



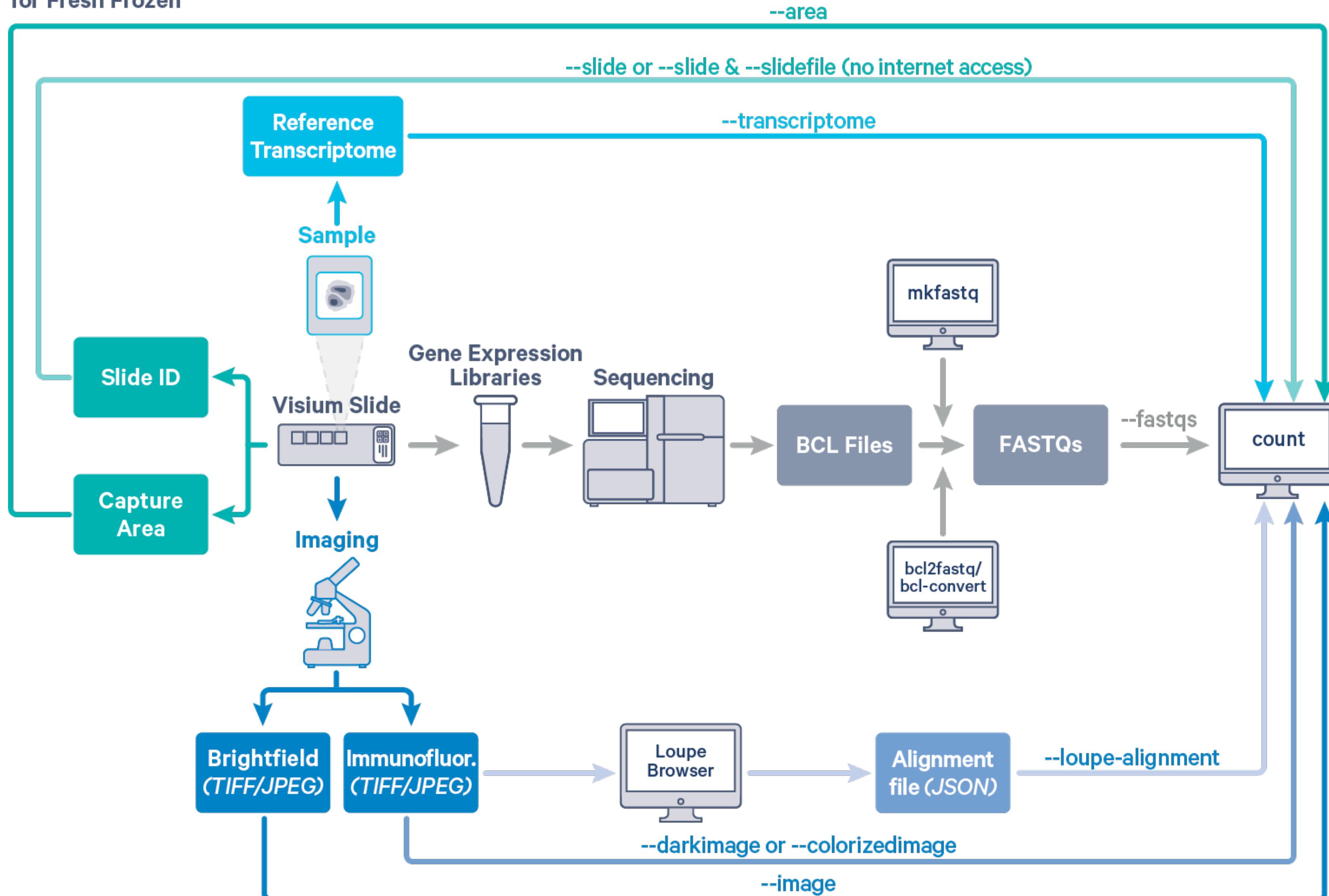
- **Visium Spatial Gene Expression** measures the **whole transcriptome** of intact fresh frozen sections in a spatially resolved manner.
- **Positional Barcodes** (instead of Cell Barcodes) are used for mRNA hybridization.
- Gene expression is mapped over a high-resolution microscope **image of the H&E- or IF-stained tissue**.
- Each spot has a **diameter of 55 μM** and (average cell size 1 - 100 μM) contains several cells.
- **Spot deconvolution** can help to estimate the abundance of each cell type in a spot

