



IPMC Bioinformatics Hub

Kévin Lebrigand and Marin Truchi

Computational Biology and Omics Data Analysis

IPMC, CNRS, Côte d'Azur University, France

 lebrigand@ipmc.cnrs.fr, truchi@ipmc.cnrs.fr

 @kevinlebrigand



Who and where are we ?

B07: open space (10 desks)

Committed to support the bioinformatics of IPMC research teams and core facilities



Kevin Lebrigand, IRHC CNRS
Spatial transcriptomics, imaging support



Marin Truchi, IR UniCA
Bulk and single-cell transcriptomics, proteomics, cytometry

Carrying out their own research projects



Maryem Ben Kedher, Post-doc (BM)
Single-cell Pharmacology (BPI)



Anna Diamant, Phd Student (GV/KL)
Single-cell long-read data analysis workflow



Eamon Mcandrew, Phd Student (PB/KL)
Single-cell long-read functional interpretation using AI



Thomas Hermet, Master2 Student (BM)
CrispR data analysis workflow

IPMC2 R-1 B07, an optimal working environment

- ❑ to group bioinformaticians recruited by teams and facilities
- ❑ to share knowledge, ideas, and resources
- ❑ to secure methodological developments
- ❑ to train and mentor people around common methods
- ❑ discuss about IPMC projects and results



Our missions

Activities of the bioinformatics hub

Strengthen bioinformatics expertise and provide support for the quantitative biology projects led by IPMC's research teams and technical platforms

Communicate
and animate

- ☐ Promote bioinformatics at IPMC
→ web site, blog post, workshops, internal seminars

Expertise
transfert

- ☐ Training of IPMC researchers/engineers/students in bioinformatics
→ best practices, guidelines for data processing and FAIR data management

Analyse
datasets

- ☐ Developing and maintaining standardized bioinformatics workflows
- ☐ Support experimental design, funding requests and publication
→ figures drawing, methods writing, data public submission (EGA, GEO)

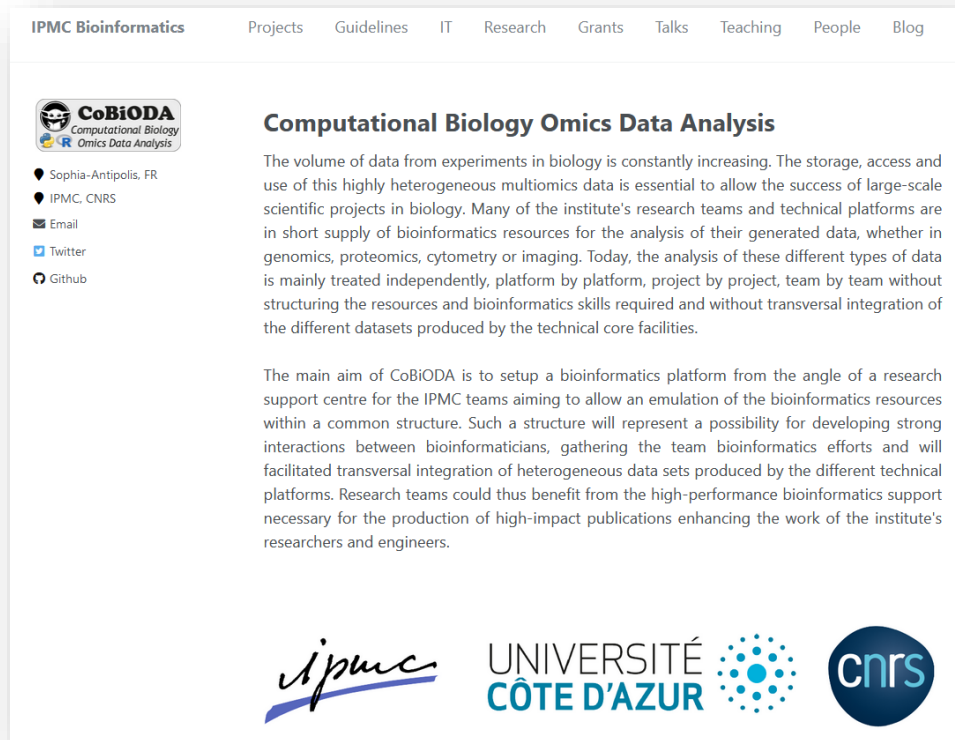
Methodological
developments

- ☐ Constant technological watch in the top priority areas defined by the institute
→ spatial / single-cell transcriptomics and proteomics, epigenetics

