



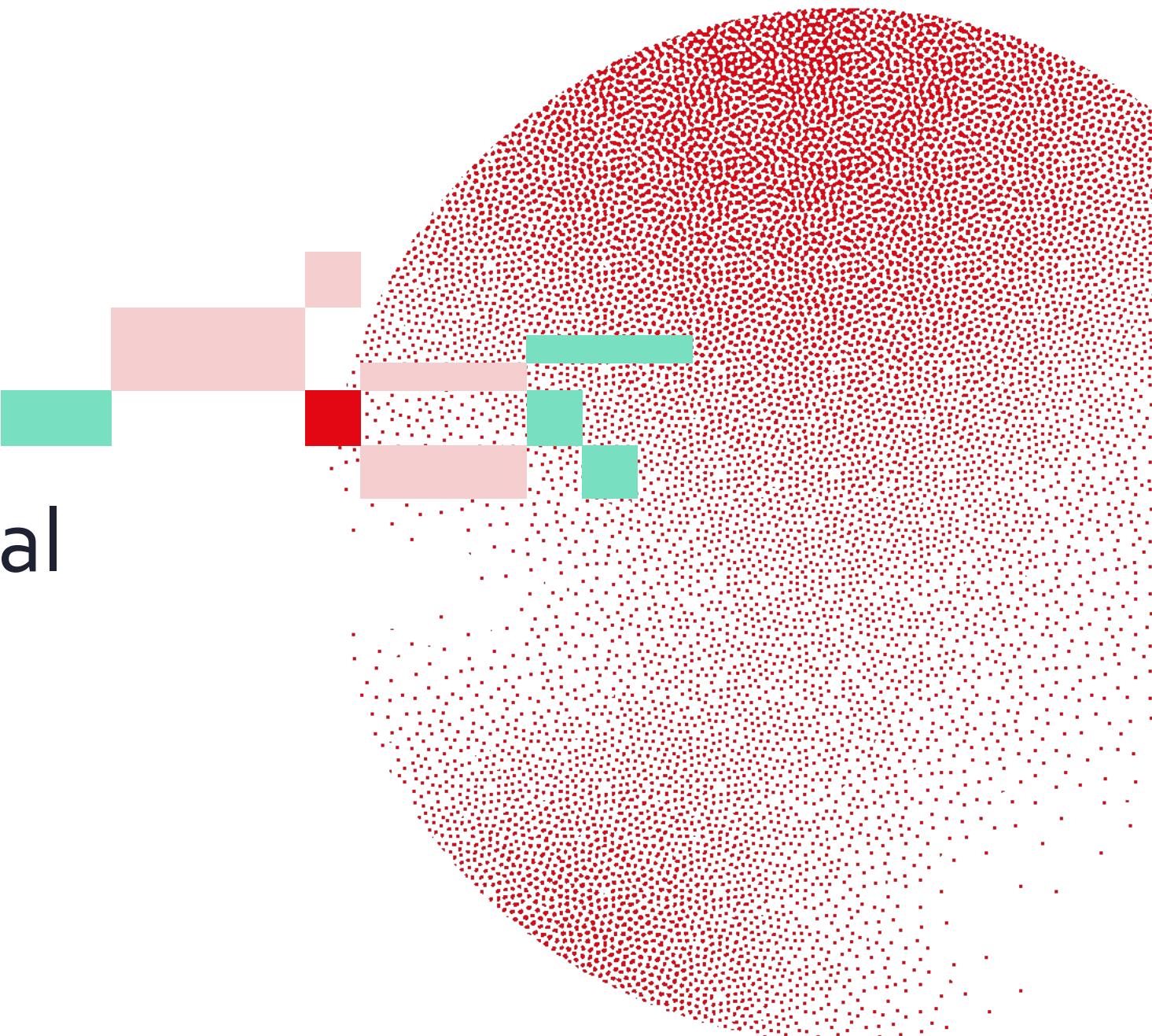
Swiss Institute of
Bioinformatics

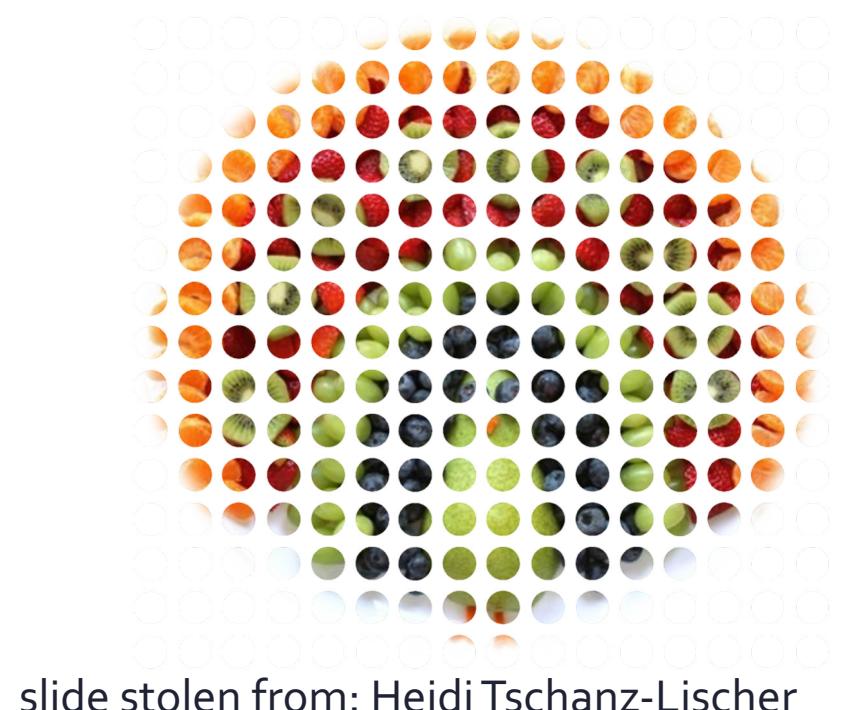
SIB DAYS TUTORIAL

Introduction to spatial transcriptomics

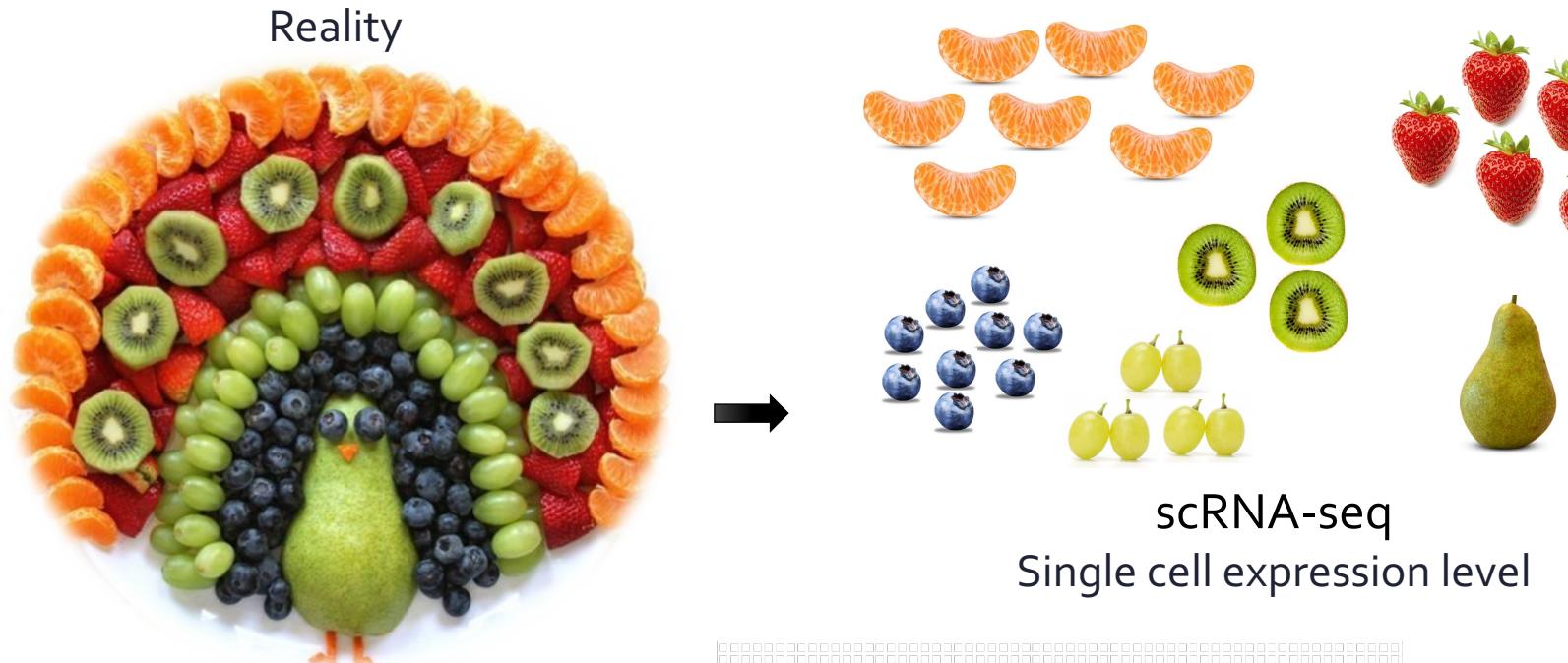
Geert van Geest

