**Introducing …**



**The new bioinformatics hub of IPMC !**

# Who and where are we ?

Members

## Committed to support research teams and facilities of IPMC

- Kevin Lebrigand, IRHC CNRS

- Marin Truchi, IR UniCA

## Carrying out their own project

- Maryem Ben Kedher, Post-doc (BM)

- Anna Diamant, Phd Student (BM)

- Eamon Mcandrew, Phd Student (PB)

## IPMC2 R-1 B07, an optimal working environment :
- to group bioinformaticians recruited by teams and facilities
- to share knowledge, ideas, and resources
- to train and mentor people
- discuss about your project and your results

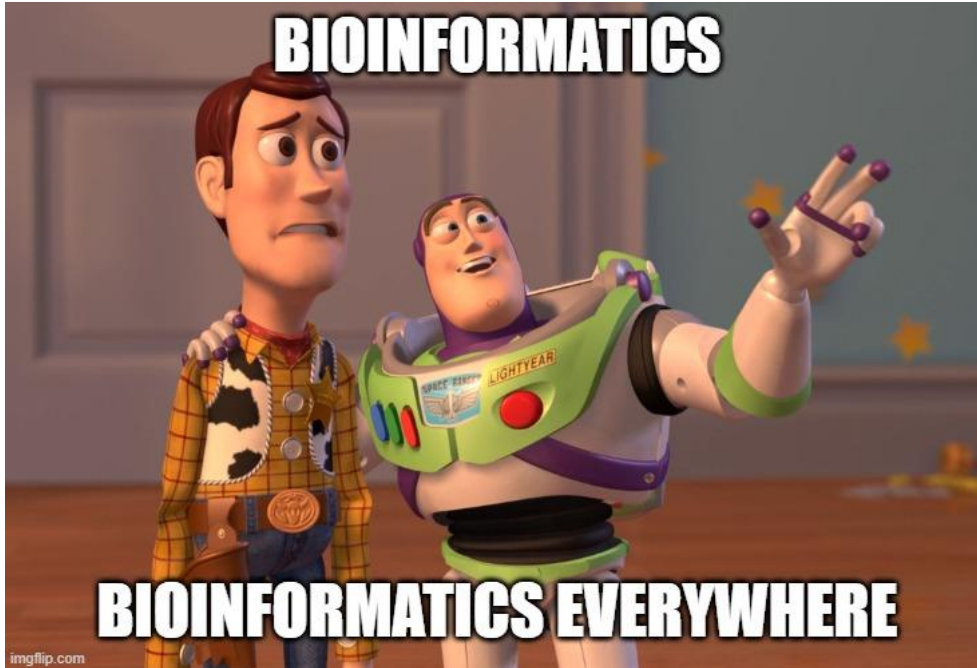# A bioinformatics hub … For what purpose?

Bioinformatics is a field of study that uses computation to extract knowledge from biological data



Nature Methods « Method of the year » :

2022 : long-read sequencing

2021 : protein structure prediction

2020 : spatial transcriptomics

2019 : single-cell multi-omics

2018 : imaging in freely behaving animals

2017 : organoids

2016 : epitranscriptome analysis

2015 : single-particle cryo-electron microscopy

2014 : light-sheet fluorescence microscopy

2013 : single-cell sequencing

2012 : targeted proteomics

➢ Growing need of bioinformatics support for processing biological data

# Our missions

Activities of the bioinformatics hub

**Reinforce bioinformatics expertise and providing support for quantitative biology projects by the IPMC's research teams and technical platforms**

- Setup standardized workflows to analyse quantitative biology data

- Support experimental design setup, funding requests (DMP) and writing of publication (figures, methods, data submission)

- Training of IPMC personnel in bioinformatics (best practices and guidelines for data processing, management and analysis)

- Methodological development

- Constant technological watch in the priority technological areas defined by the institute

- Support and promote bioinformatics at IPMC (formations, internal seminars)