Structure
bioinformatics

- ☐ Setting-up of a common IPMC technical Infrastructure and data analysis workflow (ODIN)
- ☐ Integration with local (Idex), regional (4D-Omics) and national (IFB) networks

<https://cobioda.github.io/>



The screenshot shows the CoBiODA website. At the top is a navigation bar with links: IPMC Bioinformatics, Projects, Guidelines, IT, Research, Grants, Talks, Teaching, People, and Blog. Below the navigation bar is a sidebar on the left with the CoBiODA logo and contact information: Sophia-Antipolis, FR; IPMC, CNRS; Email; Twitter; and Github. The main content area has the title "Computational Biology Omics Data Analysis" and a paragraph explaining the volume of data in biology and the need for a platform. Below this is another paragraph about the main aim of CoBiODA. At the bottom are logos for ipmc, UNIVERSITÉ CÔTE D'AZUR, and cnrs.

IPMC Bioinformatics Projects Guidelines IT Research Grants Talks Teaching People Blog



CoBiODA
Computational Biology
Omics Data Analysis

• Sophia-Antipolis, FR
• IPMC, CNRS
✉ Email
🐦 Twitter
🏠 Github

Computational Biology Omics Data Analysis

The volume of data from experiments in biology is constantly increasing. The storage, access and use of this highly heterogeneous multiomics data is essential to allow the success of large-scale scientific projects in biology. Many of the institute's research teams and technical platforms are in short supply of bioinformatics resources for the analysis of their generated data, whether in genomics, proteomics, cytometry or imaging. Today, the analysis of these different types of data is mainly treated independently, platform by platform, project by project, team by team without structuring the resources and bioinformatics skills required and without transversal integration of the different datasets produced by the technical core facilities.

The main aim of CoBiODA is to setup a bioinformatics platform from the angle of a research support centre for the IPMC teams aiming to allow an emulation of the bioinformatics resources within a common structure. Such a structure will represent a possibility for developing strong interactions between bioinformaticians, gathering the team bioinformatics efforts and will facilitated transversal integration of heterogeneous data sets produced by the different technical platforms. Research teams could thus benefit from the high-performance bioinformatics support necessary for the production of high-impact publications enhancing the work of the institute's researchers and engineers.

ipmc UNIVERSITÉ CÔTE D'AZUR  

- ❑ Bioinformatics monthly newsletter
CoBiODA website updates
- ❑ «Open Desk» morning discussion
Thursday morning 9-12h, B07
- ❑ Bioinformatics internal seminars
External speaker invitation and journal clubs
- ❑ Bioinformatics workshops
 - Public dataset re-analysis(Marin Truchi)
 - Spatial Transcriptomics (Kévin Lebrigand)
 - AI in biological research (Eamon Mcandrew)

Interacting with the Hub

Example of operating mode

Analyse
datasets



Service request

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



Data acquisition

- Either in collaboration with IPMC technical core facilities
- or accessible public dataset download
- Implementation of analysis workflows (methodological developments)



Exploratory analysis

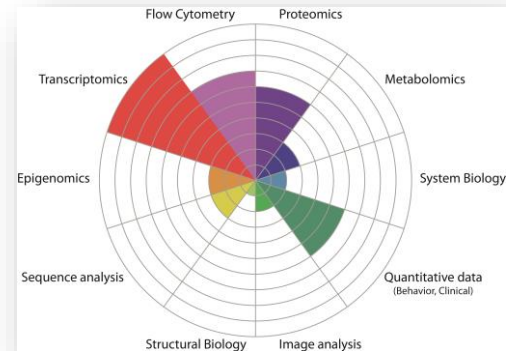
- Regular milestone meetings about project evolution
- Definition of secondary biological questions to be addressed
- Requires a close collaboration between the team and the bioinformatics hub



