

Single-cell spatial transcriptomics

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Computational Biology and Omics Data Analysis

 <https://cobioda.github.io>

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 @kevinlebrigand

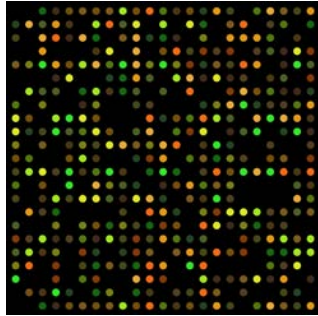


01

Introduction

20 years of transcriptomics

Driven by microfluidics technological developments

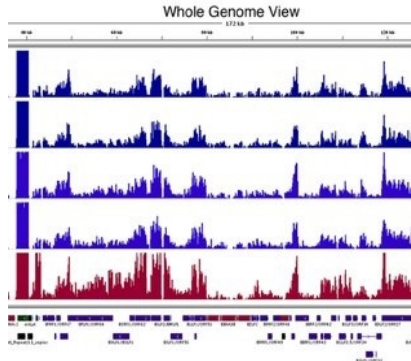


Early 2000's: DNA microarray

- Large-scale transcriptome
- Oligonucleotide probe tiling
- Fluorochrome signal analysis
- Bulk resolution



Cost : 4k€
20 samples
25k genes
0,5M matrix

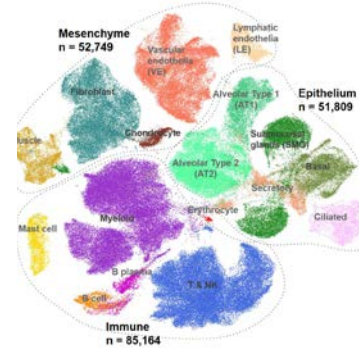


Late 2000's : RNA sequencing

- Whole transcriptome
- Next Generation Sequencing
- Full-transcript coverage
- Bulk resolution



Cost : 4k€
20 samples
50k genes
1M matrix

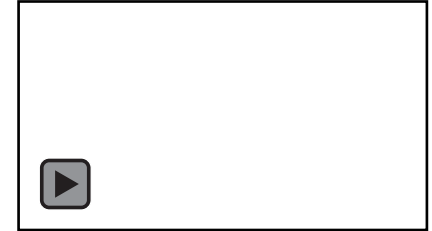


Mid 2010's: Single -cell

- Whole transcriptome
- Microfluidics + NGS
- 3p-end gene signal (UMI)
- Sensitivity (6%)
- Single-cell / state resolution



Cost : 4k€
5k cells
50k genes
250M matrix



2020's : Spatial

- 500-1000 gene targets
- Imaging analysis
- Multiplexing FiSH (single molecule)
- Sensitivity (30-80%)
- Sub-cellular resolution

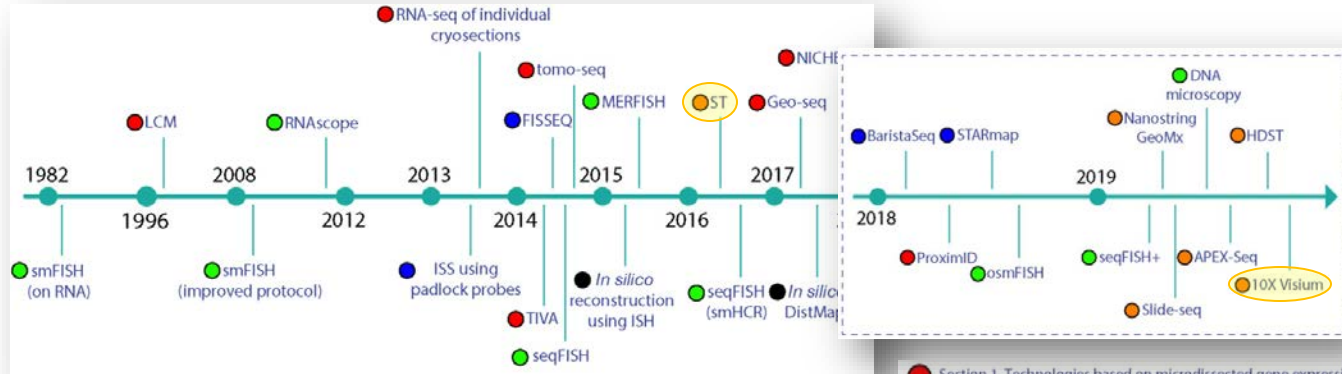


Cost : 4k€
250k cells
1k genes
250M matrix
+ Spatial dimension

Spatial Transcriptomics approaches

Historical timeline

- Spatial transcriptomics aims to directly visualize gene expression in their original environment,
- It tackles the main limitation of single cell experiment missing the spatial organization,
- A lot of developments in the last years thanks to recent advances in different fields,

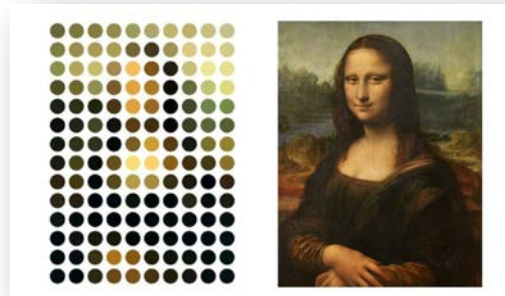
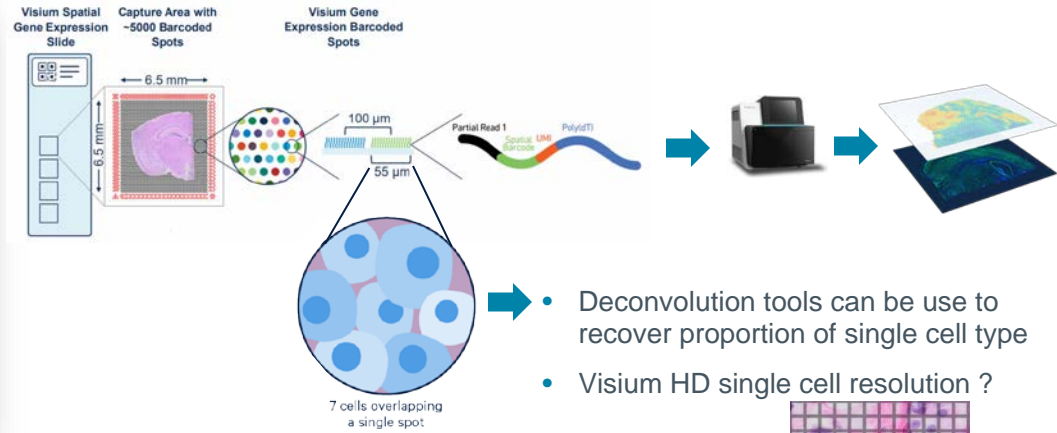
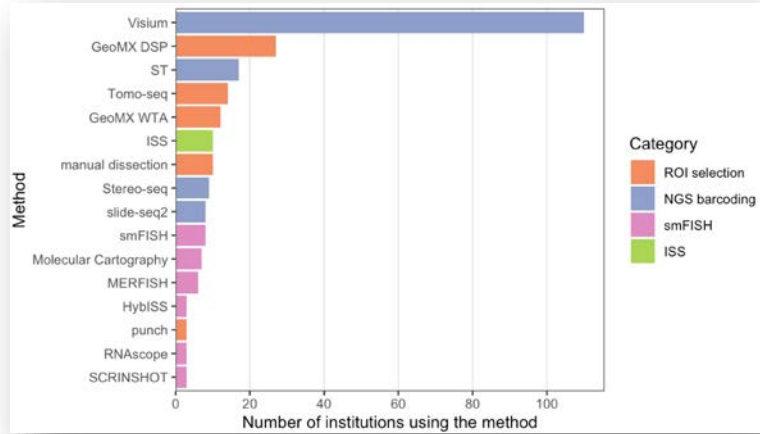


Spatially Resolved Transcriptomes Next Generation Tools for Tissue Exploration
Asp et al., BioEssays 2020

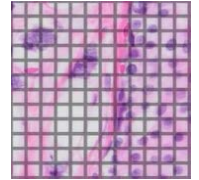
- Section 1. Technologies based on microdissected gene expression
- Section 2. *In situ* hybridization technologies
- Section 3. *In situ* sequencing technologies
- Section 4. *In situ* capturing technologies
- Section 5. *In silico* reconstruction of spatial data

Spatial transcriptomics (2017 -2022)

Visium is widely adopted by academics



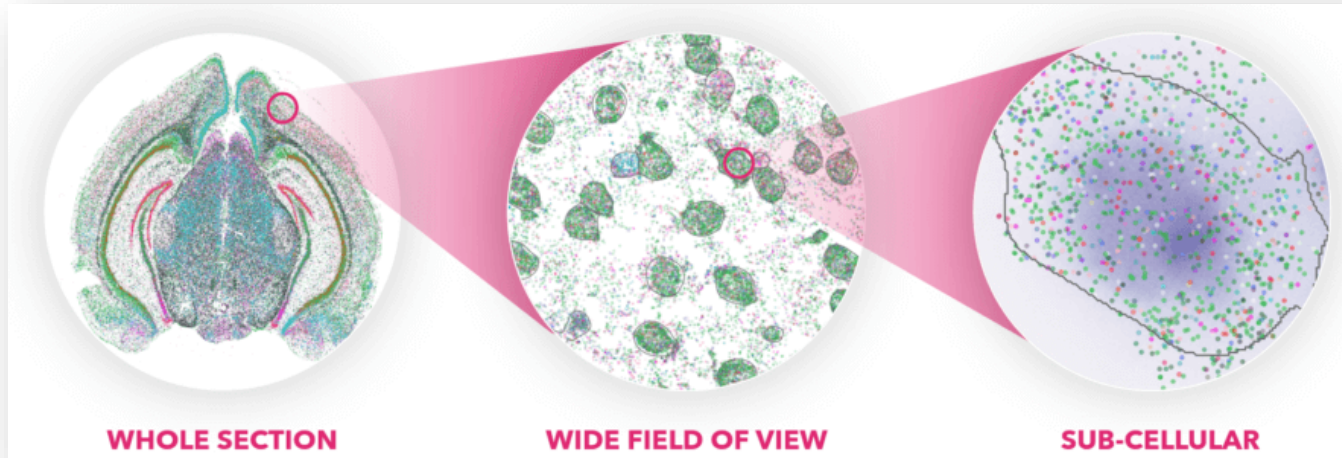
But is not the ideal readout for spatial biology
(Akoyacredit rough caricature)



Spatial imaging -based transcriptomics (2022)

No more sequencing for direct singlecell resolution

- Lower gene panel targets (from whole transcriptome to ~1,000 genes)
- Higher sensitivity (from ~6% to 30-80%)
- Larger imaging area (42 to 236 mm²)
- Higher resolution (from 55 μ m to subcellular)



