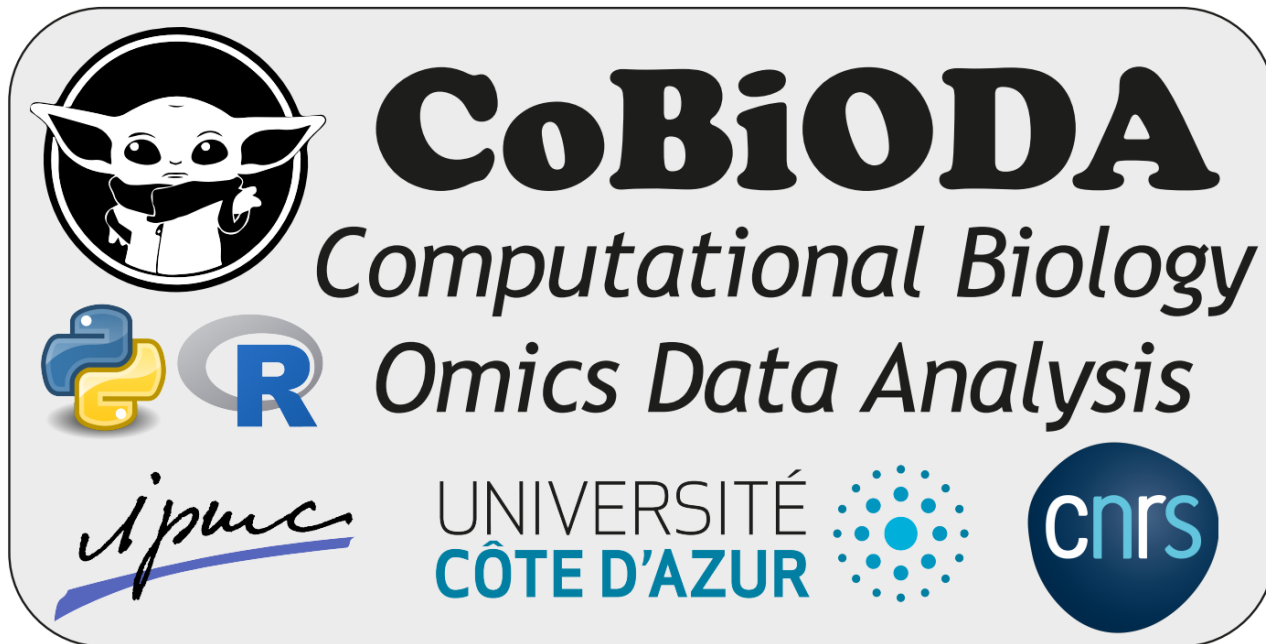


Introducing ...



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)

Dedicated space

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

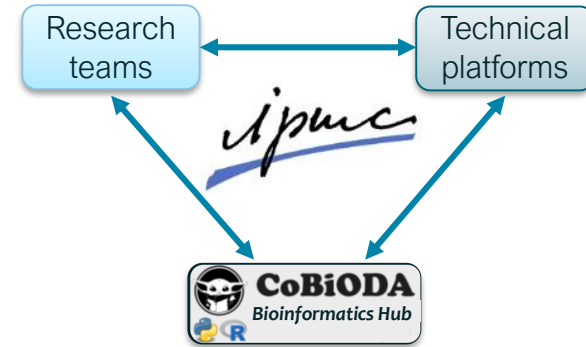


Our missions

Activities of the bioinformatics hub

Strengthening 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 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 ...)