24.06.2024 SIB days



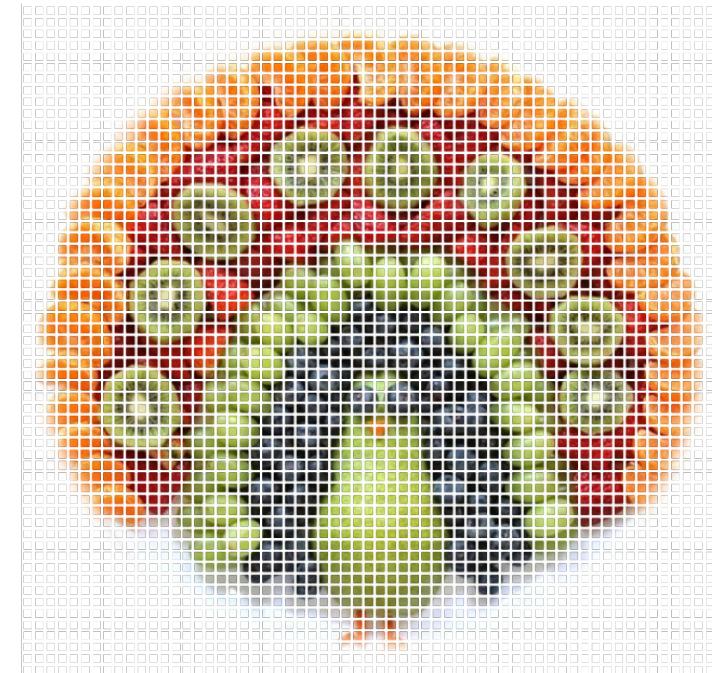


RNA-seq
Average expression level



Spatial transcriptomics
Spatial resolved expression level

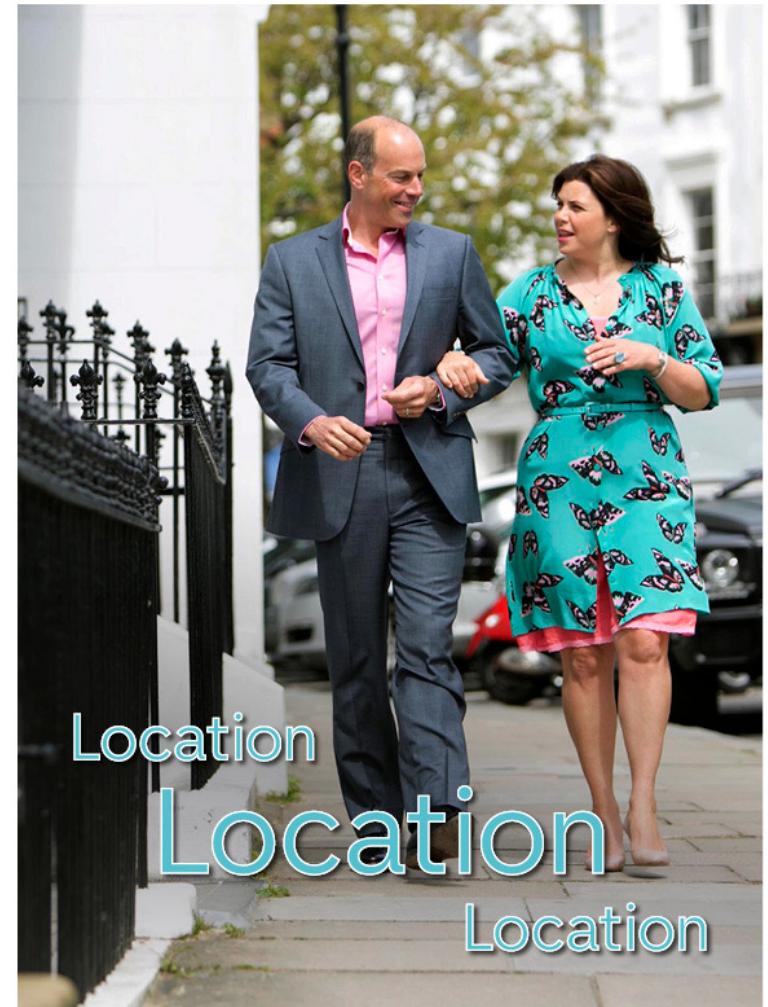
Different resolutions



Why spatial transcriptomics?