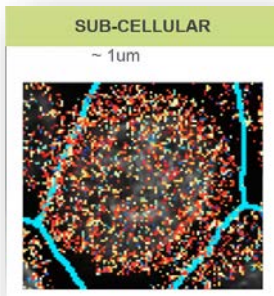
Spatial imaging -based transcriptomics (2022)

No more sequencing for direct single-cell resolution



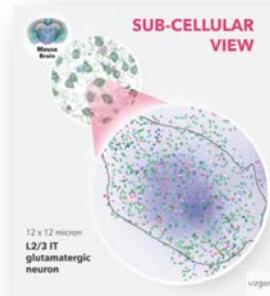
Nanostring CosMx

- Limited availability
- 960 targets (panel 20k, AGBT24)
- Sensitivity: << 30-80% (+)
- Imaging area: 16 mm² (2 days)
- Resolution: 200 nm



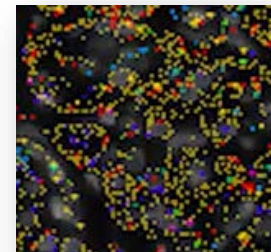
Vizgen Merscope

- Available (oct.22)
- 1,000 targets
- Sensitivity: 30-80% (+++)
- Imaging area: 100 mm² (2 days)
- Resolution: 100 nm



10xGenomics Xenium

- Available (jan.24)
- 400 targets (panel 6k)
- Sensitivity : 530% (++)
- Imaging area: 236 mm² (4 days)
- Resolution: 200 nm



Spatial imaging -based transcriptomics (2022)

No more sequencing for direct single-cell resolution



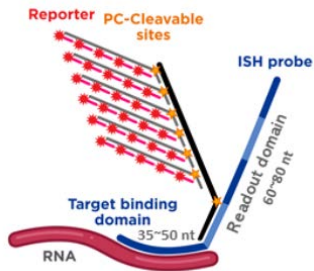
Nanostring CosMx
ISH-based



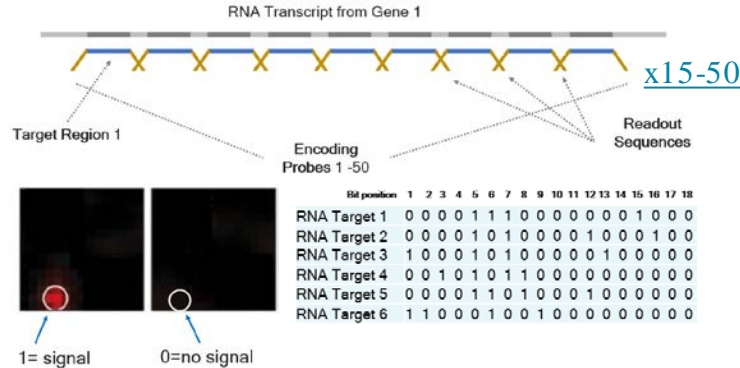
Vizgen Merscope
Multiplex ErrorRobust FISH



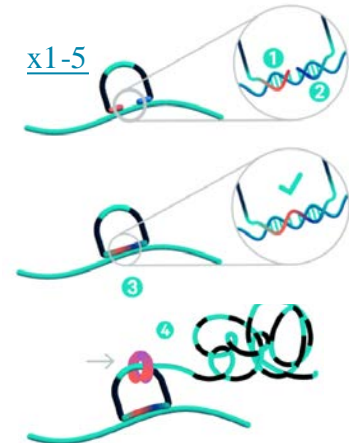
10xGenomics Xenium
Cartana ISS, padlock probes /RCA



x4-8 / target gene



Cyclic *in situ*Hybridization Chemistries

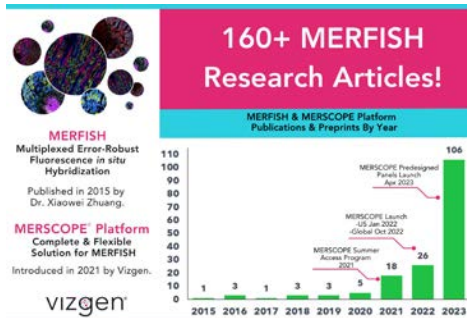


Spatial imaging -based technologies comparison

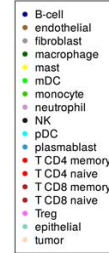
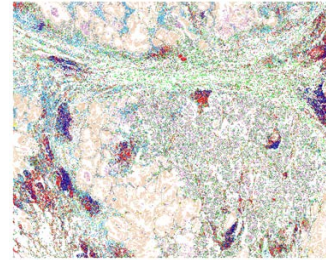
Compare available datasets

Vizgen Merscope

- XiaoweiZhuang'slab merfishpublications
 - Chen et al., Science (2015)
 - Moffitt et al., PNAS (2016), Science (2018)
 - EmanuelG et al., Nature Methods (2017)
 - Xia C. et al., PNAS (2019, Scientific Reports (2019)
 - Zhang M. et al., Nature (2021)
- Internal data release program
 - Human Immuno-oncology (**breast**, colon,**lung**, liver, skin, prostate, uterine and ovarian) 500 genes, >4 billion transcripts, 9 million cells
 - Mouse Liver Map(347genes)
 - Mouse brain Receptor Map (483 genes)

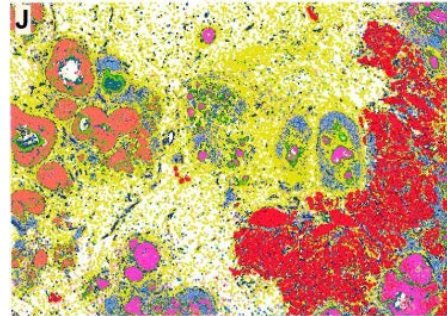


Nanostring CosMx



- Release date: 11/2021
- FFPE Human NSCLC (**Lung**)
- 960 gene targets
- 8 sections for 800k cells
- Imaging area: 8 x 16 mm²
- 259,604,214 transcripts
- Mean transcripts/cell: 265

10xGenomics Xenium



- Release date: 10/2022
- FFPE Human **Breast** cancer
- 313 gene targets
- 167,885 cells,
- 36,944,521 transcripts
- Imaging area: 40 mm²
- Mean transcripts/cell: 193

Spatial imaging technologies comparison

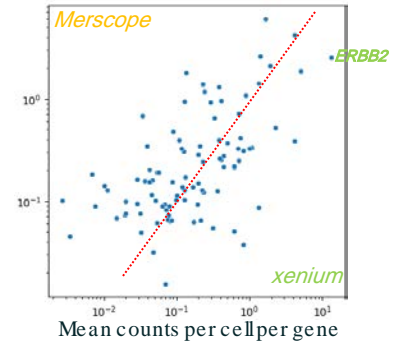
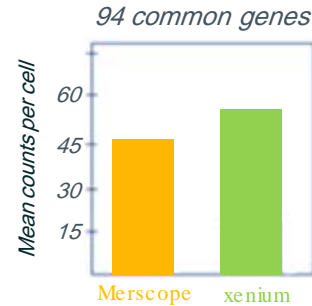
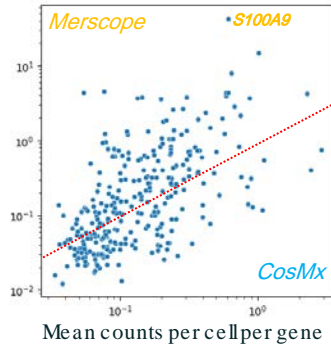
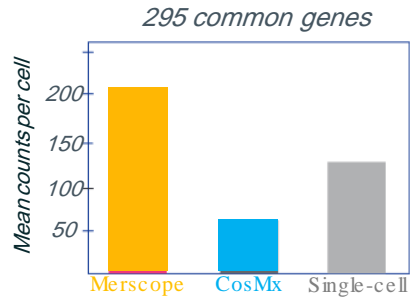
Compare available datasets: Lung and Breast cancer samples



FFPE Human Lung Cancer	Merscope	CosMx
Total cells	353 k (x4)	92 k
Detected transcripts	107 M (x4)	26 M
Gene targets	500	960
Total RPKM	9,204	61,680 (x6)
Mean transcripts/cell	302	284



FFPE Human Breast Cancer	Merscope	Xenium
Total cells	713 k (x4)	168 k
Detected transcripts	353 M (x10)	32 M
Gene targets	500	313
Total RPKM	9,909	7,912
Mean transcripts/cell	495	193



<https://vizgen.com/wp-content/uploads/2022/12/Vizgen-Spatial-Genomics-Data-Quality-eBook1.pdf>

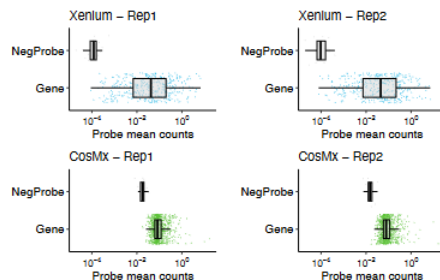
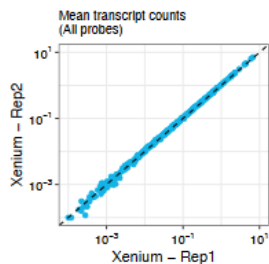
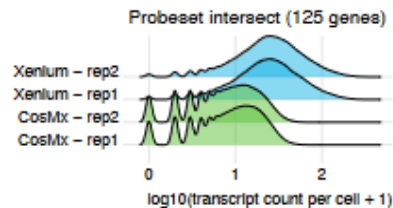
Spatial imaging technologies comparison

Recent biorxiv comparative studies

A Comparative Analysis of Imaging-Based Spatial Transcriptomics Platforms

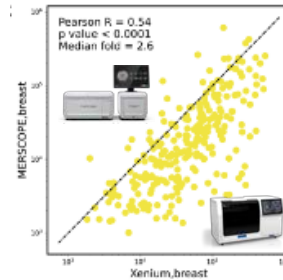
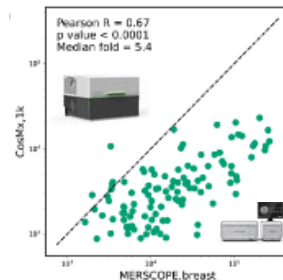
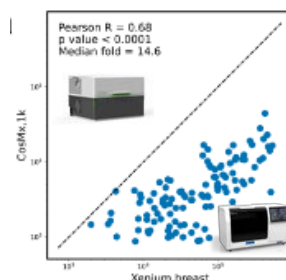
David P. Cook¹, Kirk B. Jensen^{2,3,4}, Kellie Wise^{2,3}, Michael J. Roach^{2,3}, Felipe Segato Dezem^{6,7}, Natalie K. Ryan^{3,5}, Michel Zamojski⁹, Ioannis S. Vlachos^{10,11,12}, Simon R. V. Knott^{13,14}, Lisa M. Butler^{3,5}, Jeffrey L. Wrana^{1,15}, Nicholas E. Banovich¹⁶, Jasmine T. Plummer^{6,7,8*}, Luciano G. Martelotto^{2,3*}