- Development of an IT infrastructure and integration with local, regional and national networks (4D-OMICS, ODIN …)
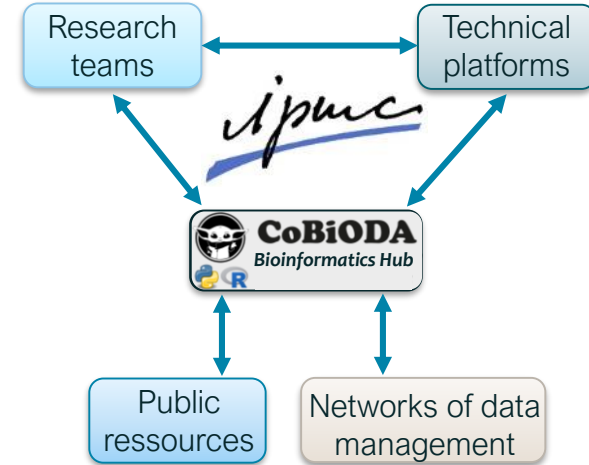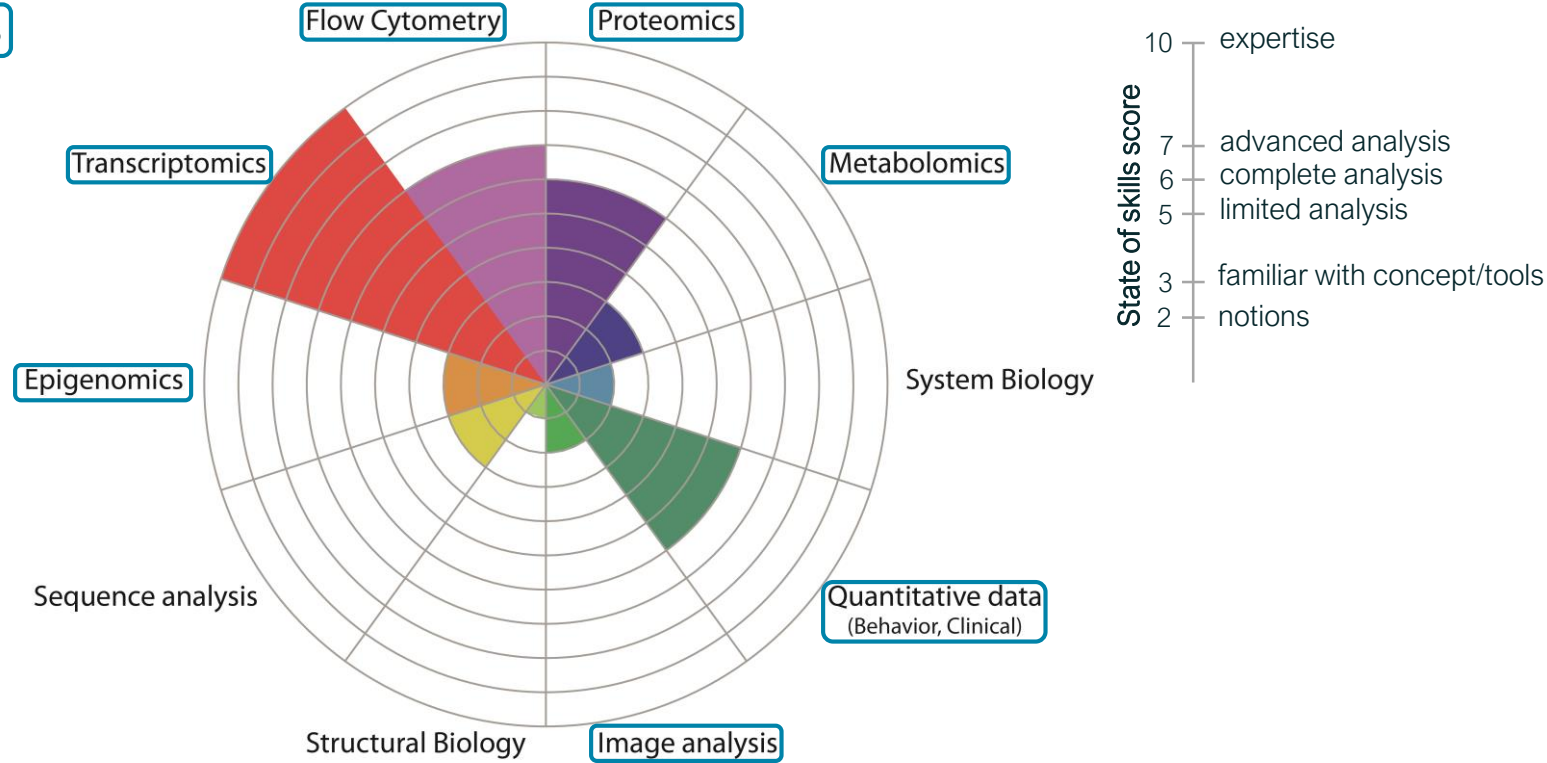
# Our scope of action
… within the Bioinformatics spectrum