- » **Cells are diverse in shape and size**
 - » Single cell not always possible
 - » How cells interact matters

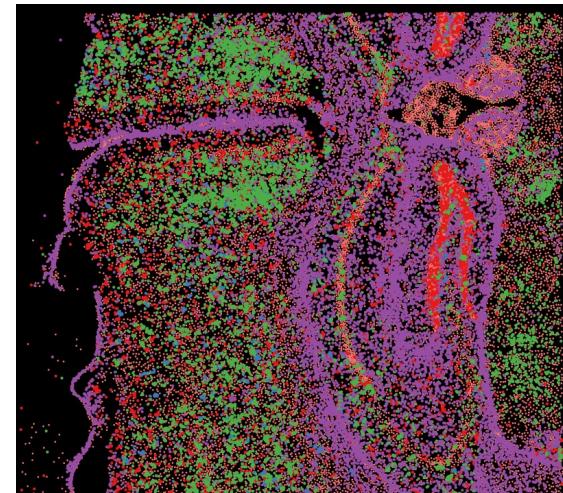
- » **Location, location, location:**
 - » Cell-cell interaction depends on proximity
 - » RNA molecules move



Methods

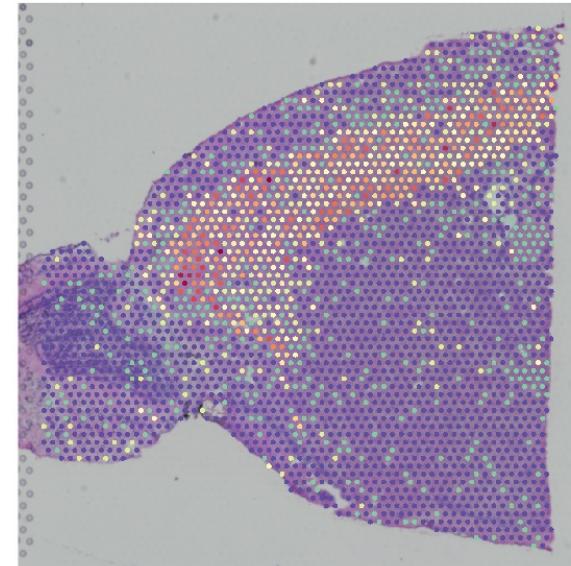
- » **Image based:**

- » Nanostring CosMx
- » vizgen MERFISH
- » 10X Xenium (in situ sequencing)



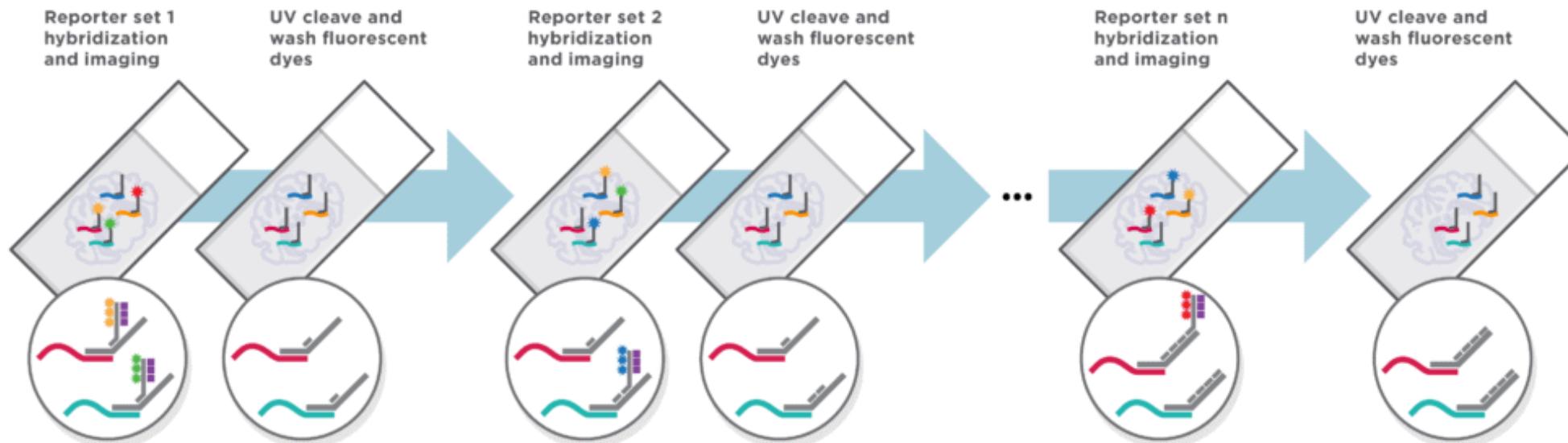
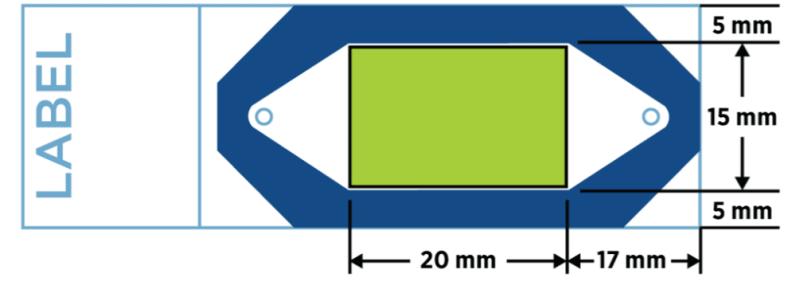
- » **Spot based:**

- » Curio seeker (SlideSeq2)
- » Nanostring GeoMx ('microdissection')
- » 10X Visium



Nanostring CosMx

- » Single molecule FISH (smFISH)
- » FFPE and FF
- » Combinatorial hybridization
- » Up to 6000 genes



vizgen MERFISH

- » Single molecule FISH (smFISH)
- » Combinatorial labelling
- » Microscopy imaging
- » Commercial panel: 1000 genes
- » Fresh frozen