	Xenium Rep 1	Xenium Rep 2	CosMx Rep 1	CosMx Rep 2
Gene target #	377	377	1000	1000
Total cell count	99,852	102,608	96,139	98,767
Median gene count per cell	33	34	75	71
Median transcript count per cell	88	92	113	99
Median transcript count / gene target count	0.23	0.24	0.11	0.10
Median transcript count (intersecting targets only)	23	24	8	7



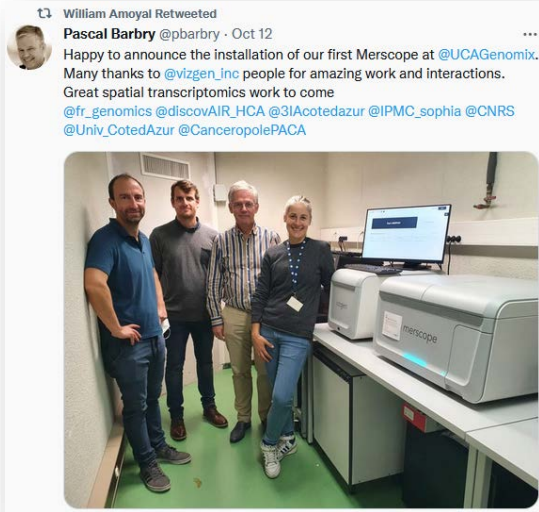
Systematic benchmarking of imaging spatial transcriptomics platforms in FFPE tissues

Huan Wang^{1*}, Ruixu Huang^{2*}, Jack Nelson^{1*}, Ce Gao³, Miles Tran³, Anna Yeaton⁴, Kristen Felt⁵, Kathleen L. Pfaff⁶, Teri Bowman⁷, Scott J. Rodig^{6,7}, Kevin Wei^{3,7}, Brittany A. Goods^{2,**}, Samouil L. Farhi^{1,**}

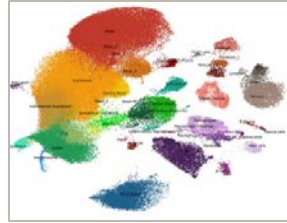


MERSCOPE @ UCAGenomiX (Nice-Sophia -Antipolis)

October 2022



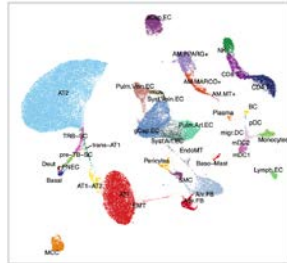
- Human Lung Cell Atlas (CZI)  **discovAIR**
Discovering the Cellular Landscape of the Airways and Lung Tissue



- 12 control / 2 IPF / 10 COPD patients
- 415,764 cells (117 samples)
- 48 cell types



- Epileptic encephalopathy Dravet Synd. (Mouse brain, M Mantegazza, Nice)
- Human embryo olfactory epithelium exploration (Paolo Jacobini, Lille)
- Pulmonary Arterial Hypertension (Christophe Guignabert, Paris Saclay)



- 7 control / 7 PAH patients
- 69,949 cells
- 39 cell types

02

Data acquisition and statistical analysis

Gene targets panel design

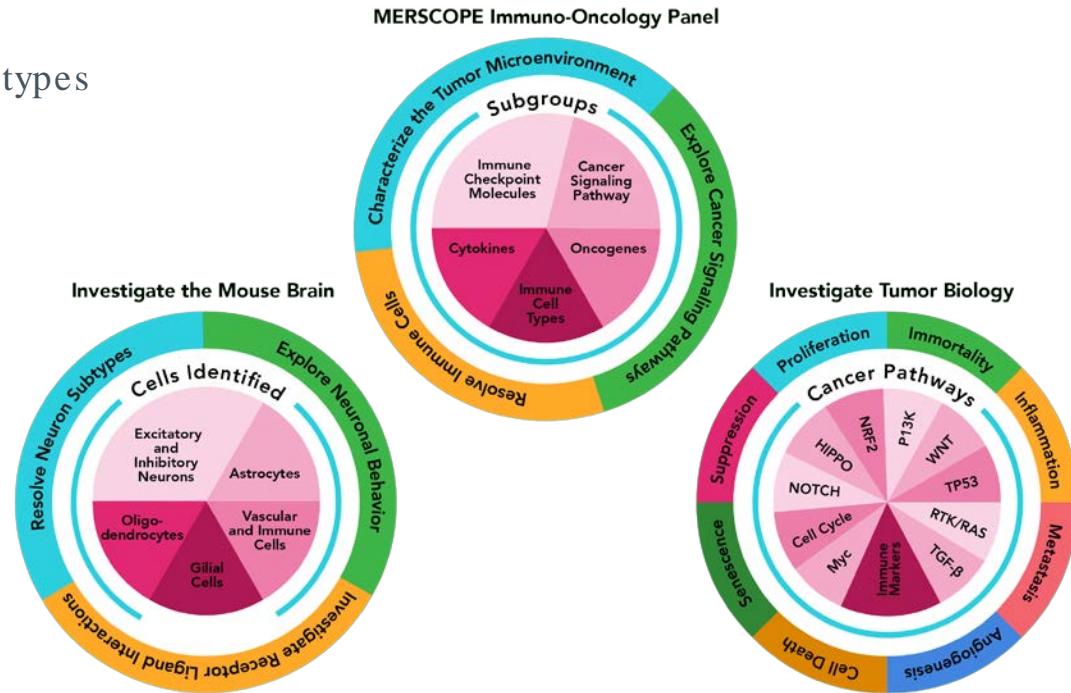
Depending on the biological question !

Depending of your specific scientific focus

- Identify all major cell types, resolve cell subtypes
- Explore functional information
- Investigate interactions between cell types
- Ligand-receptors analysis
- Explore canonical signaling pathways
- Profile immune checkpoint molecules
- ...

Satisfy technological system limitations

- Number of targets available
- Range of gene targets expression
- Total gene targets expression
- Have a nice budget to spend (~15 k€)
- ...



<https://portal.vizgen.com/>

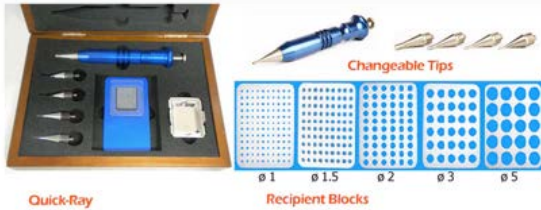
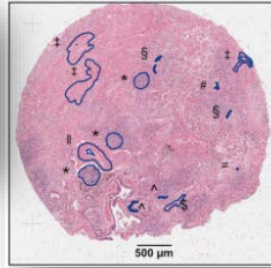
<https://cloud.10xgenomics.com/xeniumpanel-designer>

Experimental design

Take advantage of the large imaging area

Image-based spatial transcriptomics identifies molecular niche dysregulation associated with distal lung remodeling in pulmonary fibrosis

Annika Vannan^{1,4}, Ruqian Lyu^{2,3,8}, Arianna L. Williams¹, Nicholas M. Negretti⁴, Evan D. Mee¹, Joseph Hirsh⁴, Samuel Hirsh⁴, David S. Nichols⁵, Carla L. Calvi⁵, Chase J. Taylor⁶, Vasilii V. Polosukhin⁶, Ana PM Serezani⁷, A. Scott McCall⁸, Jason J. Gokey⁹, Heejung Shim³, Lorraine B. Ware^{5,7}, Matthew J. Bacchetta⁸, Ciara M. Shaver⁵, Timothy S. Blackwell^{5,9,10}, Rajat Walia¹¹, Jennifer MS Sucre^{4,9}, Jonathan A. Kropski^{5,9,10,8}, Davis J McCarthy^{2,3,8}, Nicholas E. Banovich^{1,8,*}



<https://www.ihcworld.com/products/Quick-Ray-Mold.htm>

Raymond Yip @rkhyip · Mar 4

Oh boy.. how lucky we are to have a histologist that can do this kind of magic ✂️ #xenium

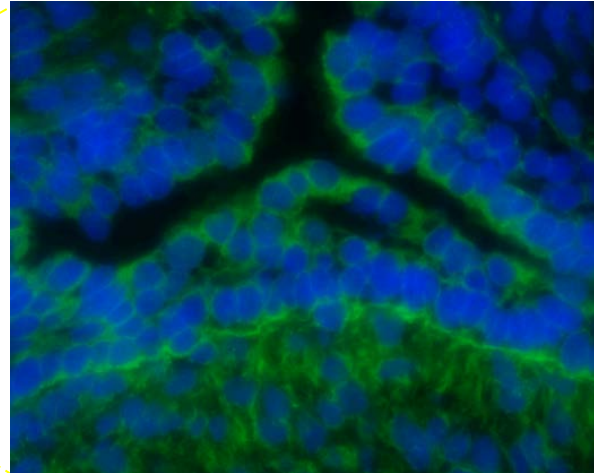
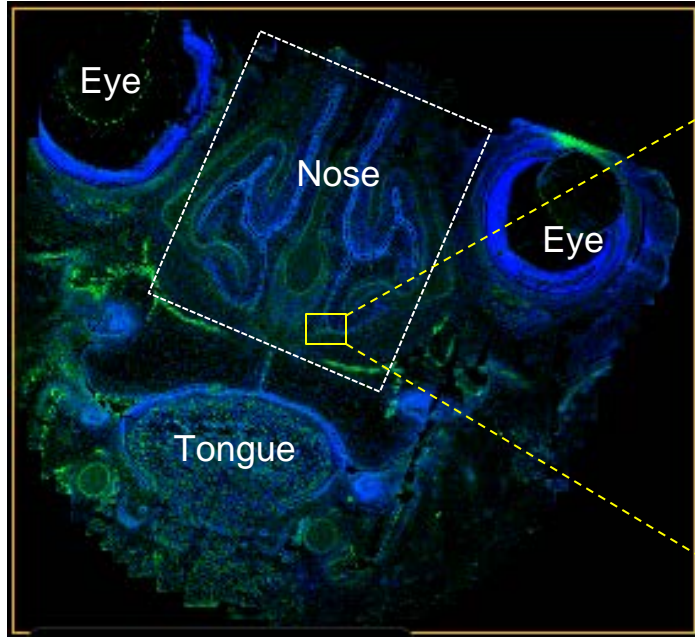