Bioinformatics is a field of study that uses computation to extract knowledge from biological data



Institute priorities

State of skills score:
- 10 — expertise
- 7 — advanced analysis
- 6 — complete analysis
- 5 — limited analysis
- 3 — familiar with concept/tools
- 2 — notions

Categories: Flow Cytometry, Proteomics, Metabolomics, System Biology, Quantitative data (Behavior, Clinical), Image analysis, Structural Biology, Sequence analysis, Epigenomics, Transcriptomics

# Organisation

Example of operating mode

## Service request

- Definition of the primary biological questions to be addressed
- Discussion on technology and experimental design
- Feasibility study: human resources, infrastructure, project timeline, deliverables

## Data acquisition

- In collaboration with IPMC technical platforms
- Downloading of public datasets
- Implementation of analysis workflows (methodological developments)

## Exploratory analysis

- Meetings about project progress
- Definition of secondary biological questions
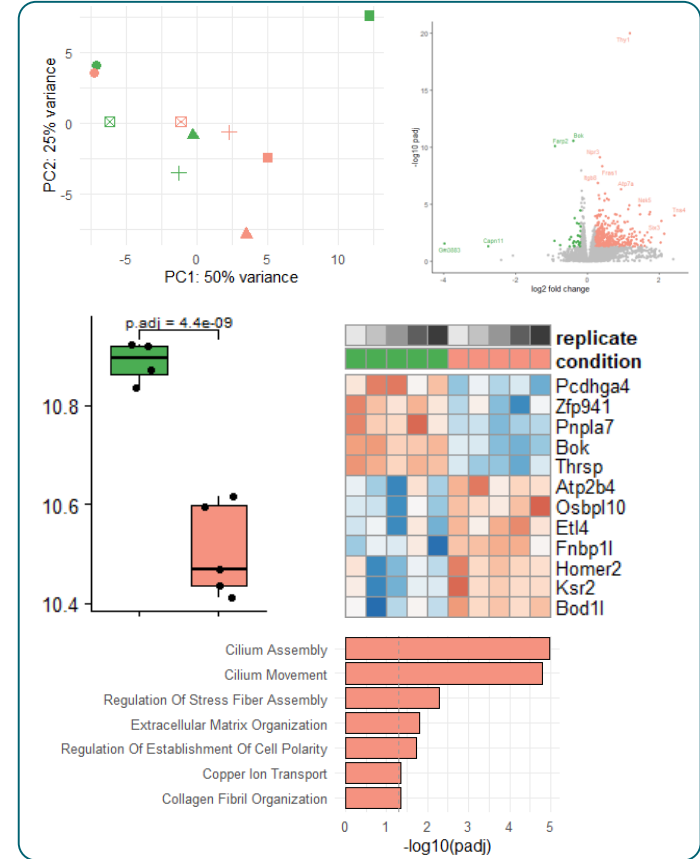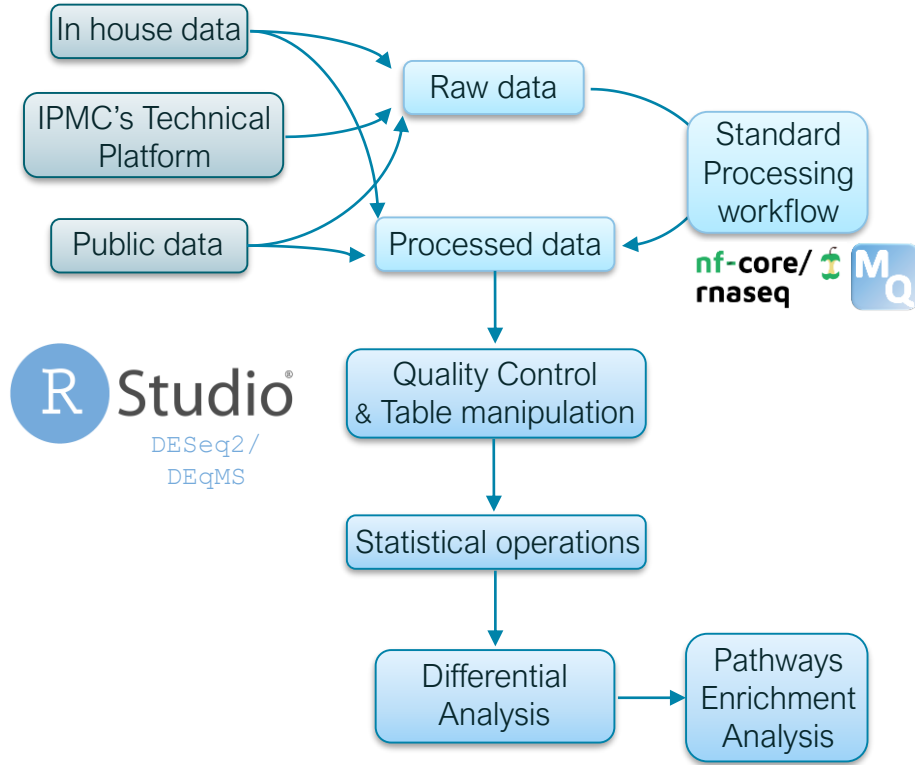- Close collaboration between the team and the bioinformatics hub