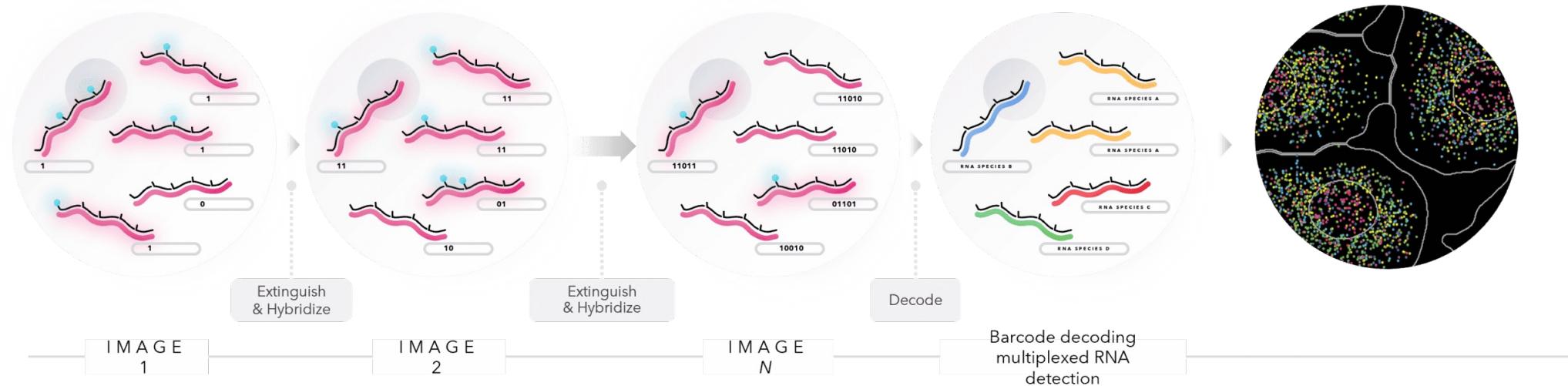
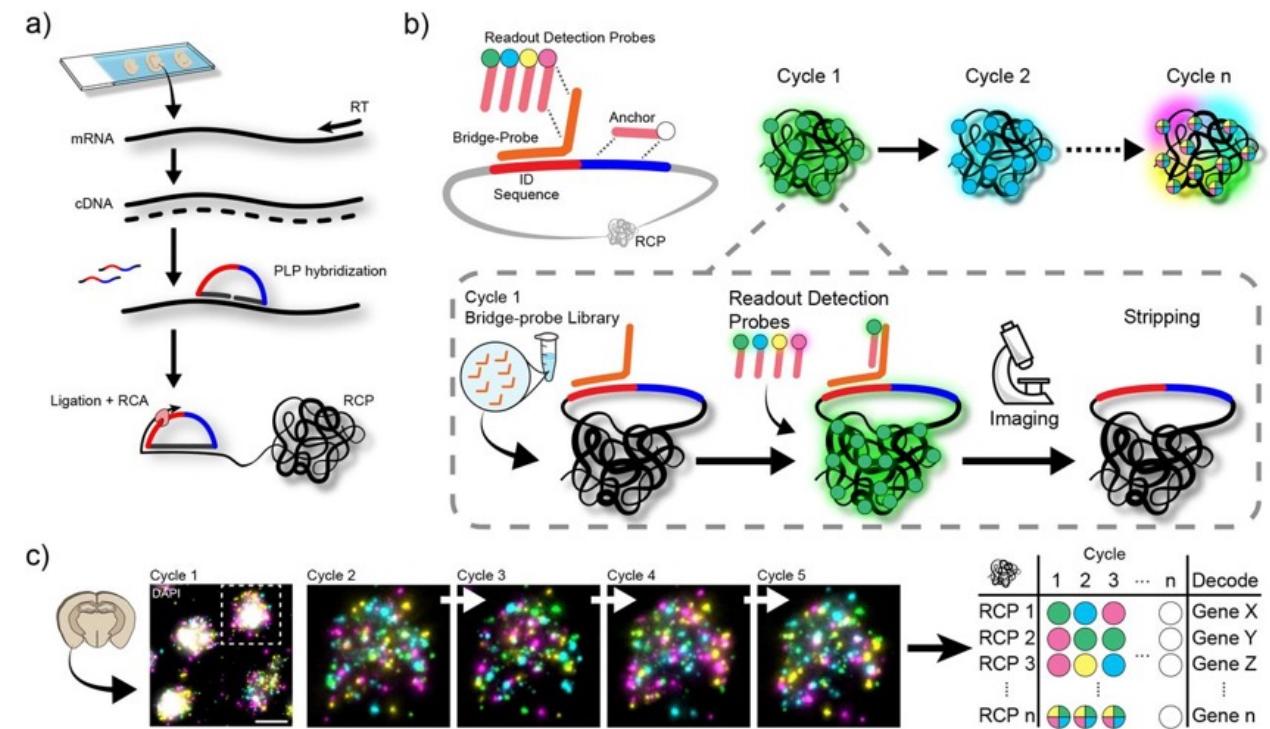


image: <https://vizgen.com/technology/>

10X Xenium and in situ sequencing

- » in-situ reverse transcription and rolling circle amplification (RCA)
- » Detection by several rounds of combinatorial probe hybridization
- » Up to ~5000 genes



<https://www.scilifelab.se/units/in-situ-sequencing/>

Gyllborg et al, Nucleic Acids Research (2020)