Each run is around 5 k€

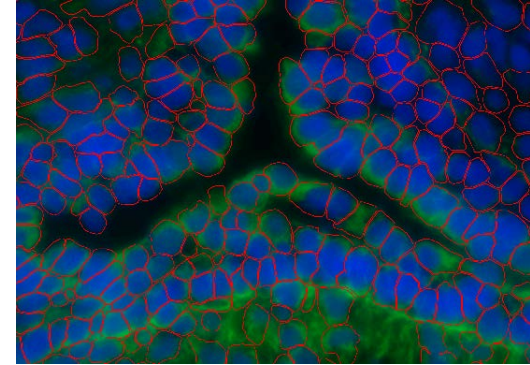
multiplexing helps removing batch effect and increase replicates for a robust statistical analysis

MERSCOPE data acquisition (7 z -stack)

Staining for cell segmentation



DAPI channel
Cell boundaries channel



Article | [Published: 14 December 2020](#)

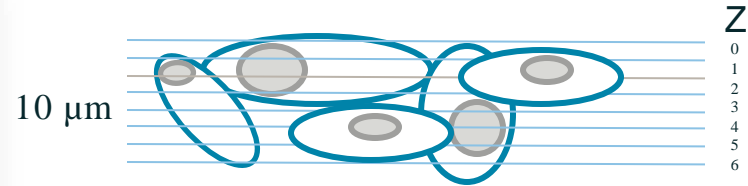
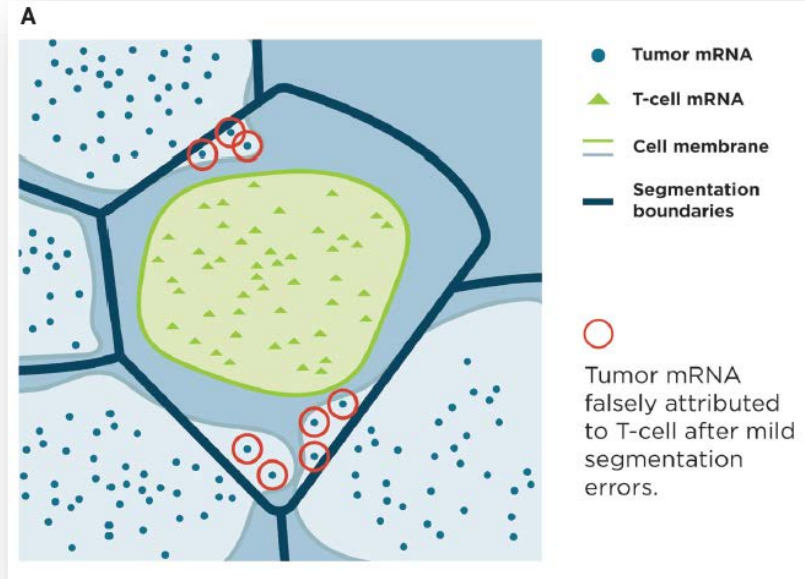
Cellpose: a generalist algorithm for cellular segmentation

[Carsen Stringer](#), [Tim Wang](#), [Michalis Michaelos](#) & [Marius Pachitariu](#) 

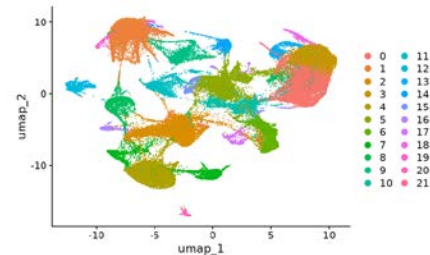
[Nature Methods](#) **18**, 100–106 (2021) | [Cite this article](#)

Cell segmentation is crucial

Cell x gene matrix purity and good subsequent biology



3D segmentation required, actually not used, 2D segmentation per Z then harmonizing and summing the detected transcripts for all Z into the harmonized segmentation mask (nuclei of full cell)



Vizgen Postprocessing tool

Run on Merscope standard analysis output folder


The Vizgen Post-processing Tool (VPT) enables users to reprocess and refine the single-cell results of MERSCOPE experiments. VPT is a command line tool that emphasizes scalable, reproducible analysis, and can be run on a workstation, a cluster, or be deployed in a cloud computing environment.

Features

- Perform cell segmentation
 - Reproduce standard Vizgen segmentation options
 - Perform reproducible custom segmentation
- Import cell segmentation from other tools
 - Supports geojson and hdf5 formats
- Regenerate single cell data with new segmentation
 - Cell by gene matrix
 - Cell spatial metadata
 - Image intensity in each cell
 - Update MERSCOPE Vizualizer file (vzg)
- Image format conversion
 - Convert large tiff files to single or multi-channel Pyramidal OME-TIFF files
- Nextflow compatible, example pipeline provided

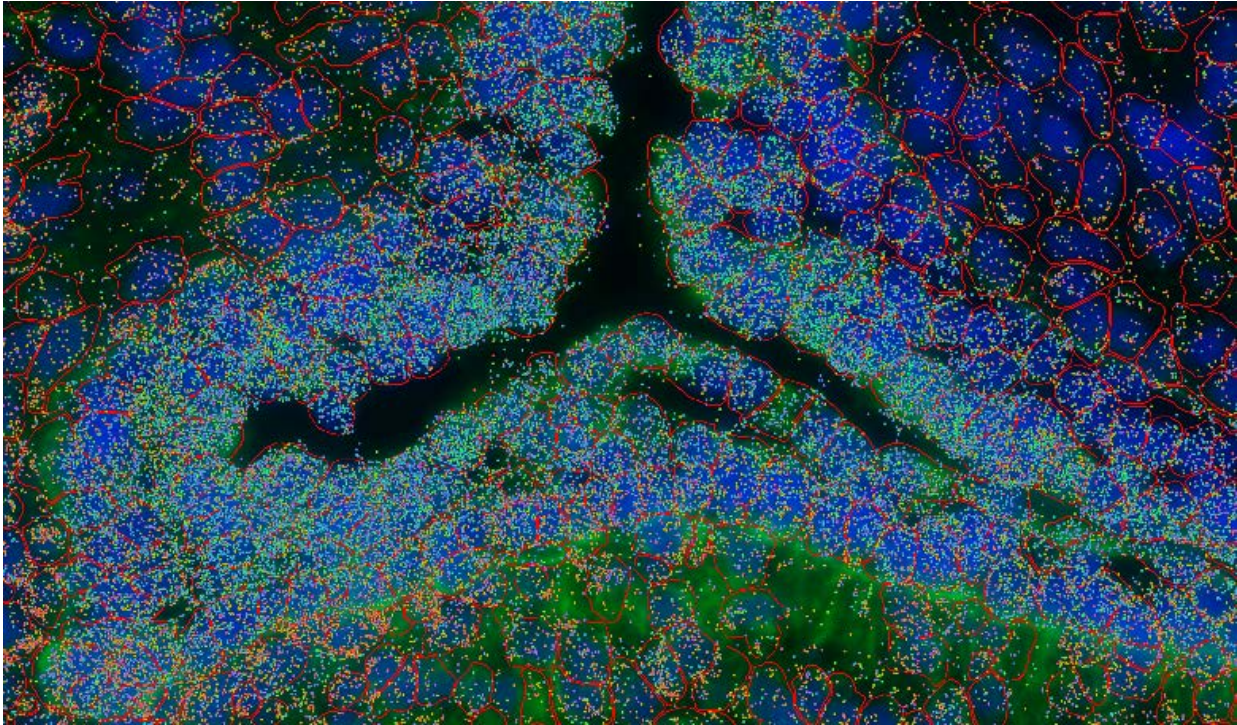


Search or jump to...

 Vizgen / vizgen-postprocessing

MERSCOPE raw data

Cell x genematrix

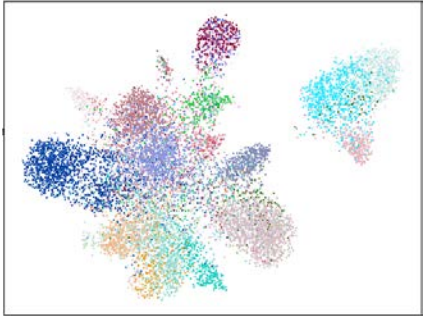


Gene-level matrix

100k's cells

Ctla	5	4	6	7	1	4	3	9	5	5	.	1	4	3	6	4	.	7	5	2	4
Myl6	5	2	5	1	2	4	13	2	5	2	4	4	1	4	8	4	2	3	3	1	1
Pkm	3	2	1	.	.	8	3	9	4	10	5	1	.	4	12	5	1	3	9	1	7
Tecr	3	1	5	2	4	6	5	9	6	3	2	2	1	4	7	1	1	1	3	2	8
Meis2	8	29	3	.	24	6	6	21	25	16	6	1	.	2	29	.	.	6	18	.	10
...																					

1,000 Genes



MERSCOPE raw data

Standard Merscope output files

```
000-giacobini/000-data/202304281610_20230428-HuDeCa-Giacobini-PGW9-2-3A_VMSCO6001/region_0:
```

```
total 13G
```

```
-rw-r--r-- 1 lebrigand solid 11G 3 mai 2023 202304281610_20230428-HuDeCa-Giacobini-PGW9-2-3A_VMSCO6001_region_0.vzq  
-rw-r--r-- 1 lebrigand solid 447M 3 mai 2023 cell_boundaries.parquet  
-rw-r--r-- 1 lebrigand solid 83M 3 mai 2023 cell_by_gene.csv  
-rw-r--r-- 1 lebrigand solid 46M 3 mai 2023 cell_metadata.csv  
-rw-r--r-- 1 lebrigand solid 2,1G 3 mai 2023 detected_transcripts.csv  
drwxr-xr-x 2 lebrigand solid 4,0K 3 mai 2023 images  
-rw-r--r-- 1 lebrigand solid 855K 3 mai 2023 summary.png
```

```
0,9K 3 mai 2023 manifest.json  
227 3 mai 2023 micron_to_mosaic_pixel_transform.csv  
6,6G 3 mai 2023 mosaic_cellbound2_z2.tif  
6,6G 3 mai 2023 mosaic_API_z2.tif
```