Conclusion of the project, publication of results

- Support for publication (figures drawing, methods writing)
- Sharing of data (FAIR) and analyses (GitHub, ODIN, bioinformatics newsletter)
- Association of the bioinformatics hub to the publication

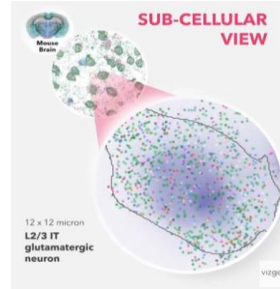
Current expertise  



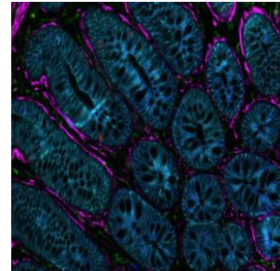
Institute priority technological areas

Spatial transcriptomics and proteomics

Methodological
developments



- Spatial transcriptomics
- 300 to 5,000 gene targets (+ proteins)
- single-molecule sensitivity: 30-80%
- large imaging area: 1 to 2,5 cm²
- sub-cellular resolution: 100 nm
- Fresh frozen and FFPE
- Functional exploration assays



- Spatial proteomics (Multiplexed antibody staining)
- 40 (hyperion) - 100 targets (phenocycler)
- semi-quantitative measurement
- large imaging area: 1 cm²
- sub-cellular resolution: 0,5 µm
- Fresh frozen and FFPE
- Cell-typing assays

All systems generate huge dimension matrices
200k cells x 40-5,000 multi-omics targets
that require complex bioinformatics analysis



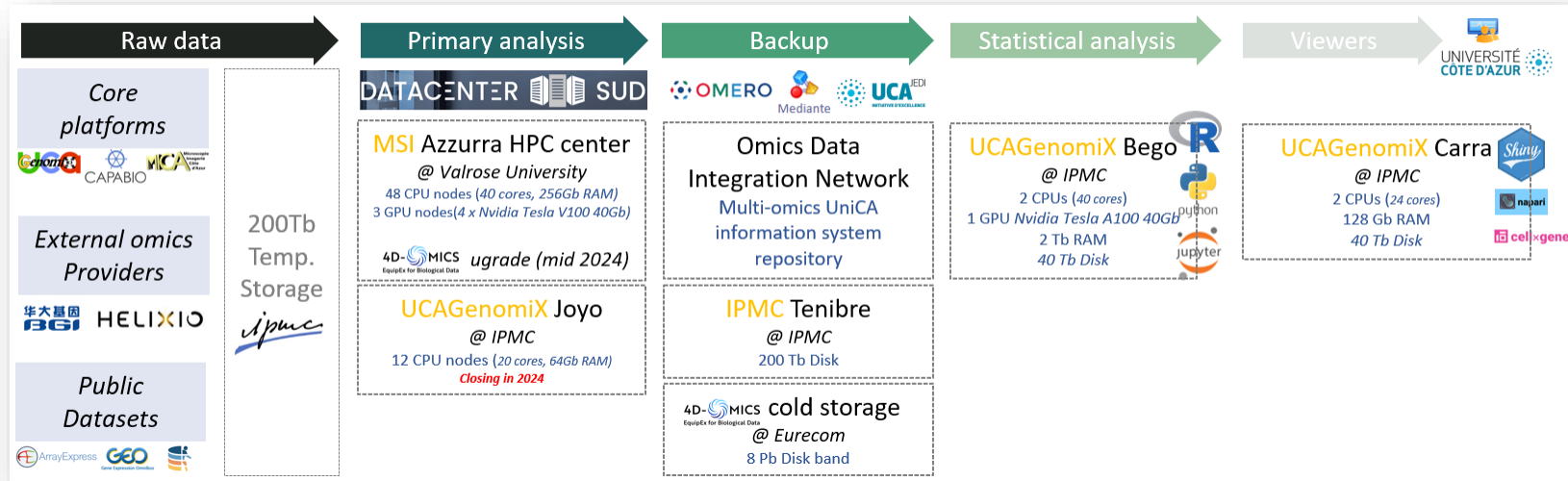
- ☐ Olfactory epithelium development (HuDeCa, Paolo Giacobini, Lille)
- ☐ Pulmonary Arterial Hypertension (Christophe Guignabert, Paris)
- ☐ Non small Lung Cancer (IHU RespirERA, Paul Hofman, Nice)
- ☐ Epileptic mouse (Massimo Mantegazza, IPMC)