Overview commercial imaging-based methods

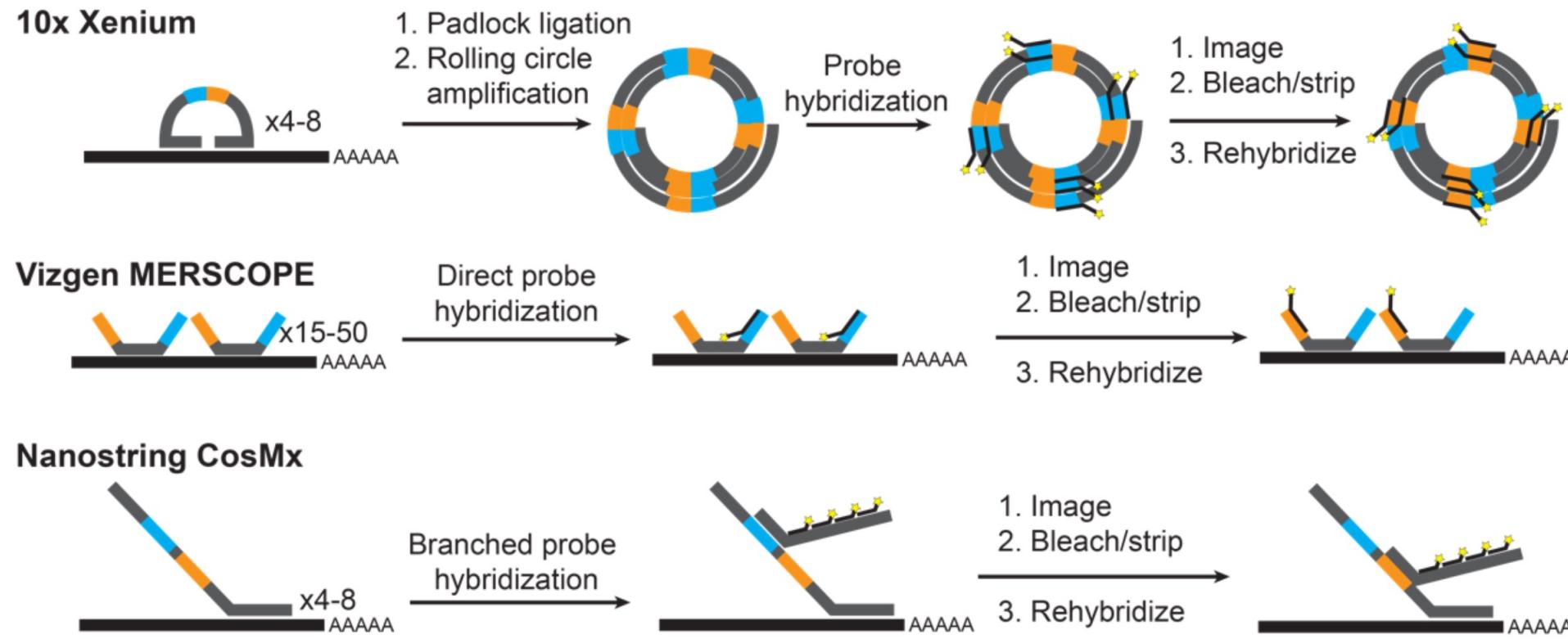
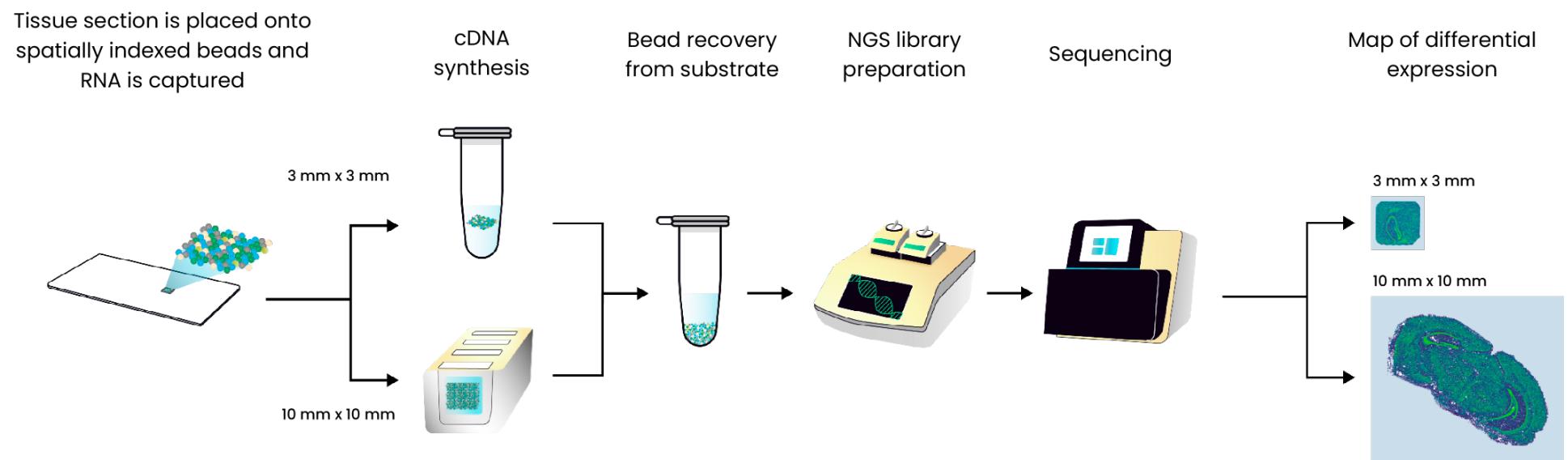


Image: Wang, Huan, et al. "Systematic Benchmarking of Imaging Spatial Transcriptomics Platforms in FFPE Tissues," 2023. <https://doi.org/10.1101/2023.12.07.570603>. CC-BY-NC-ND 4.0

Curio seeker (SlideSeq2)

- » Bead based
- » resolution: $10 \mu\text{m}$
- » $3 \text{ mm} \times 3 \text{ mm}$ or $10 \text{ mm} \times 10 \text{ mm}$
- » polyA capture
- » Fresh frozen



Nanostring GeoMx

- » Probe based
- » ROI 'Microdissection' by UV illumination
- » ROI diameter: $10 \mu\text{m}$ - $600 \mu\text{m}$ (can be any shape)
- » Sequencing probe barcodes
- » Full transcriptome possible

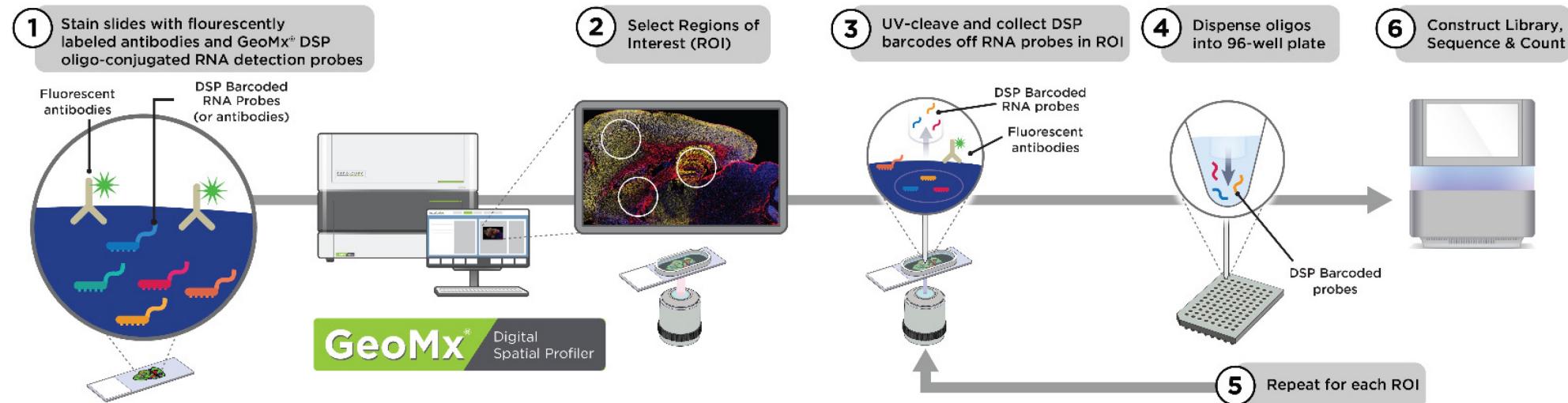
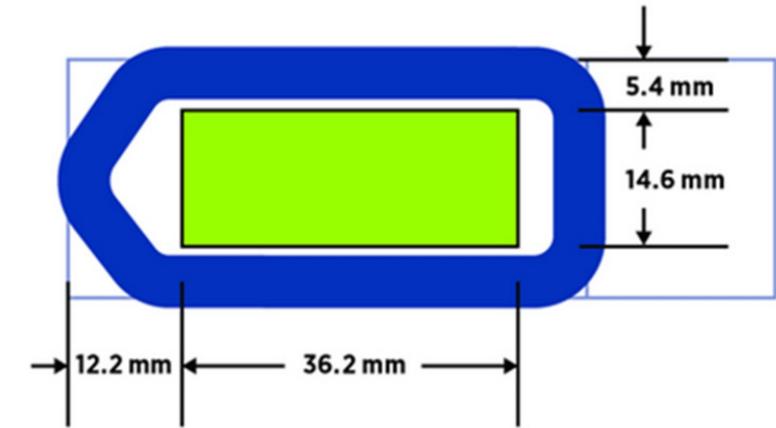
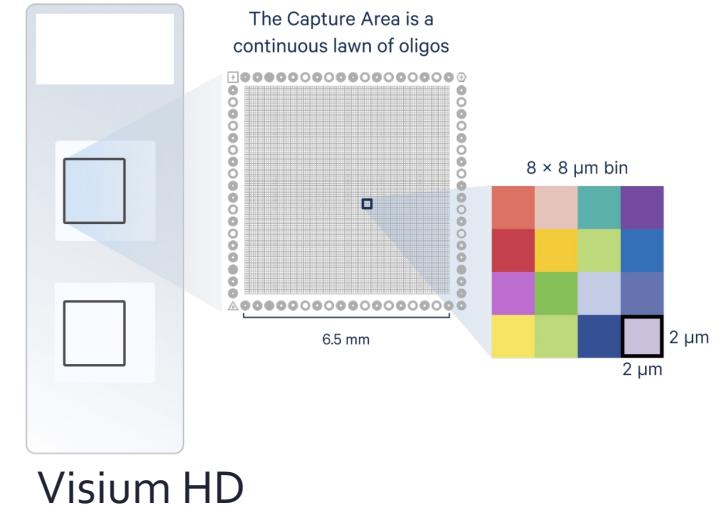