## Conclusion of the project, publication of results

- Supporting publication (figures, methods, data sharing)
- Data management following FAIR principles (4D-OMICs, ODIN)
- Recognition of the bioinformatics hub's work
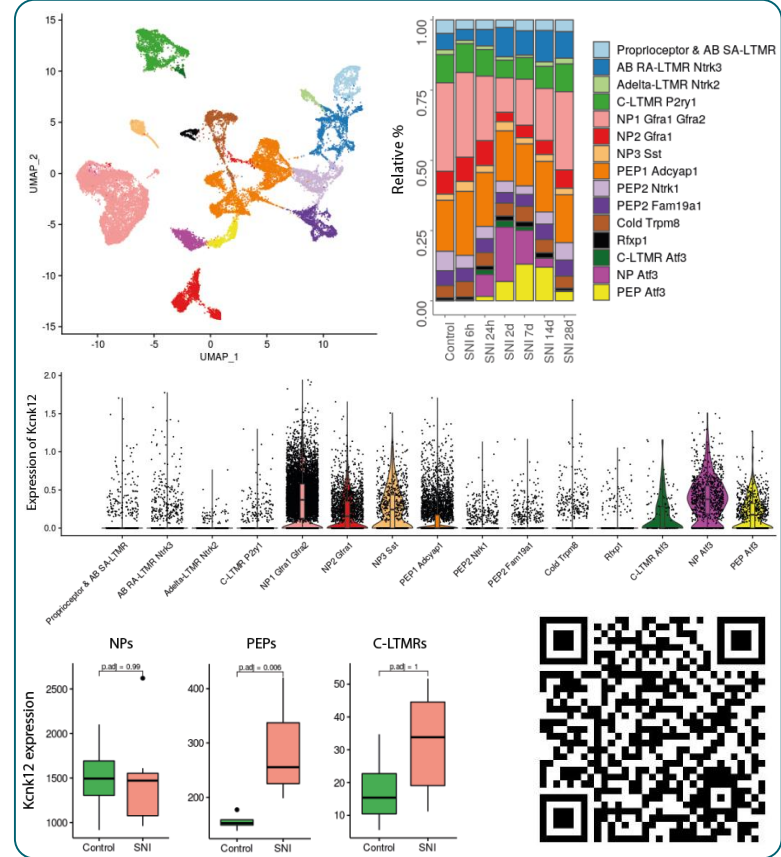
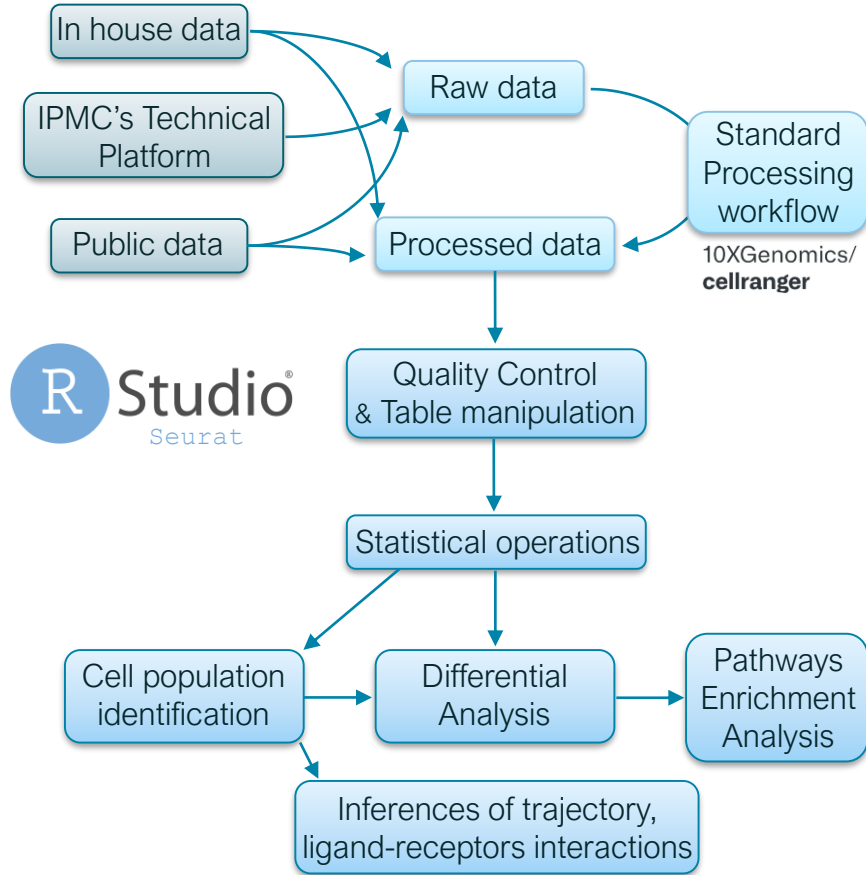# Bulk RNA-seq or Proteomics workflow

Compare gene expression or protein levels between samples of 2 conditions

# Single-cell RNA-seq workflow

Identify cell populations, explore gene expression, compare population abundances and gene expression between samples