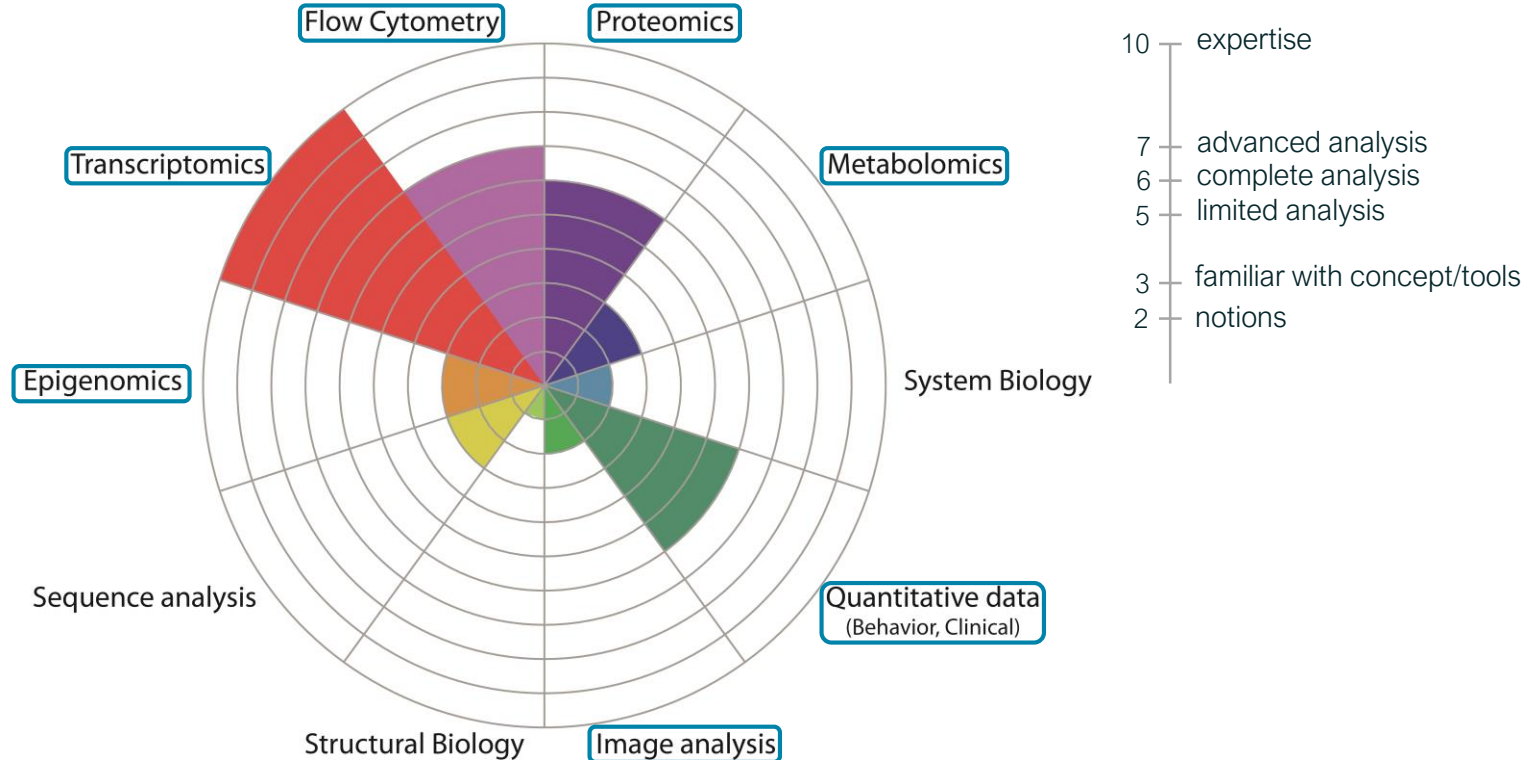


Our scope of action

... within the Bioinformatics spectrum

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

Institute priorities



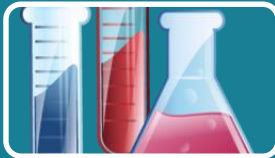
Organisation

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