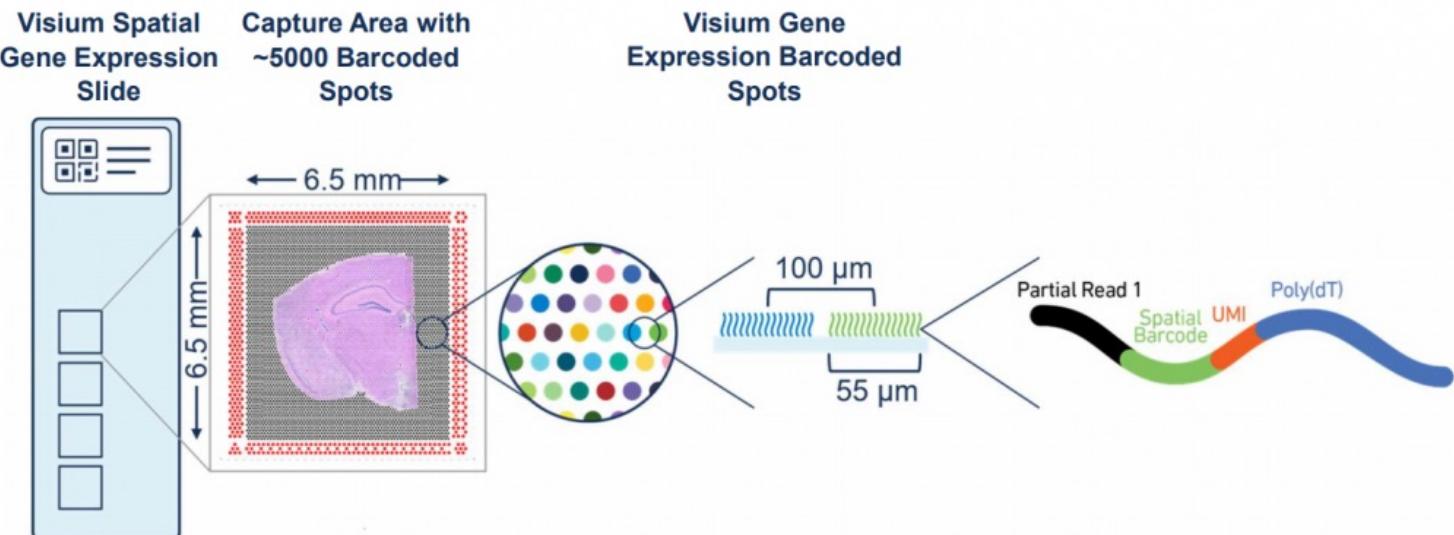
Image: Bergholtz, et al *Cancers* 13, no. 17 (2021): 4456. <https://doi.org/10.3390/cancers13174456>. CC-BY-4.0

10X Visium

- » Array based
- » resolution
 - » Standard: $55\text{ }\mu\text{m}$; $100\text{ }\mu\text{m}$ center-to-center
 - » HD: $2\text{ }\mu\text{m}$; no gaps
- » $6.5\text{ mm} \times 6.5\text{ mm}$ or $11\text{ mm} \times 11\text{ mm}$ (standard only)
- » Fresh frozen or FFPE
- » Direct placement or CytAssist (= probes)



Visium HD



Spaceranger count – 10X visium data

- » **Performs:**

- » image alignment
- » read alignment
- » spot on slice identification
- » UMI counting

- » **Input:**

- » Fastq files
- » Reference
- » Probe sets (if probes were used)
- » Slide information (ID, area)
- » Images: H&E or fluorescence



- » **Output:**

- » Images – including aligned fudicials
- » Filtered and unfiltered matrices (spot x gene)
- » Report: web_summary.html

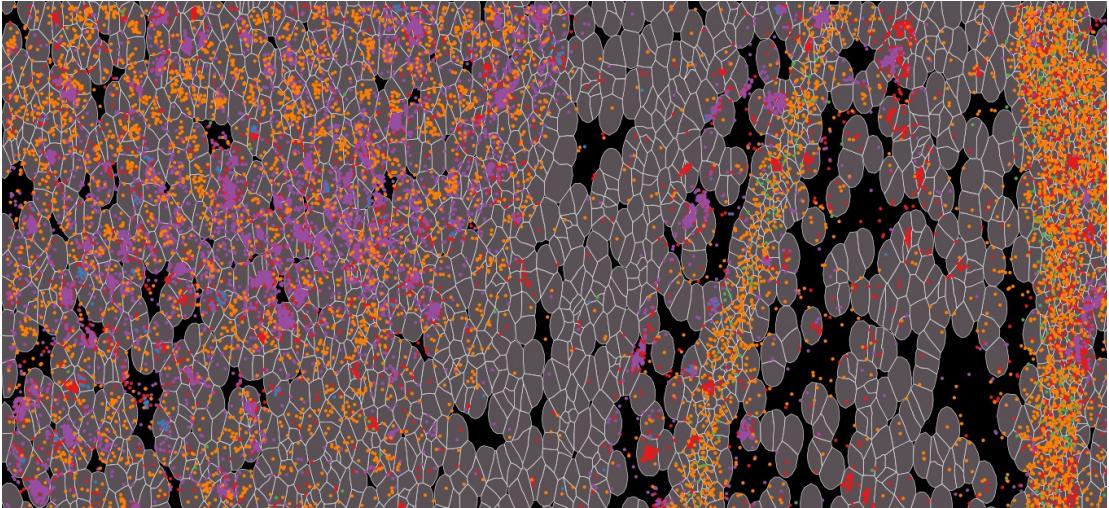
Spatial transcriptomics data

- » **Matrix:**

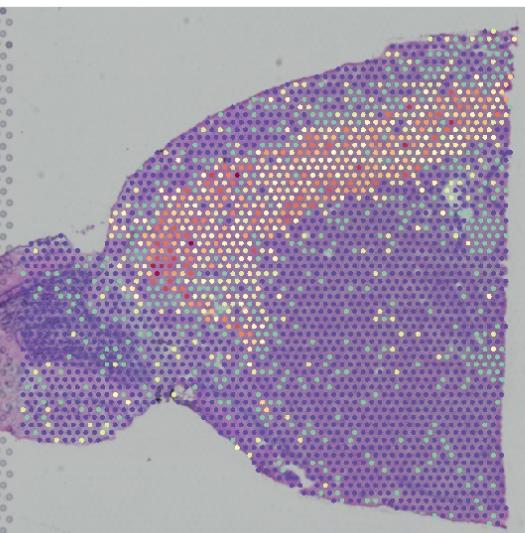
- » contains counts: transcript molecules or UMI
- » rows: genes or transcripts
- » columns: spots or cells