# Flow and Mass Cytometry workflow
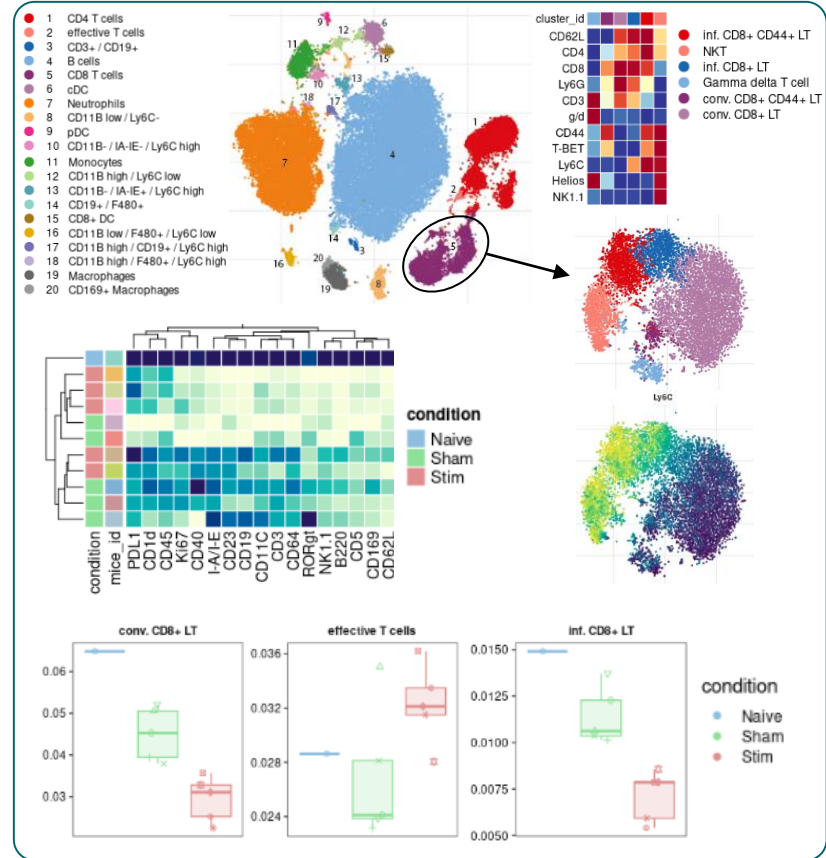
Identify cell populations, explore marker expression, compare population abundances and marker expression between samples
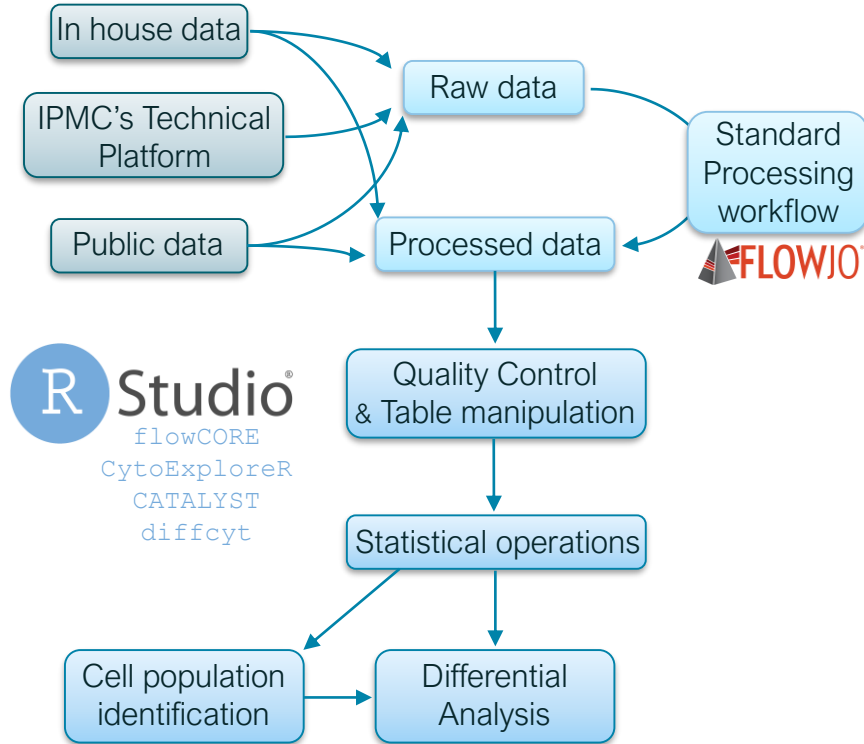
(+) Resolution, Scalability, Reproducibility, Adaptability

Examples of figures for Flow/Mass Cytometry data analysis

# Our first contributions since July 23

Completed, ongoing and planned for the coming months

- Completed analyses:
  - ➢ F.Bihl (GL), public clinical and bulk RNA-seq data (Nephropathies)
  - ➢ Gregor et Malika (EH), public bulk RNA-seq data (effect of Piezo1 mutations and activation)
  - ➢ Nihals (BM), in-house generated bulk RNA-seq data (Systemic scleroderma)
  - ➢ F.Anjuere, spatial proteomics (Codex project)
  - ➢ Nicolas (FL), public scRNA-seq data (expression of Kcnk12/13 in a mouse model of neuropathy)
  - ➢ H.Marie, bulk RNA-seq data generated by the **Genomics platform** (Alzheimer mouse model)
  - ➢ Célia (BM), in-house generated scRNA-seq data (Blocking FGF2 on IPF-derived fibroblasts)