Visium - FFPE sample



SpaceRanger - 10X Genomics

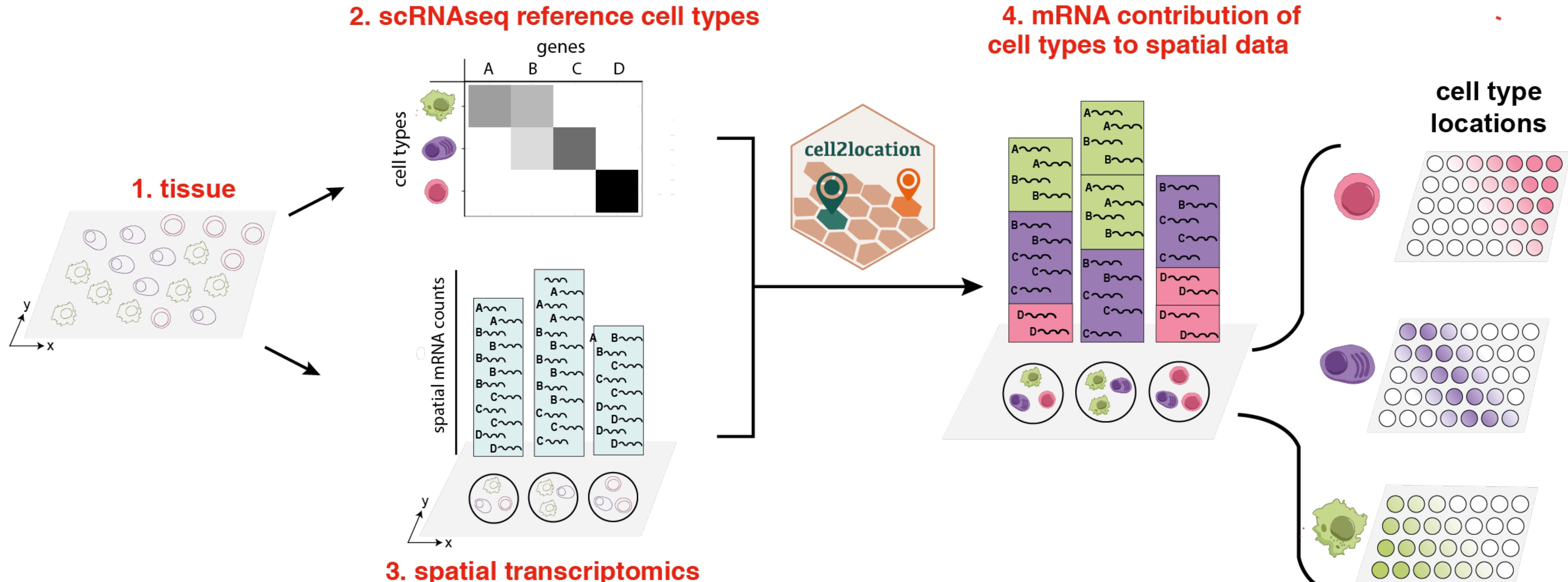
Space Ranger count
for Fresh Frozen



REQUIRED FILES:

- SLIDE information (capture area and ID)
- Reference (Fresh frozen or Probe set (FFPE))
- Images of each slides
- Optional: Additional information channels