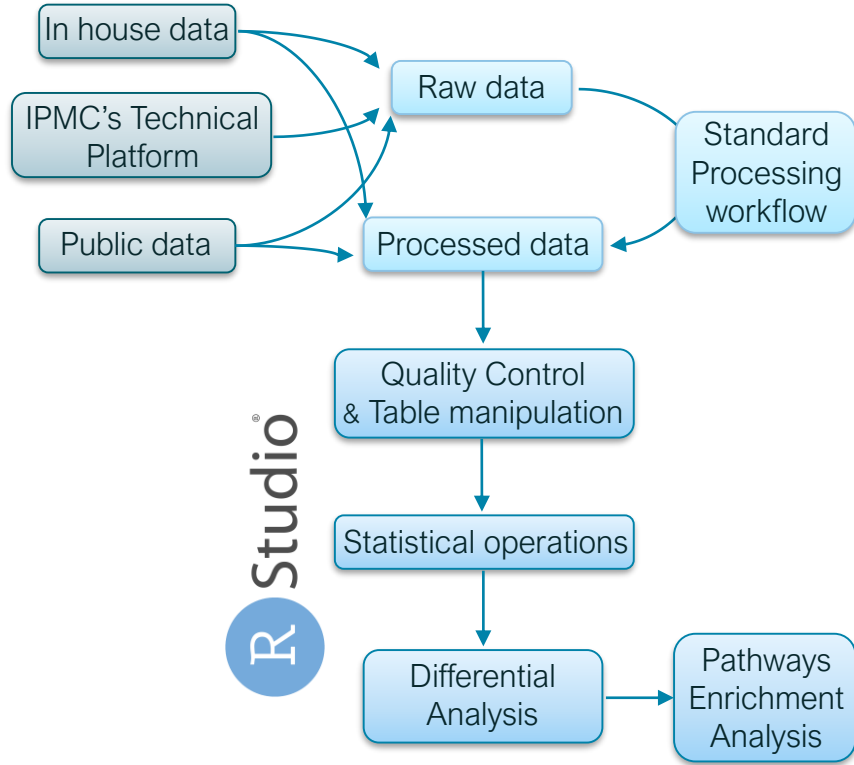


Conclusion of the project, publication of results

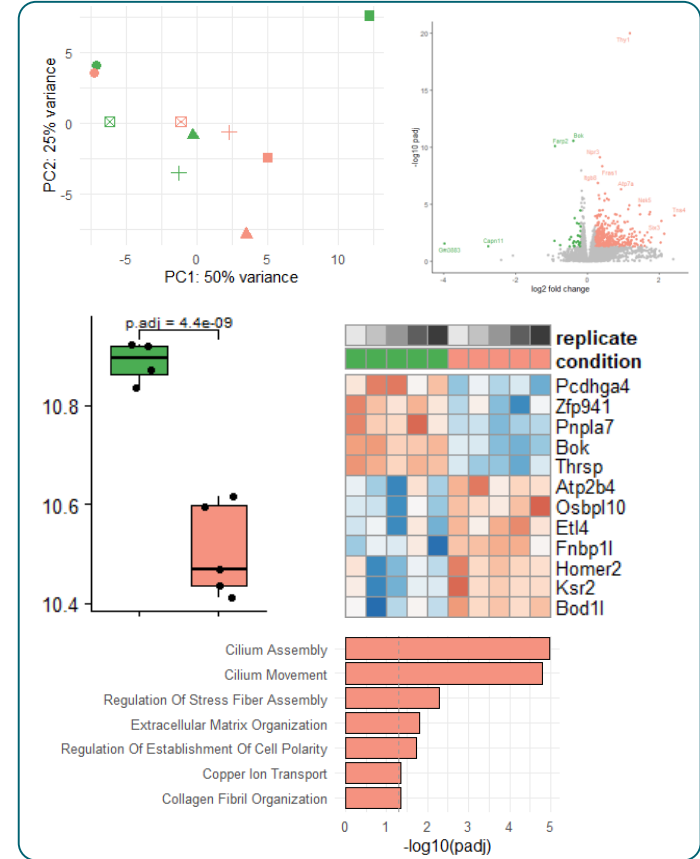
- Supporting publication (figures, methods)
- Sharing of data (FAIR) and analyses (ODIN, bioinformatics newsletter)
- Recognition of the bioinformatics hub's work