Organize and structure bioinformatics

@ IPMC and UniCA level

Structure
bioinformatics

Define and rationalize a common data flow for biological omics data analysis



SIGNALIFE

Initiative Bioinfo-UniCA

Florence Besse (Copil IdeX)

- ❑ Platforms comity
- ❑ Scientific comities

Maison de la Modélisation, Simulation et Interactions

Didier Auroux

- ❑ Pool Tech (4-6 Engineers)
- ❑ Cluster Azzurra

4D-MICS
EquipEx for Biological Data

Structurer la composante biologique de DATASUD

Pascal Barbry (UniCA, AMU)

- ❑ Projet: 2021-2029
- ❑ Budget: 6.595.999€

IRCAN, ipmc, CEA, Institut de Biologie Valrose

Omics Data Integration Network (ODIN)

Bioinformatics Platforms (UniCA)

- ❑ User-oriented multiomics research project manager
- ❑ Académie 4 (CDD 1 an)

Take home messages

- ❑ Bioinformatics can be quite complex for biologists but in fact is easy for bioinformaticians, come to see and discuss about your research projects
 - CoBiODA website updates
 - « Open Desk » morning discussion (thursday 9-12h, B07)
- ❑ Bioinformatics needs highly accurate datasets, wetlab part is crucial
- ❑ Bioinformatics is not free, just as generating datasets cost money, grants need to secure the bioinformatics support too
 - Bioinformatics resources is limited
 - Project's team exclusive support or co-financed contract across IPMC teams
 - Recurrent IPMC or UniCA contract for an IPMC shared research engineer
- ❑ Marin Truchi: IPMC bioinformatics projects