- Ongoing Projects:
  - ➢ Nicolas (TS), multi-organs time series flow cytometry data preprocessed by J.Cazareth (**Cytometry platform**)
  - ➢ P.Barbry, processing and analysis of spatial transcriptomics data (Tests, PAH et Olfactory epithelium)
  - ➢ A.Gay, (**Proteomics platform**), testing workflow analysis of proteomics data
  - ➢ Jacqui (MM), supporting the analysis of transcriptomics data (Epilepsy project)
  - ➢ Juliette (LD), organizing and analysing Live Mouse Tracker data, set up with **ANIMEX**
  - ➢ Developing IT infrastructure (4D-OMICS, ODIN)

- Planned :
  - ➢ R.Barres, epigenomics data analysis
  - ➢ D.Debayle, metabolomics data analysis
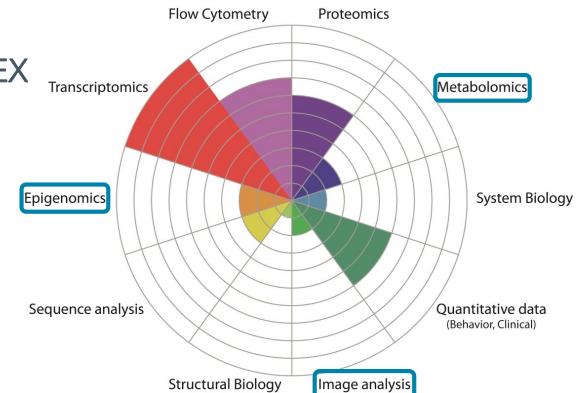
# Spatial transcriptomics imaging

Quantify single-cell gene expression in a spatial context without sequencing, with higher sensitivity and resolution

- Late 2000's: RNA sequencing

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

- Mid 2010's: Single-cell

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

- 2020's : Spatial

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



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## nature methods

Method of the Year 2020:
Spatially resolved transcriptomics

- Lower gene targets (from whole transcriptome to 500-1,000 genes)
- Higher sensitivity (from <10% to 30-80%)
- Keeps the spatial information (Imaging area range 16-100mm2)
- Higher resolution (cellular to subcellular)



WHOLE SECTION    WIDE FIELD OF VIEW    SUB-CELLULAR
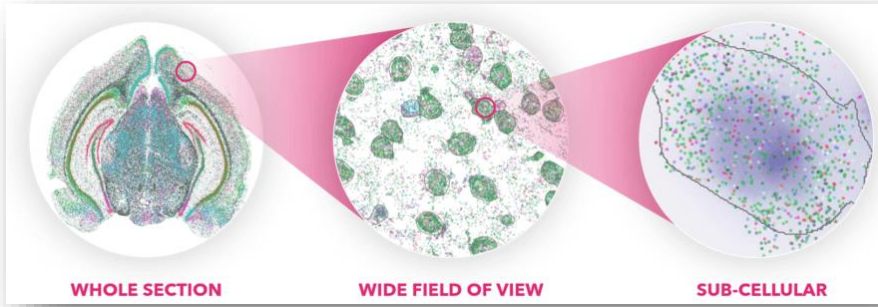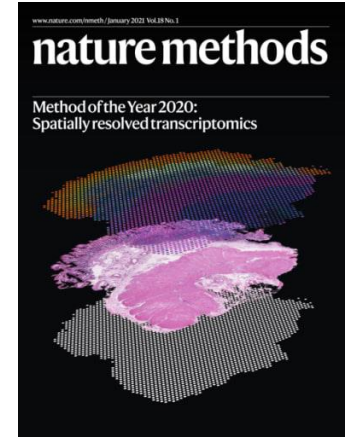


Vizgen Merscope (acquired by the Genomics Platform one year ago)

➤ We want to give the institute's research teams the capacity to analyse this type of data

# Thanks for your attention !

Don't hesitate to contact us or to come to the office to discuss about your projects and data !

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