Bulk RNA-seq or Proteomics workflow

Compare gene expression or protein levels between samples of 2 conditions



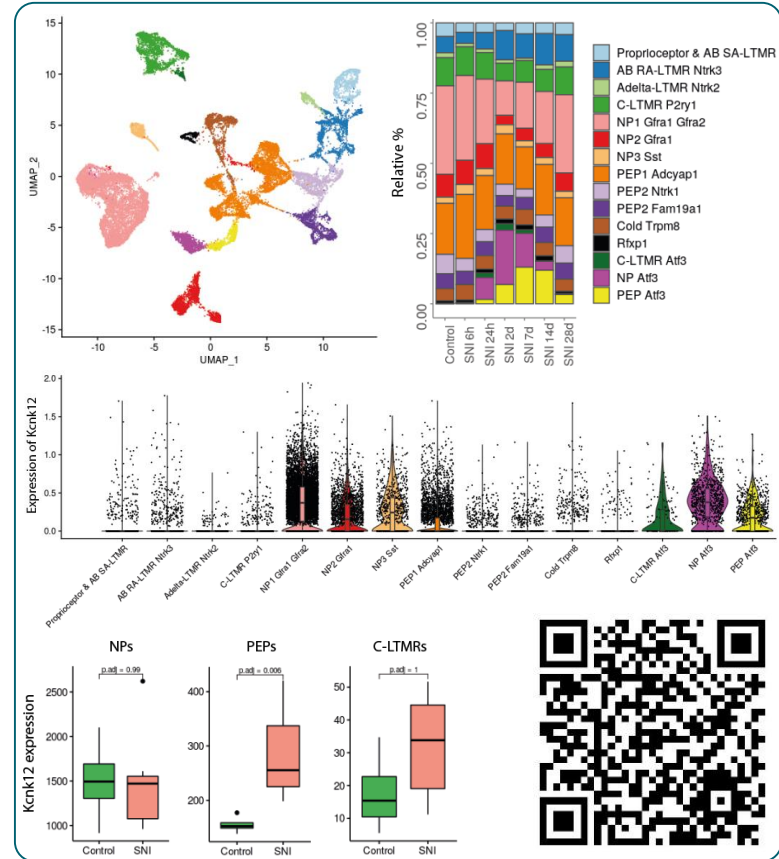
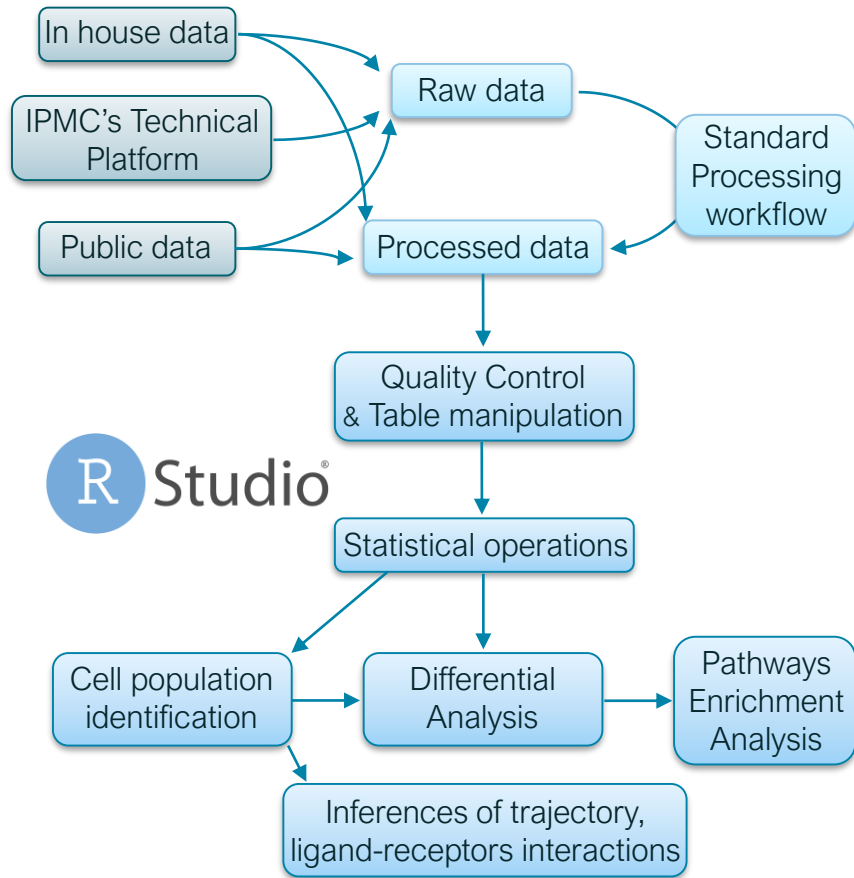
R Studio®