0,5-2 Tb

```
1 sdata.shapes['P11_region_0_polygons']  
✓ 0.0s  
  
geometry  
3613852200009100002 POLYGON ((4702.379 302.065, 4704.864 304.790, ...  
3613852200009100005 POLYGON ((4709.067 304.517, 4709.887 305.673, ...  
3613852200009100006 POLYGON ((4767.177 301.994, 4767.475 303.202, ...  
3613852200009100007 POLYGON ((4723.735 306.300, 4723.939 307.090, ...  
3613852200009100008 POLYGON ((4764.231 307.210, 4764.805 312.376, ...
```

```
1 sdata.table.layers['counts']  
✓ 0.0s  
  
array([[0, 1, 1, ..., 1, 0, 0],  
       [0, 1, 0, ..., 2, 0, 0],  
       [0, 3, 4, ..., 0, 0, 0],  
       ...,  
       [0, 0, 0, ..., 0, 0, 0],  
       [0, 0, 0, ..., 0, 0, 0],  
       [0, 2, 6, ..., 4, 0, 0]])
```

```
1 sdata.table.obs  
✓ 0.1s  
  
fov volume center_x center_y min_x min_y max_x max_y anisotropy  
3613852200009100002 NaN 841.761444 4707.689677 298.299088 4702.379316 292.031852 4713.603506 305.207677 1.990932  
3613852200009100005 NaN 762.740701 4713.532399 299.961526 4709.066587 293.764119 4718.738288 306.280330 1.812676  
3613852200009100006 NaN 1243.613805 4774.139602 300.963756 4767.176971 293.701627 4780.340526 307.566412 1.069031  
3613852200009100007 NaN 391.378917 4727.286292 305.141647 4723.734863 301.881750 4730.984004 308.291885 1.194130  
3613852200009100008 NaN 680.804739 4768.106763 308.764922 4764.065981 303.609728 4772.968368 313.933532 1.204513
```

```
1 sdata.points['P11_region_0_transcripts'].compute()  
✓ 15.7s  
  
x y gene Unnamed: 0 global_z transcript_id fov barcode_id cell_id  
0 76.288345 6615.9116 CFTR 138 0.0 ENST00000003084 0 0 -1  
1 -0.706320 6656.7720 CFTR 480 0.0 ENST00000003084 0 0 -1  
2 56.071490 6741.6104 CFTR 1284 0.0 ENST00000003084 0 0 3613852200420100110  
3 -6.401468 6764.1587 CFTR 1479 0.0 ENST00000003084 0 0 -1  
4 12.010611 6604.1650 CFTR 1808 1.0 ENST00000003084 0 0 3613852200390100641
```

MERSCOPE data analysis

Data analysis workflows

Seurat 5.0.1 | Install | Get started | Vignettes | Extensions | FAQ | News | Reference | Archive

SEURAT

stable

Search docs

GENERAL

- Installation
- API
- Classes
- Release Notes
- References

GALLERY

- Tutorials
- Examples

SpatialData

Simplify infrastructure with MongoDB Atlas, the leading developer data platform

All by @theislab

Seurat v5

We are excited to release Seurat v5! To Ins new features and functionality:

Satija'slab, NYGC

Theis'slab, h

(A) storage format

- tables
- points
- shapes
- labels
- images

OME

NGFF

(C) convenient readers

Xenium

Visium

Cytos

IMC

(D) interactive annotation and visualization

(B) python library

spatially-aligned datasets

spatial queries

transforms

- translate
- scale
- rotate
- chain

observation aggregation

(E) deep learning interface

PyTorch

(F) ecosystem integration

MONAI

Giotto

Edit on GitHub

Spatial transcriptomic and proteomic technologies have provided new opportunities to investigate cells in their native microenvironment. Here we present Giotto, a comprehensive and open-source toolbox for spatial data analysis and visualization. The analysis module provides end-to-end analysis by implementing a wide range of algorithms for characterizing tissue composition, spatial expression patterns, and cellular interactions. Furthermore, single-cell RNAseq data can be integrated for spatial cell-type enrichment analysis. The visualization module allows users to interactively visualize analysis outputs and imaging features. To demonstrate its general applicability, we apply Giotto to a wide range of datasets encompassing diverse technologies and platforms.

Example Functionalities

monkeybread

Edit on GitHub

monkeybread

monkeybread is a Python package that facilitates the analysis of single-cell resolution spatial transcriptomics data such as those generated by the MERSCOPE or Xenium platforms.

monkeybread provides tools that enable:

- Identification of cellular niches (i.e., regions with distinct compositions of cell types)
- Visualization of density of cell types across the tissue
- Statistical tests for testing for colocalization between cell types
- Statistical tests and visualization for ligand-receptor co-expression between neighboring cells

monkeybread operates on datasets stored as AnnData objects and thus, can be integrated into pipelines that use packages from the scverse such as scanpy or squidpy.

monkeybread was developed at Immunitas Therapeutics.

CS

Product | Solutions | Open Source | Pricing

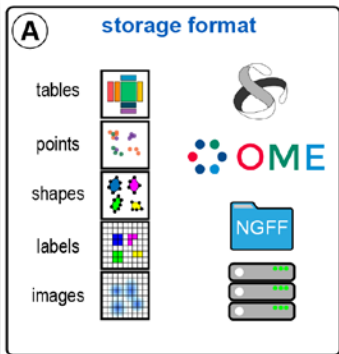
cobioda / scispy Public

Scverse ecosystem, Oliver Stegle & Fabian J. Theis

<https://github.com/cobioda/scispy/>

spatialdata data architecture

Scverse ecosystem



```
1 sdata
✓ 2.1s

SpatialData object with:
├── Images
│   └── 'P11_region_0_z2': MultiscaleSpatialImage
├── Points
│   ├── 'P11_region_0_transcripts': DataFrame with shape: (22, 2)
│   └── 'celltypes': DataFrame with shape: (22, 1)
├── Shapes
│   ├── 'P11_region_0_polygons': GeoDataFrame with shape: (22, 2)
│   ├── 'anatomical': GeoDataFrame shape: (22, 2)
│   └── 'arteries': GeoDataFrame shape: (22, 2)
└── Table
    └── AnnData object with n_obs × n_vars = 22 × 10
        obs: 'fov', 'volume', 'center_x', 'center_y', 'mean', 'std'
        uns: 'leiden', 'leiden_colors', 'neighbors'
        obsm: 'X_pca', 'X_umap', 'blank', 'spatial'
        varm: 'PCs'
        layers: 'counts', 'scaled'
        obsp: 'connectivities', 'distances': AnnData object with coordinate systems:
            └── 'microns', with elements:
                P11_region_0_z2 (Images), P11_region_0_z2 (Points)
```

spatialdata-plot

Rapidly visualise different modalities

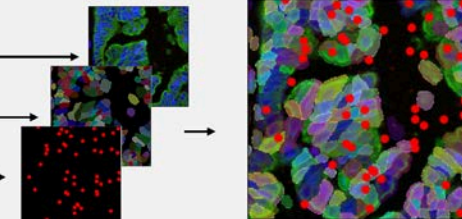
cosmx_sdata

`.pl.render_images(...)`

`.pl.render_labels(...)`

`.pl.render_points(...)`

`.pl.show(...)`



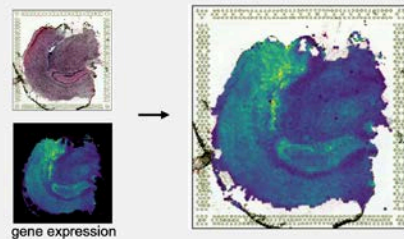
Enrich visualisation with metadata

visium_sdata

`.pl.render_images(...)`

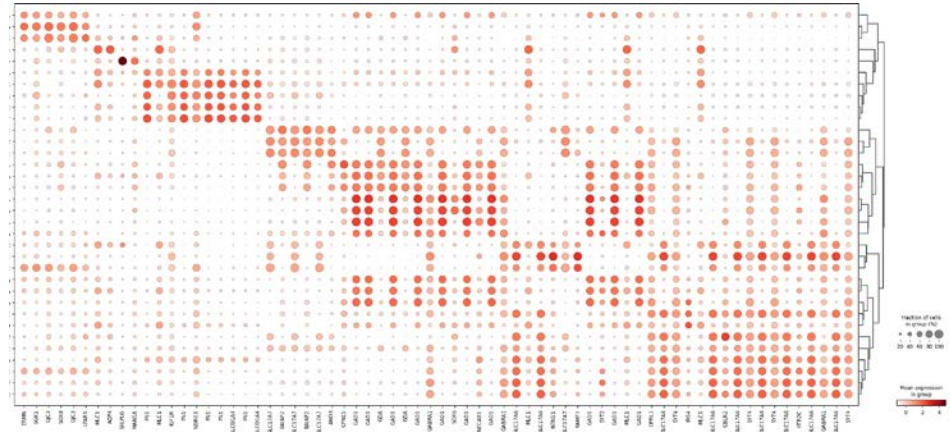
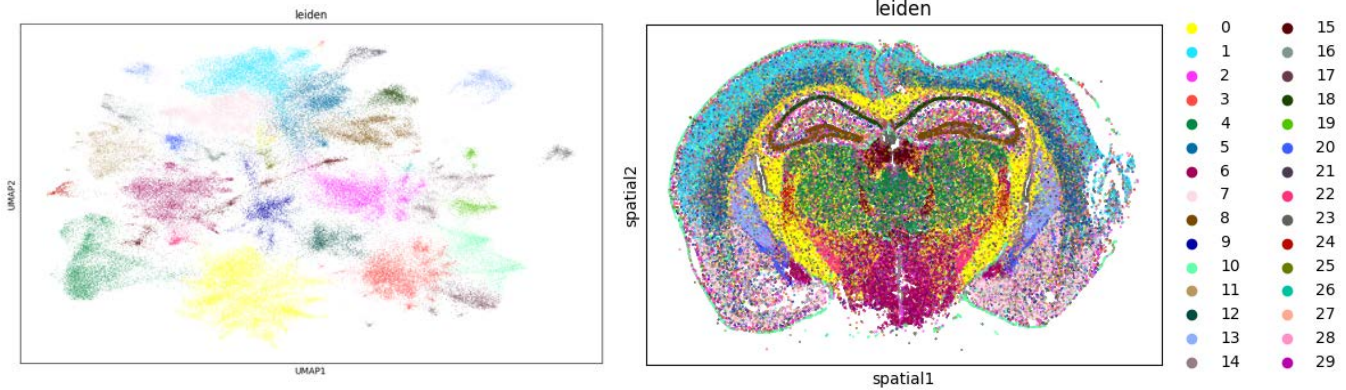
`.pl.render_shapes(
 color_key = "mt-Cytb"
>)`