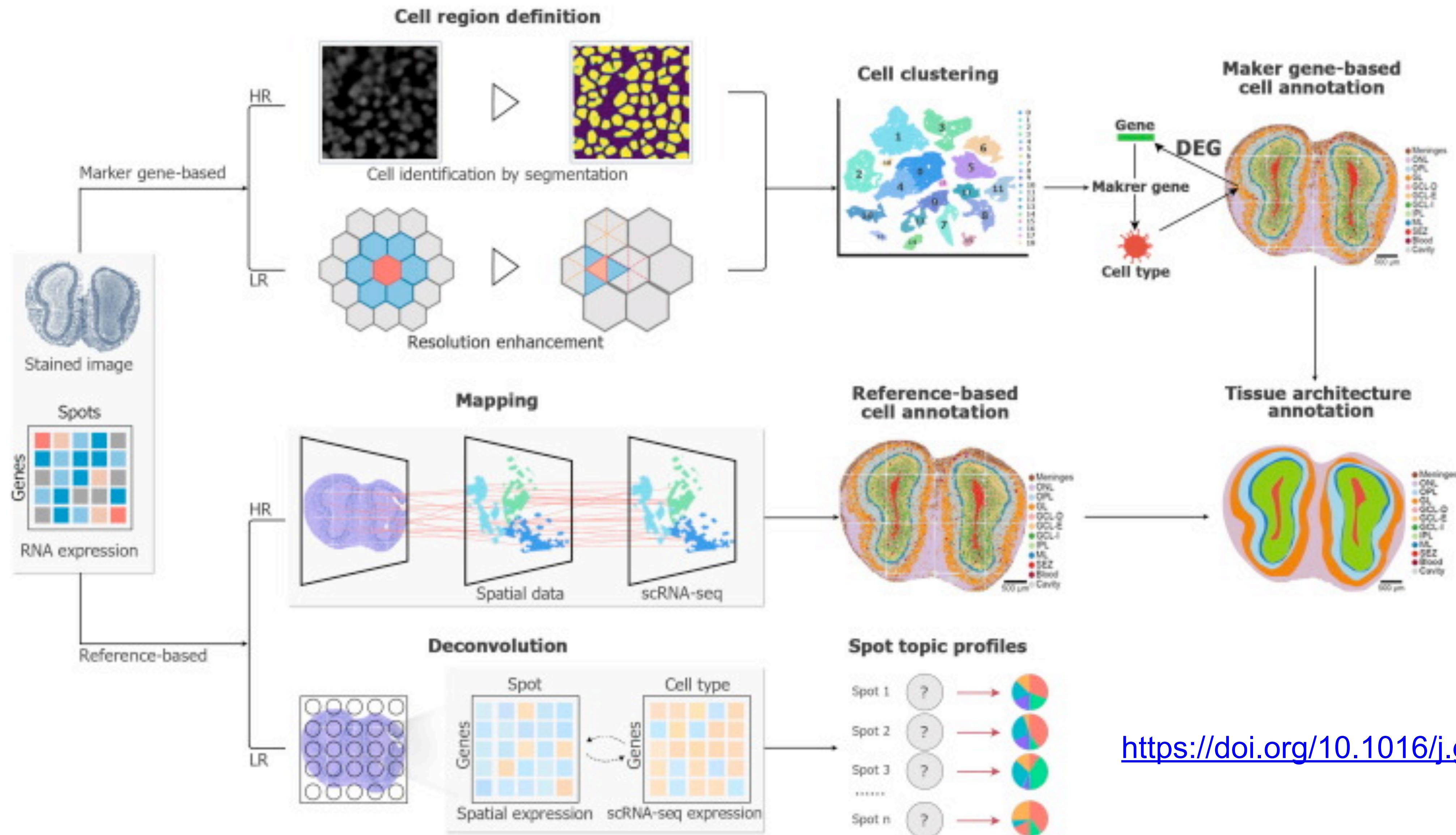
Spot deconvolution - Cell2location



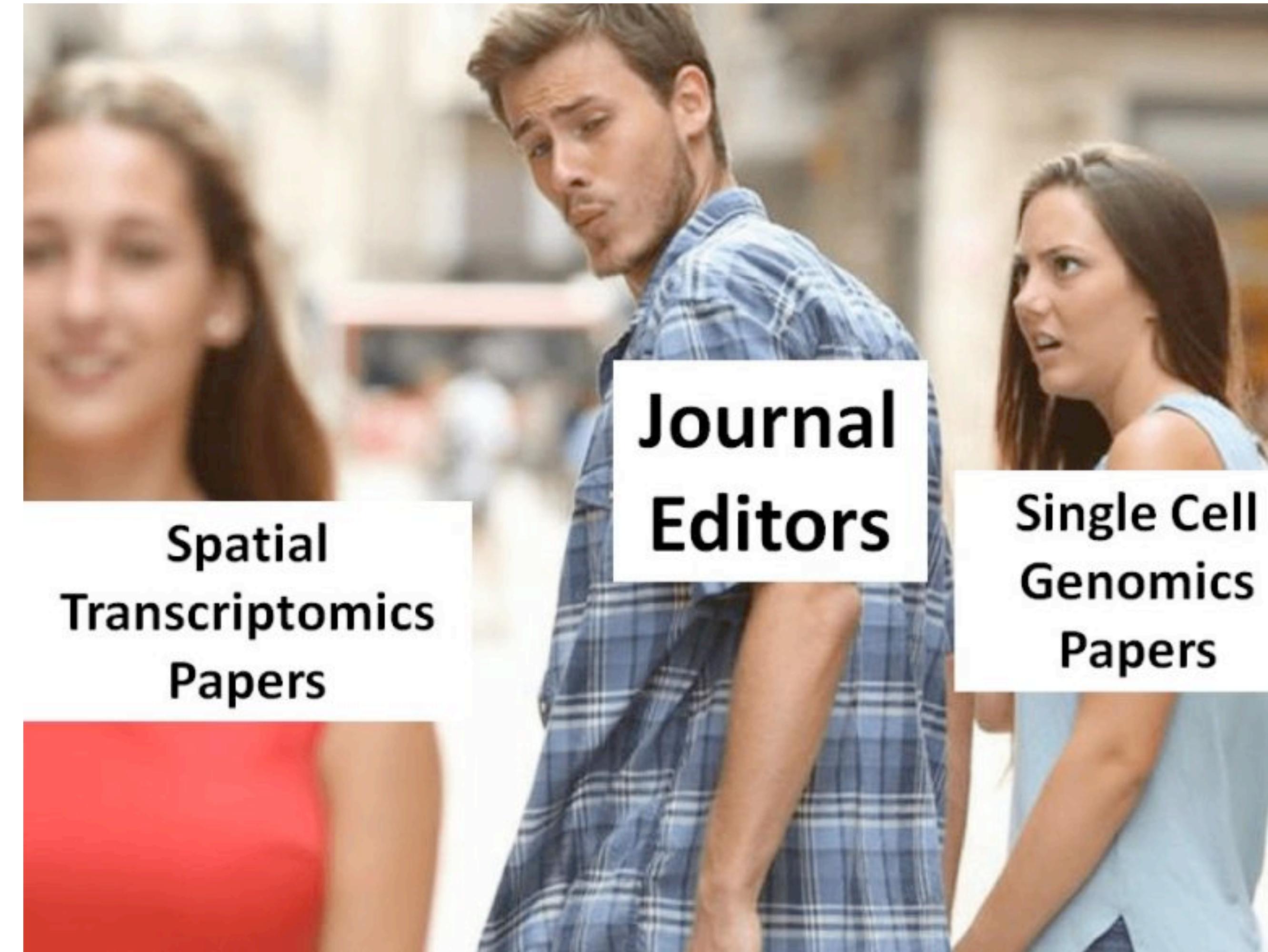
Negative Binomial Regression
for Gene signature of the
reference data

Mapping of the reference to
estimates cell type abundance
for each spot

Spatial transcriptomics - Pipeline



Visium - Hands-on



**Spatial
Transcriptomics
Papers**

**Journal
Editors**

**Single Cell
Genomics
Papers**

https://github.com/hayatlab/singlecell_workshop/blob/main/03_Visium_Heart_Workshop_GCB23.ipynb

Visium - Recap

How does spatial transcriptomics (Visium) of the human heart
compare to
Single-nuclei data?

Advantages

Disadvantages

Future perspectives