Examples of figures for RNA-seq/Proteomics data analysis

Single-cell RNA-seq workflow

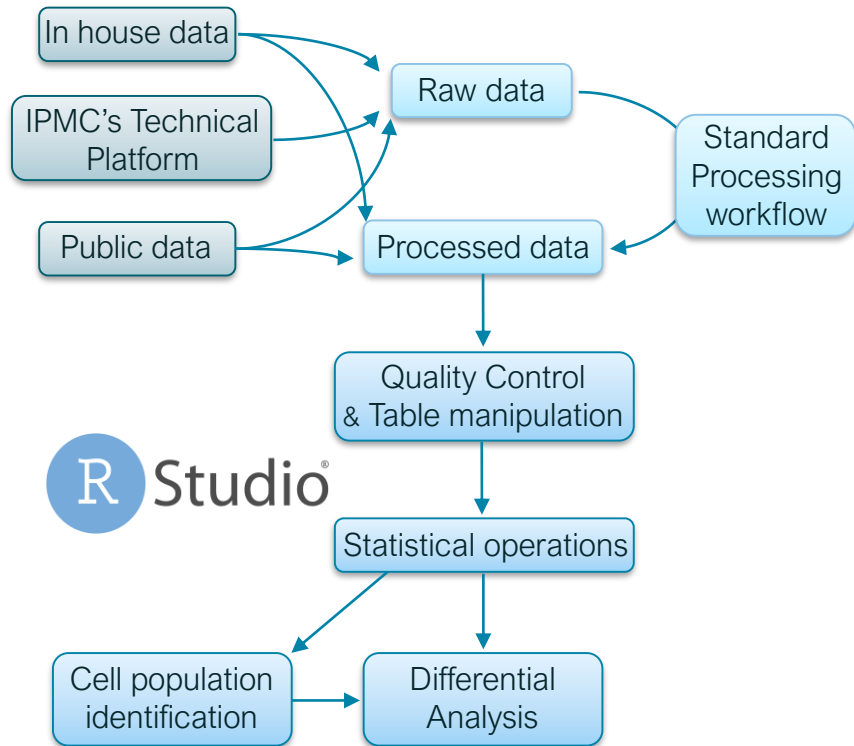
Identify cell populations, explore gene expression, compare population abundances and gene expression between samples



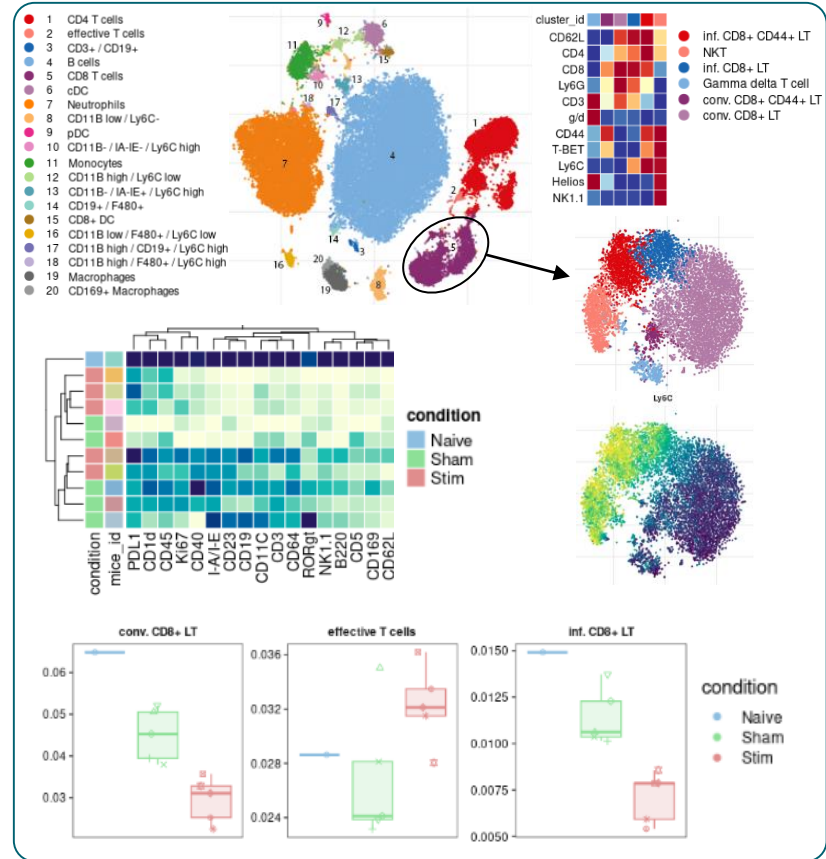
Examples of figures for scRNA-seq data analysis

Flow and Mass Cytometry workflow

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



R Studio®



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**)
 - A.Gay, (**Proteomics platform**), testing workflow analysis of **proteomics data**
 - P.Barbry, processing and analysis of **spatial transcriptomics** data (Tests, PAH et Olfactory epithelium)
 - 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