CoBiODA involvements summary

Already running and coming soon projects

Structuration

Architecture Logiciel
ODIN

Architecture
Informatique
4D-Omics

Structuration
Bioinformatique
Labex Signalife

Core platform

Animalerie
Eq. Davidovic
Live Mouse Tracker

Cytometrie
Eq. Simon
multiorgan time serie

Proteomique
Eq. Bardoni
FMRP

Imagerie
Eq. Davidovic
ClearMap

CrispR
Eq. Mari

Research teams projects

Eq. Honoré
Gregor / Malika
Extern RNA-seq oxLDL

Eq. Marie
RNA-seq MISEPA2

Eq. Bardoni
Carole / Wassila
FMRP

Eq. Lambeau
Franck Bihl
Kidney GEM clinical data

Eq. Lesage
Nicolas G.
Extern scRNA-seq

Eq. Mari
Bernard
scRNA-seq Fibrose

Eq. Mantegazza
Spatial Merfish
Epileptic mice

Eq. Anjueres
Spatial Hyperion
Breast Cancer

Eq. Lambeau
Spatial Merfish
Mouse brain Pla2

Developments

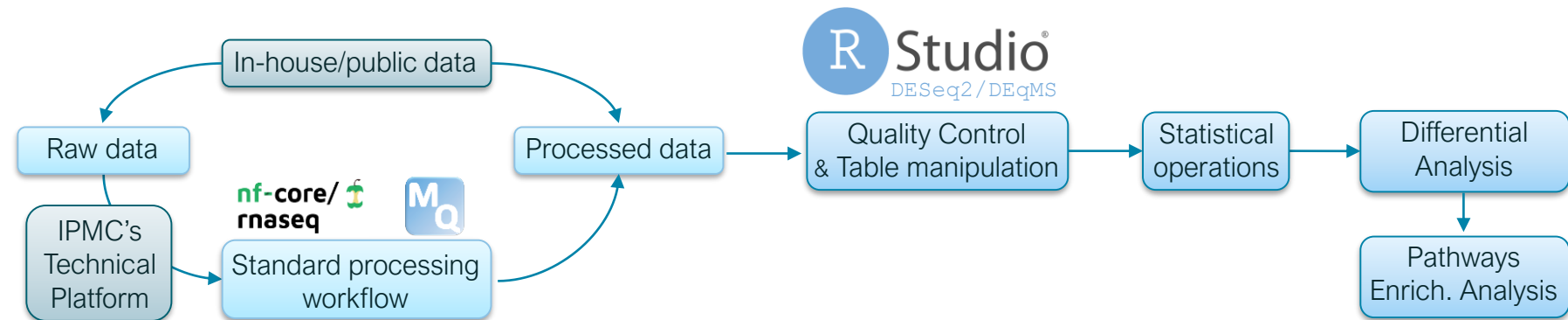
Eq. Barrès
MC. Dumargne
Epigenomics

Eq. Barbry
Spatial Merfish
PAH

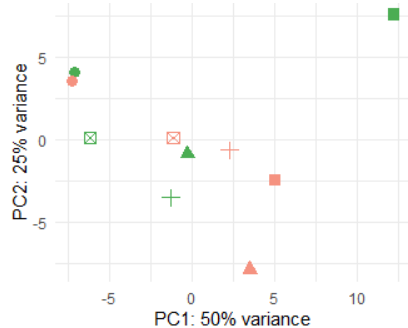
Eq. Roux
Smart-seq
Live cell imaging

Bulk RNA-seq or Proteomics workflow

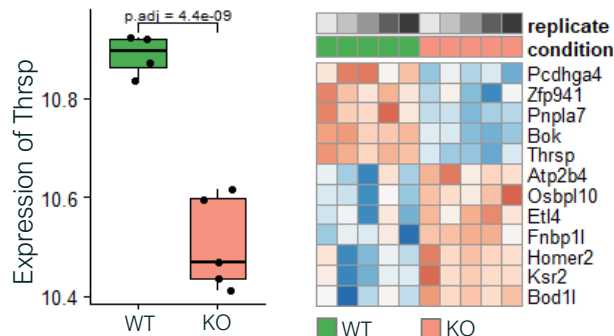
Compare gene expression or protein levels between 2 experimental conditions



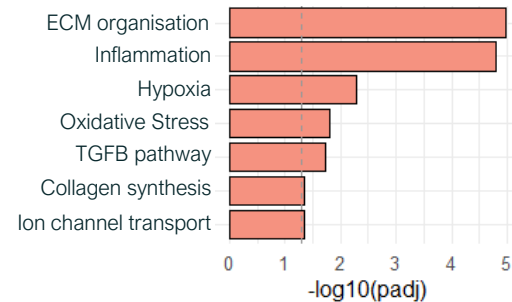
Assess data quality, detect outlier samples & bias (technical, experimental)



Produce standard statistical analysis with “publication ready” and customizable plots