`.pl.show(...)`



Cell type labeling

Directly from your target gene panel statistical analysis




Mouse coronal brain section
135 merfish gene panel

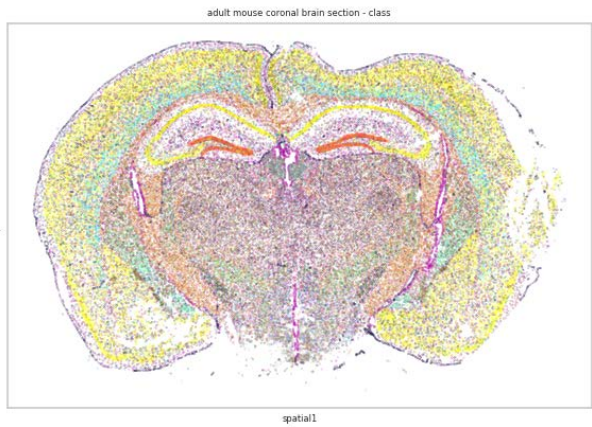
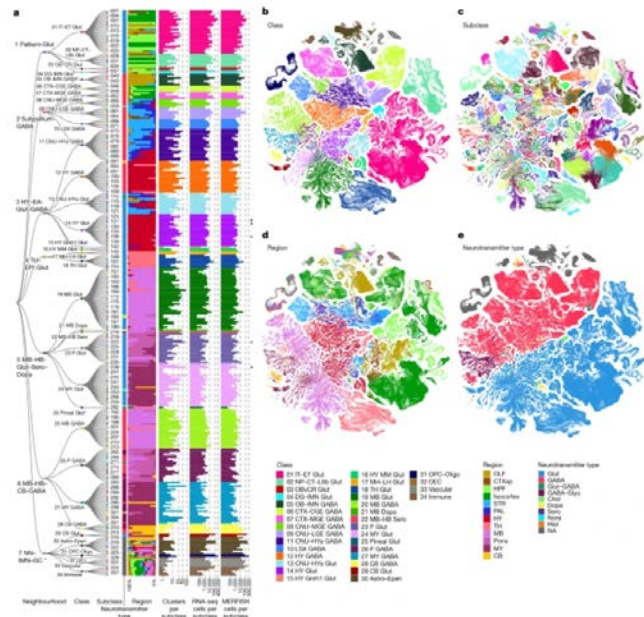
Cell type labeling using annotation transfer

Based on a reference singlecell dataset using SCANVI

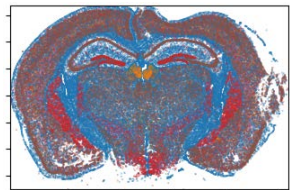
Article | [Open access](#) | Published: 13 December 2023

A high-resolution transcriptomic and spatial atlas of cell types in the whole mouse brain

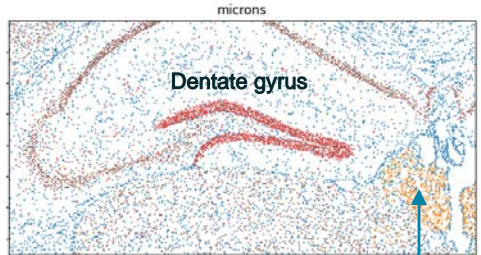
Zizhen Yao , Cindy T. J. van Velthoven, Michael Kunst, Meng Zhang, Delissa McMillen, Changkyu Lee, Won Jung, Jeff Goldy, Aliya Abdelhak, Matthew Aitken, Katherine Baker, Pamela Baker, Eliza Barkan, Darren Bertagnoli, Ashwin Bhandiwad, Cameron Bielstein, Prajal Bishwakarma, Jazmin Campos, Daniel Carey, Tamara Casper, Anish Bhaswanth Chakka, Rushil Chakrabarty, Sakshi Chavan, Min Chen, ... Hongkui Zeng



Transfer based on 132 genes



- Chol
- Dopa
- GABA
- GABA-Glyc
- Glut
- Glut-GABA



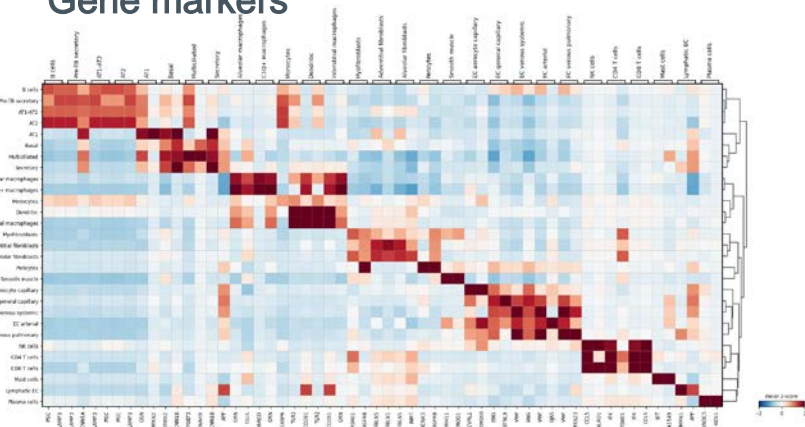
- Chol
- Dopa
- GABA
- GABA-Glyc
- Glut
- Glut-GABA

Medial Habenula
Cholinergic System in
Addiction and Emotion
Associated Behaviors

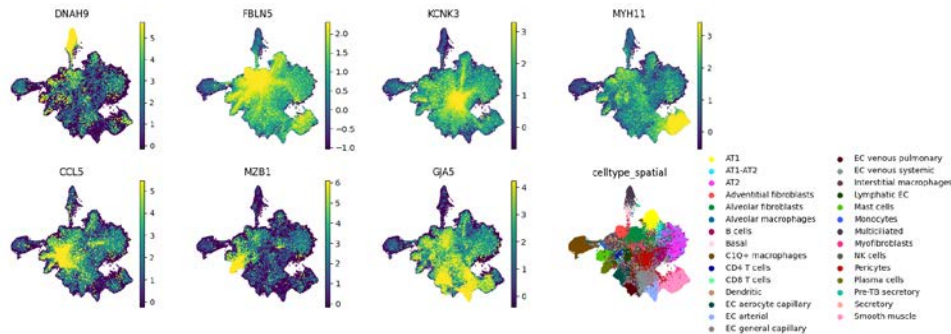
Standard single -cell data analysis

Scanpy package

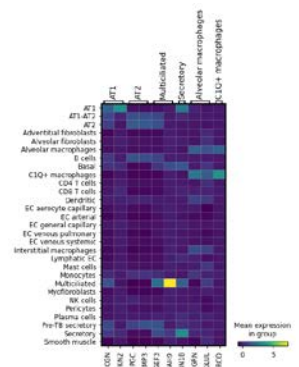
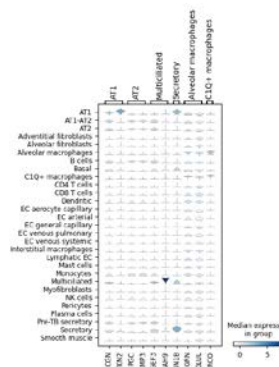
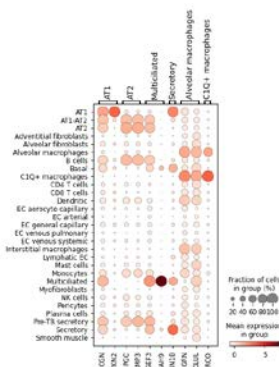
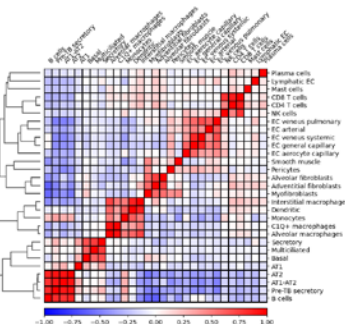
Gene markers



Gene markers

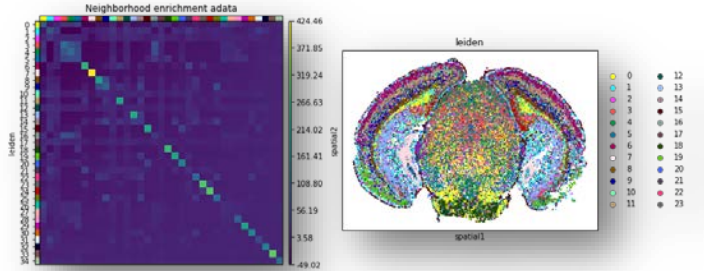


Cell type correlation



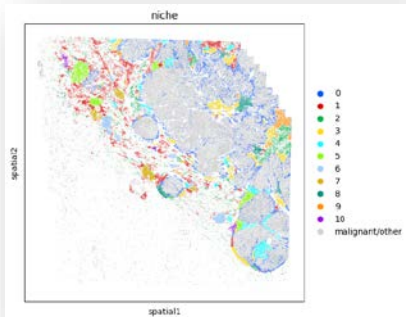
Standard single -cell spatial data analysis

New vast area for computationalbiologists (just like single-cell 5 years ago !)



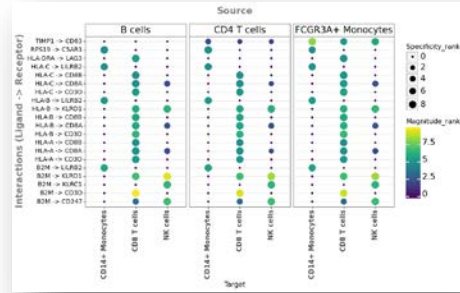
Neighbors enrichment analysis

Test if cells belonging to 2 clusters are close to each other more often than expected (**co-occurrenceprobability**)



Cellular niches analysis

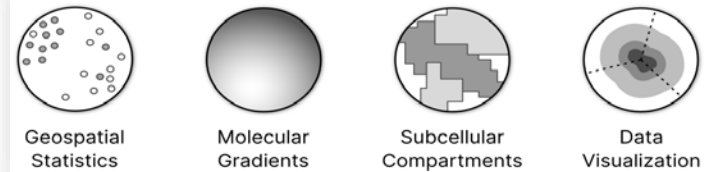
for each cell, we count the number of neighbors that are of each cell type thus forming a “neighborhood profile” vector of length C, where C is the number of cell types. We then cluster all neighborhood profiles and call each cluster a “niche”.



Ligand-Receptor analysis

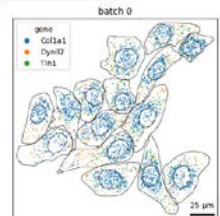
- Need to be in gene panel !!
- CellPhoneDB[Efremova et al., 2020]
- Omnipath[Türeiet al., 2016].

Machine Learning & Statistical Analysis



Sub-cellular exploration

Bento is a Python toolkit for performing subcellularanalysis of spatialtranscriptomics data.