- » **Spatial information:**

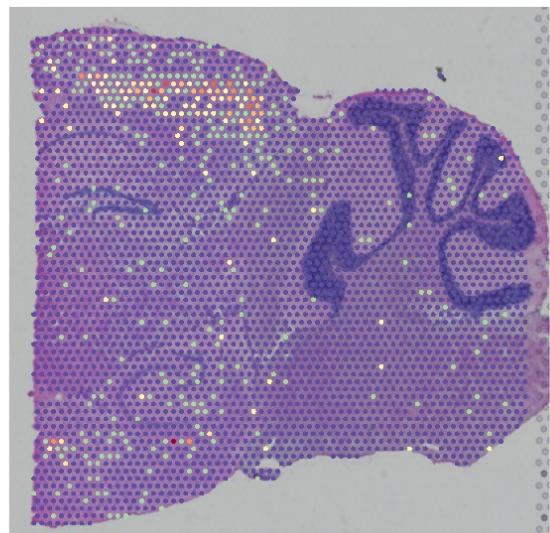
- » Sequencing based: Spot position
- » Imaging based: cell centroids, cell boundaries, molecule positions



10x xenium - cells



10x visium - spots



Spatial transcriptomics analysis

- » Python
 - » Squidpy
- » R:
 - » Seurat
 - » Bioconductor: SpatialExperiment, scater, scran

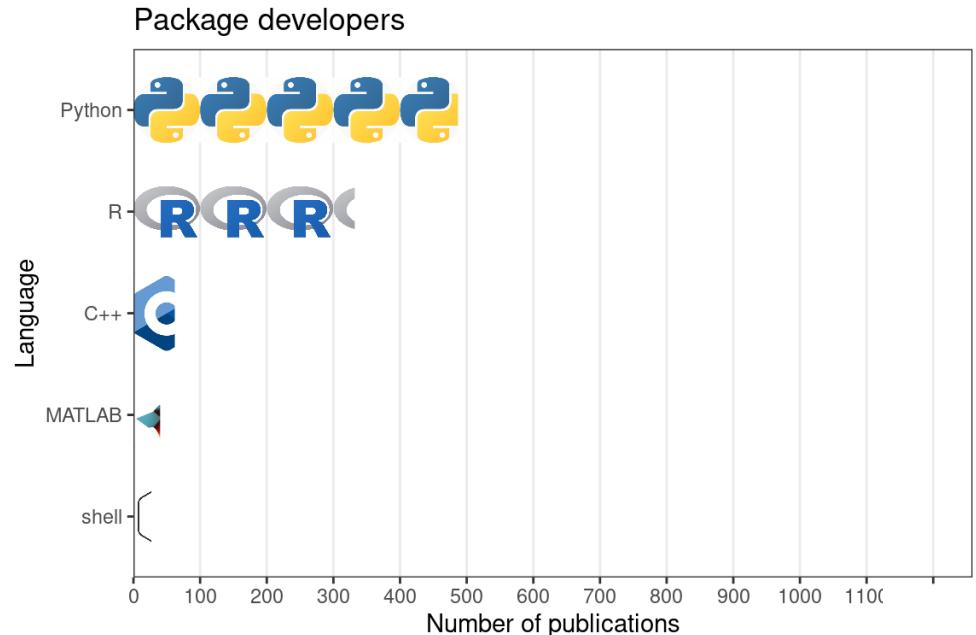
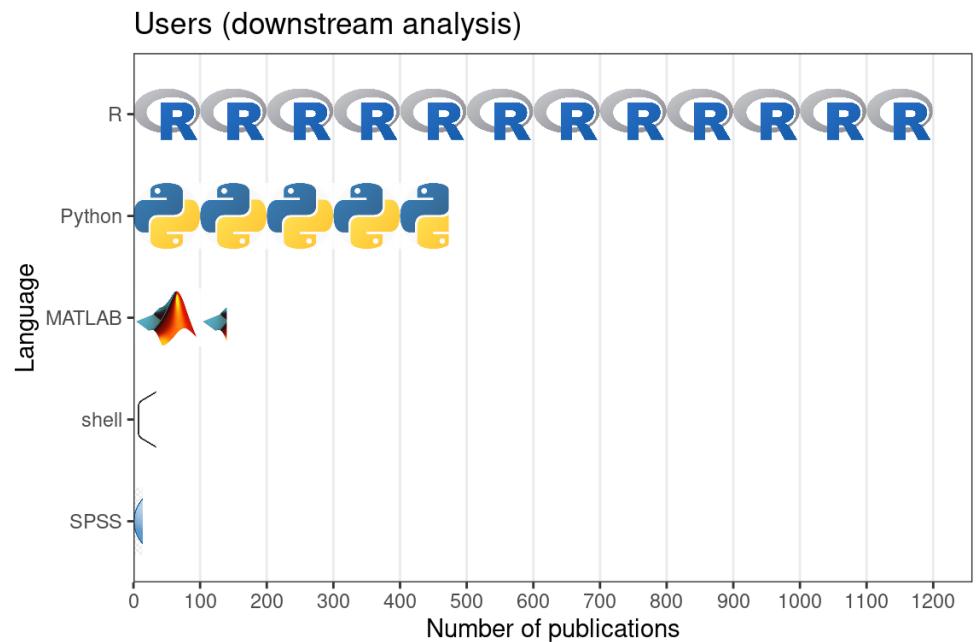
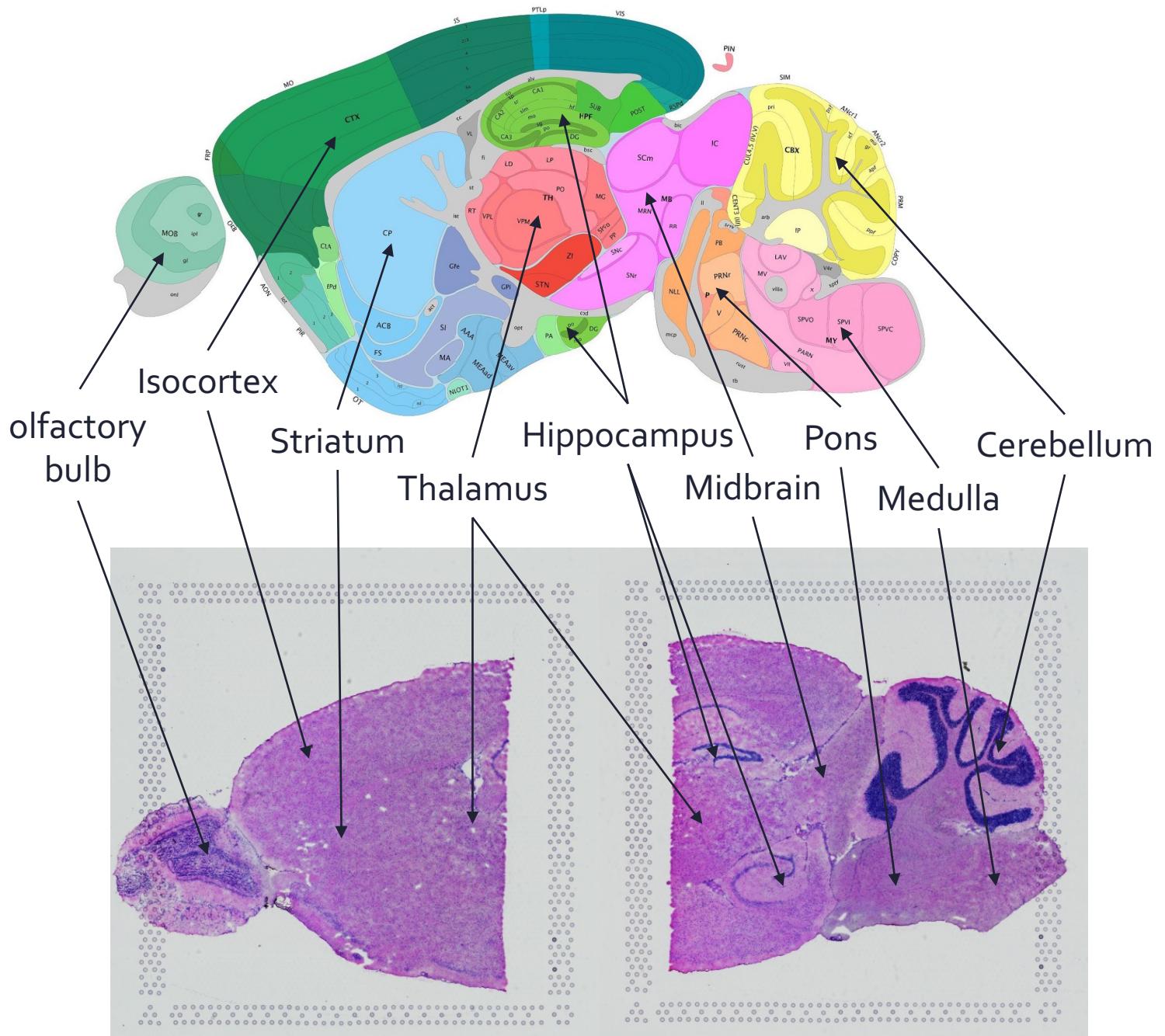