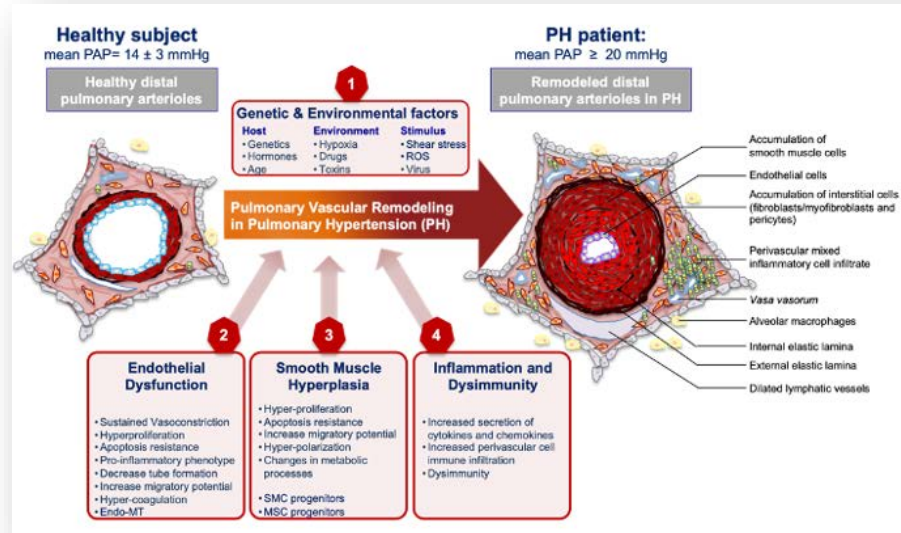
03

Ongoing projects

PAH : Pulmonary Arterial Hypertension

A rare vascular disorder

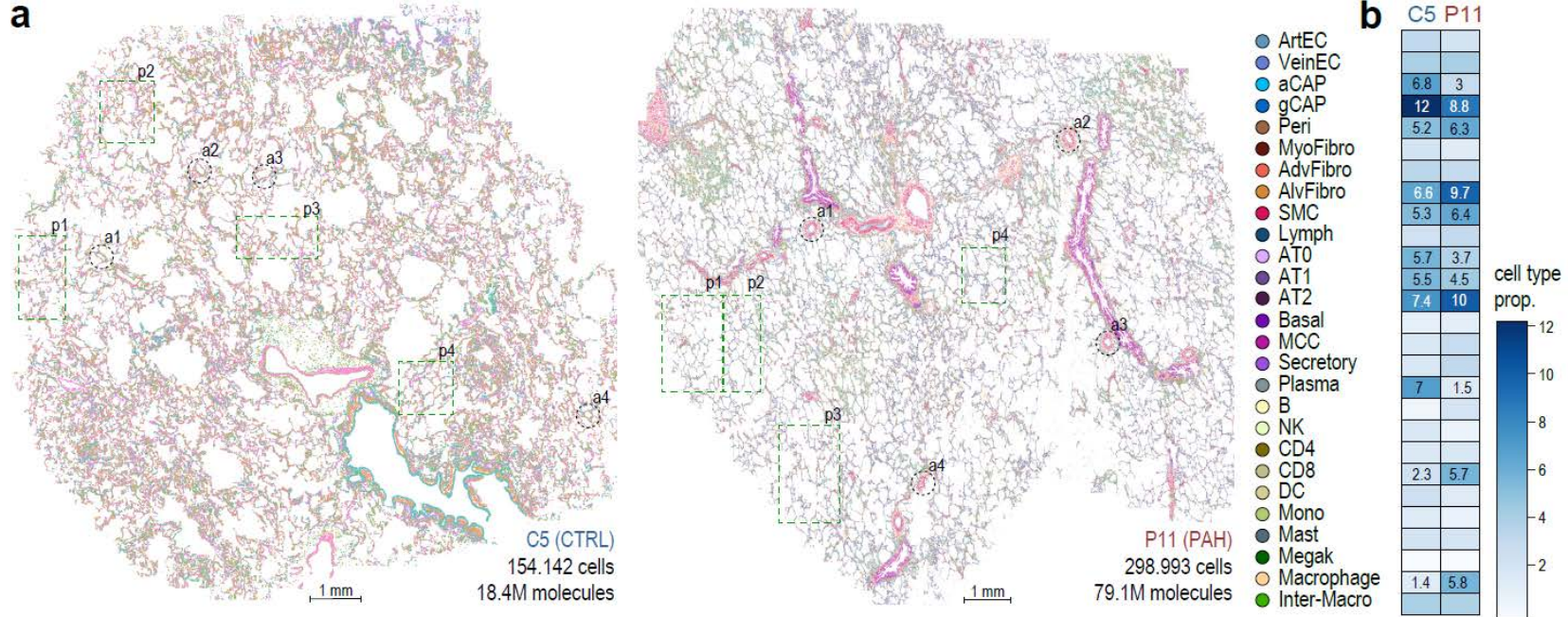
Characterized by the presence of occluded pulmonary arterioles resulting from the proliferation of pulmonary artery endothelial cells (PAECs), pulmonary artery smooth muscle cells (PASMCs) and fibroblasts, which leads to right heart hypertrophy and eventual cardiac failure



- Defined by a mean pulmonary arterial pressure >20mmHg
- More frequent in women to men(2:1 to 4:1)
- Different origins:
 - IPAH (idiopathic or sporadic cases),
 - HPAH (heritable case family history) 6-10% monogenic autosomal-dominant - 14% ♂, 42% ♀
 - APAH (associated forms), anorexigens / liver / congenital heart / connective tissue disease

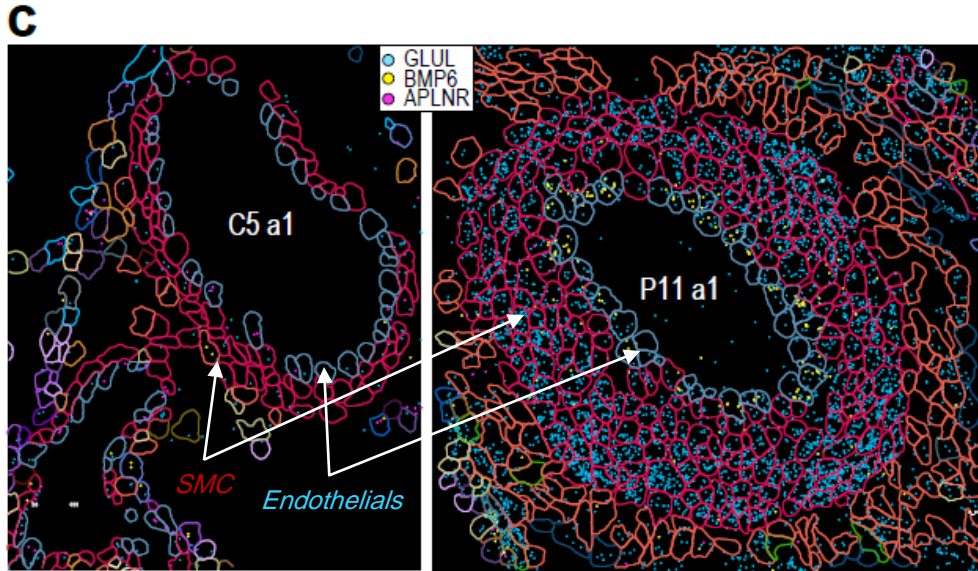
PAH : Pulmonary Arterial Hypertension

A rare vascular disorder

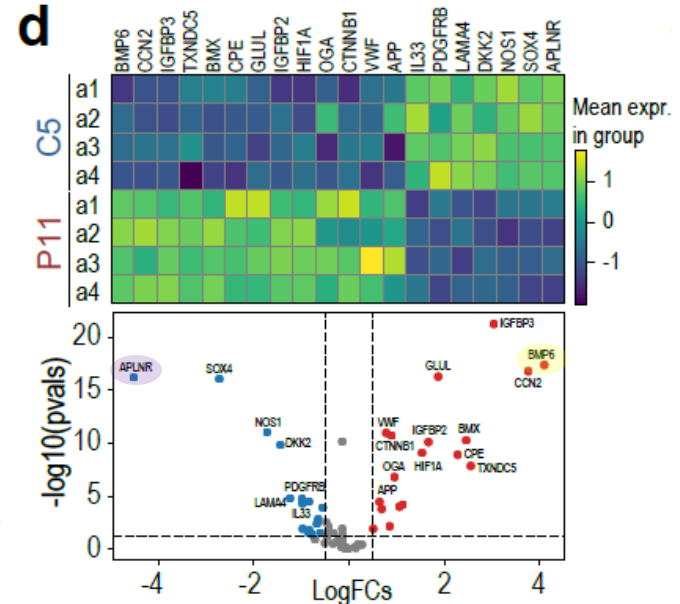


PAH : Pulmonary Arterial Hypertension

A rare vascular disorder



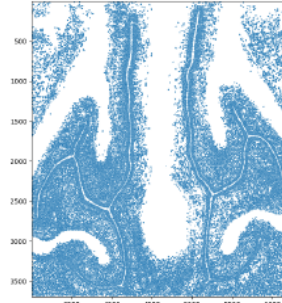
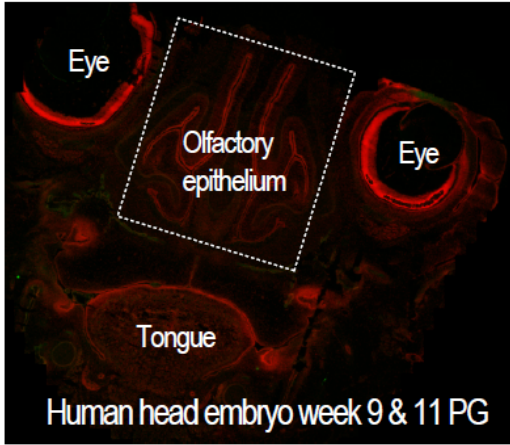
GLUL up in PAH artEC SMC
BMP6 up in PAH artEC
APLNR down in PAH artEC



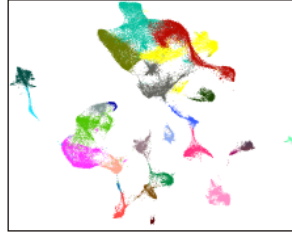
Artery Endothelial Cells
pseudo-bulk analysis

HuDeCa project

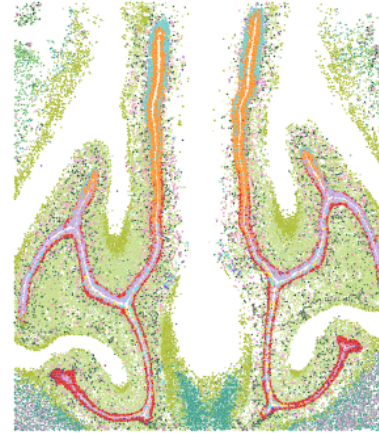
human fetal nose from 7 to 12 post-conceptual weeks (PCW) at singlecell resolution



Extraction
Rotation
Segmentation



Automatic classification
using snRNA-seq



Spatial data exploration

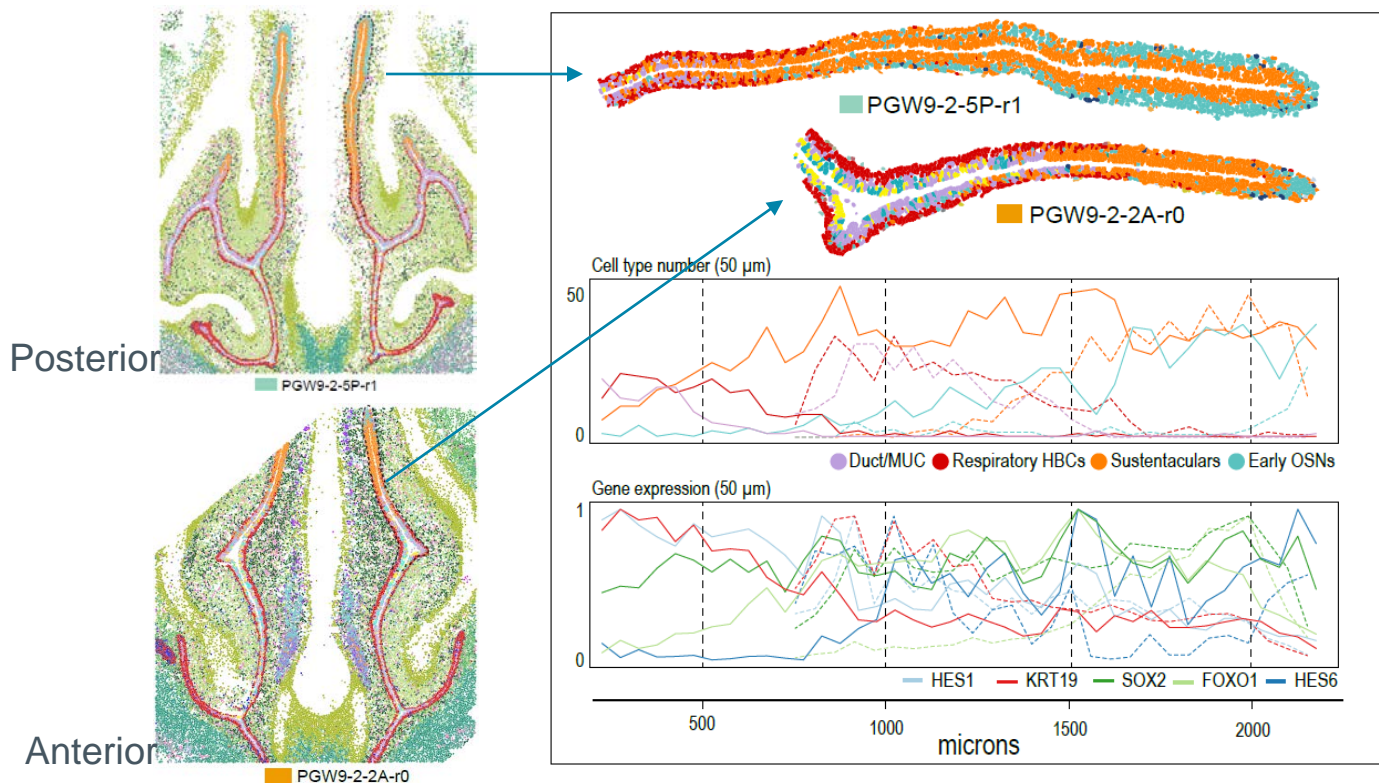
Cell types

- Cartilage
- Stromal
- Lymphatic EC
- Vascular EC
- Pericytes
- Respiratory HBCs
- Olfactory HBCs
- Duct/MUC
- Multiciliated
- Deuterosomal
- Sustentaculars
- GBCs
- Early OSNs
- Excitatory neurons
- Inhibitory neurons
- GnRH neurons

HuDeCa project

human fetal nose from 7 to 12 post-conceptual weeks (PCW) at singlecell resolution

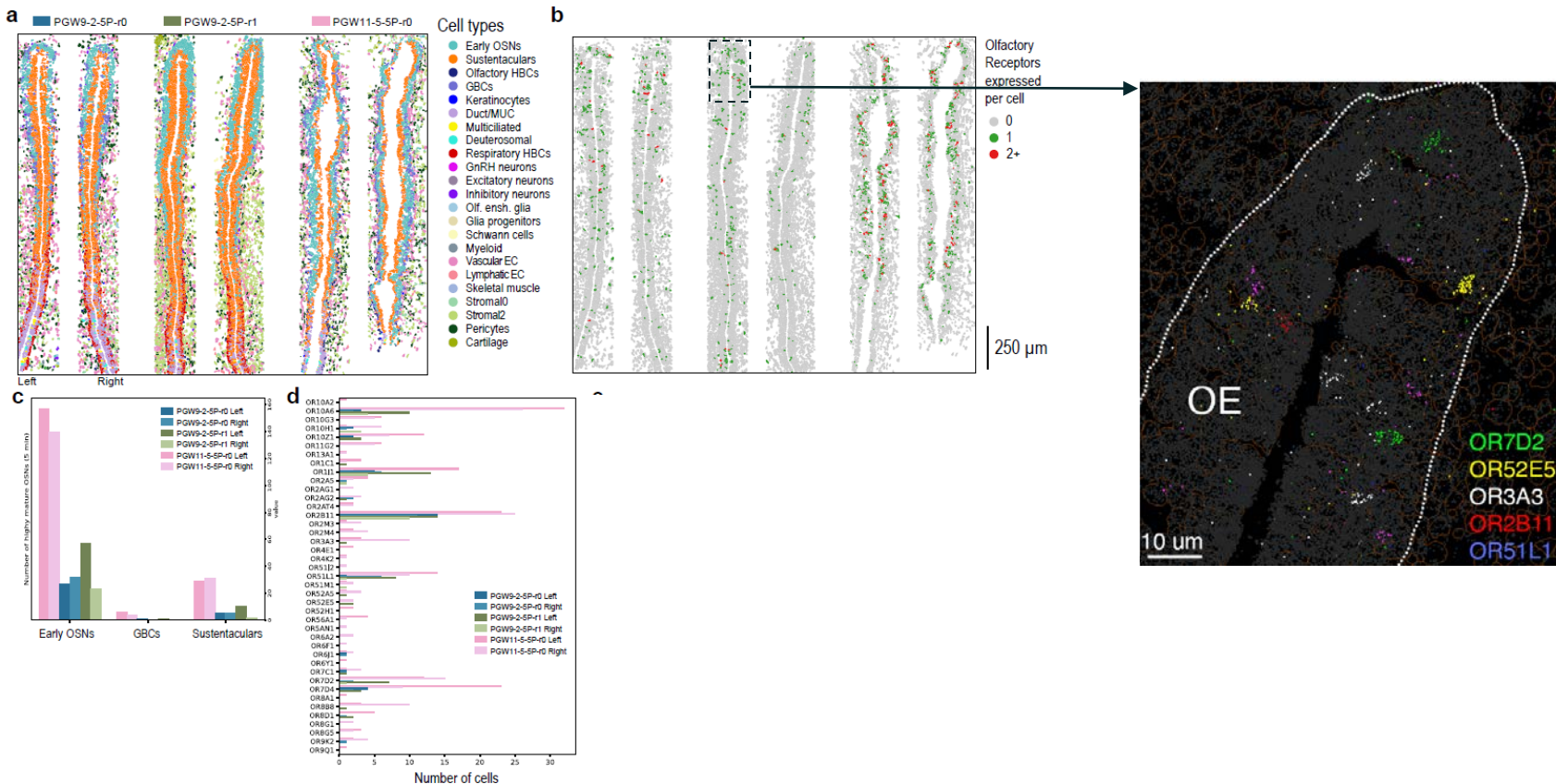
Posterior versus Anterior Olfactory epithelium comparison



HuDeCa project

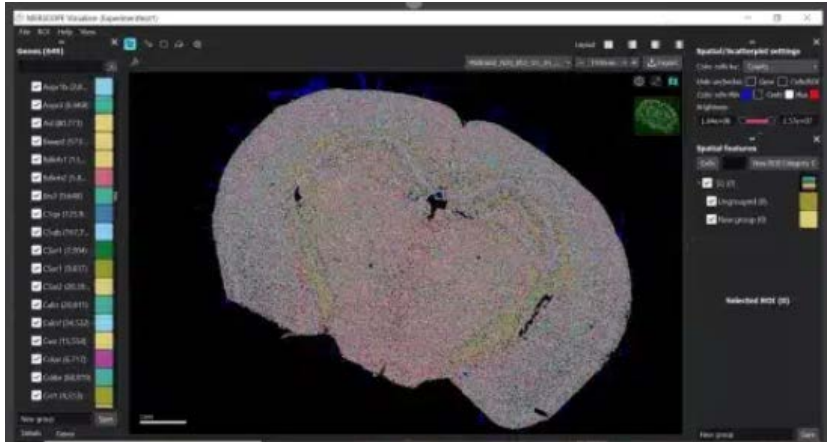
human fetal nose from 7 to 12 post-conceptional weeks (PCW) at singlecell resolution

Posterior Olfactory epithelium Week9 versus week11 comparison

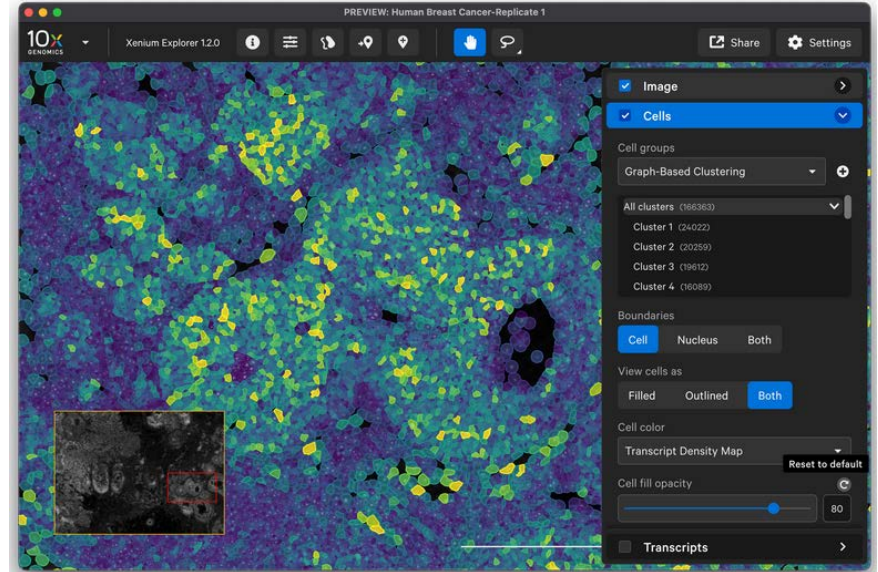


Spatial transcriptomics explorer

MERSCOPEVizualizersoftware



Xeniumexplorer



https://github.com/quentinblampey/spatialdata_xenium_explorer

Acknowledgments

Institut de Pharmacologie Moléculaire et Cellulaire



Pascal Barbry's Lab (IPMC, CNRS France)

- Virginie Magnone
- G radine Rios
- Marie Couralet
- Valentine Freschi
- Marie-Jeanne Arguel



CoBiODA IPMC bioinformatics

- K vin Lebrigand
- Marin Truchi
- Morgane Fierville
- Eamon McAndrew