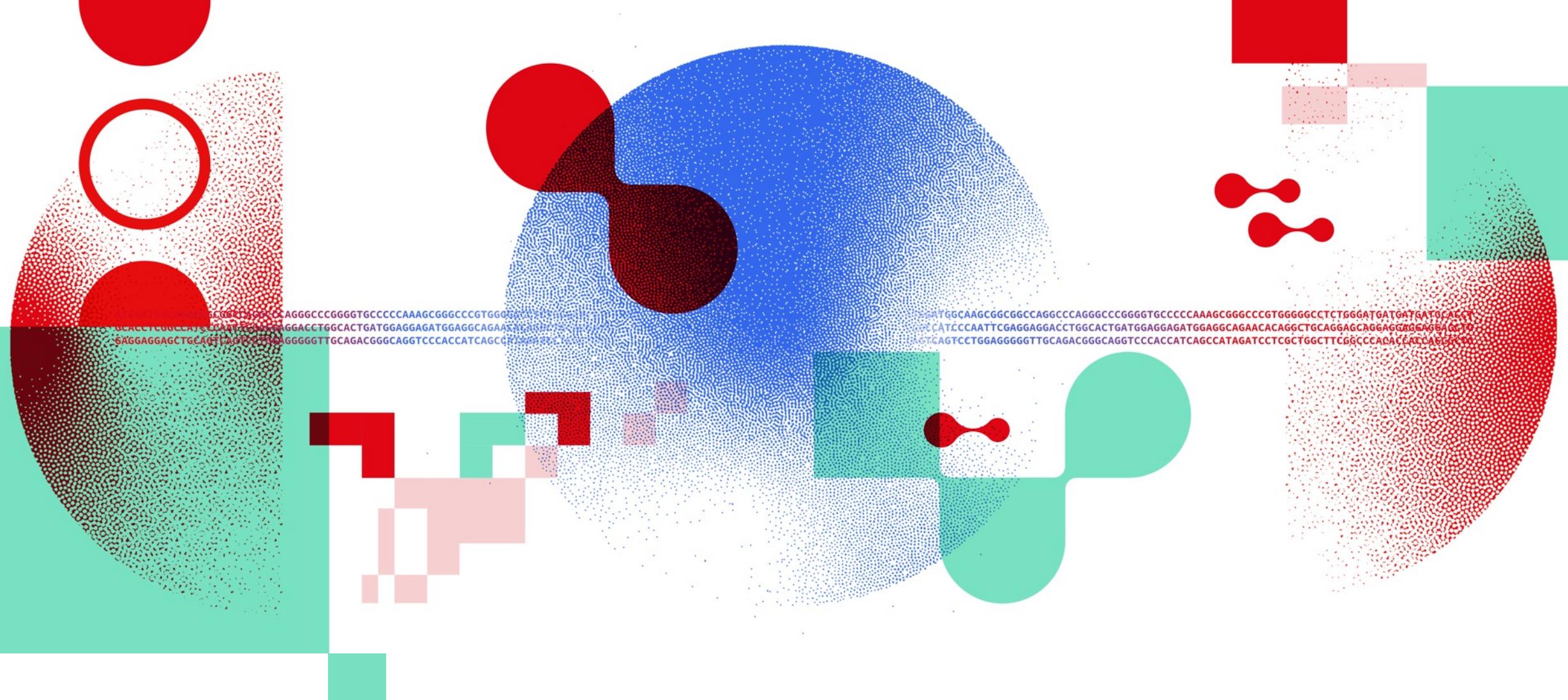
Image from: https://pachterlab.github.io/LP_2021/

Our dataset

- » 10X visium v1
- » Direct placement
- » Mouse brain
- » Two slices - sagittal

- » Perform quality control
- » Integration and clustering
- » Marker gene identification
- » Basic annotation





Time for exercises!

DATA SCIENTISTS FOR LIFE

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