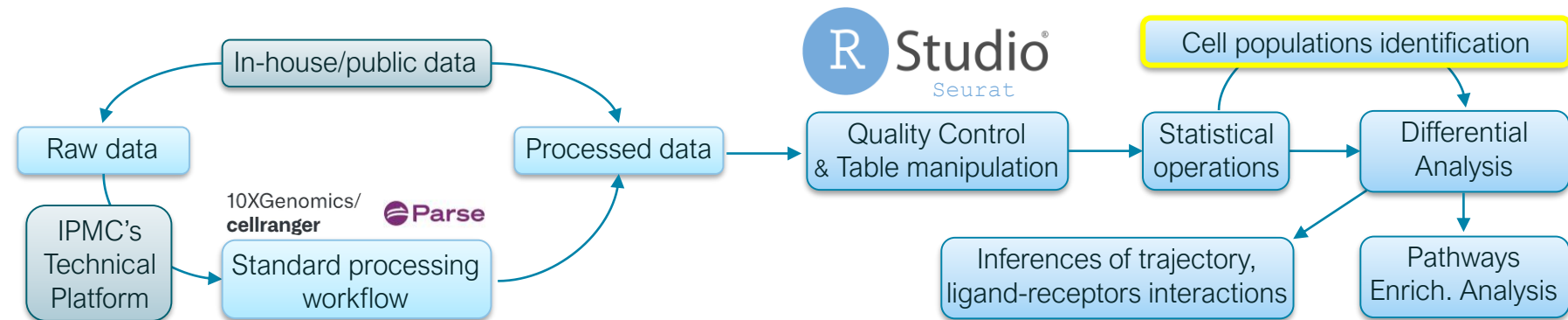
Infer functional hypothesis



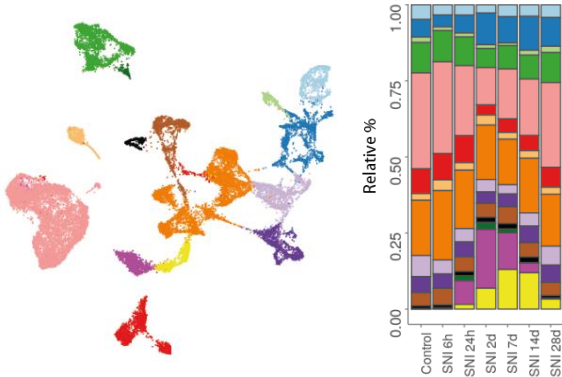
Run on a laptop

Single-cell RNA-seq workflow

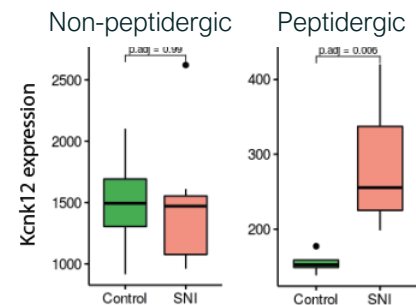
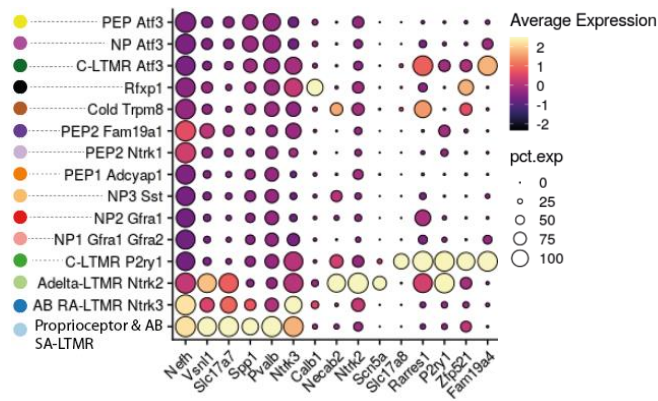
Identify cell populations, explore gene expression, compare population abundances and gene expression between samples



❑ Explore public datasets to increase your knowledge of your model

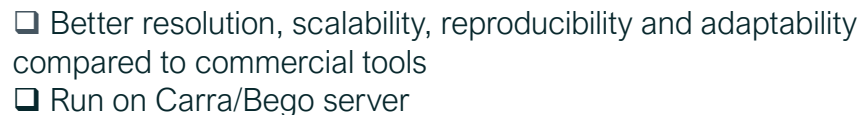


❑ Characterize the expression of your favorite gene between populations & conditions

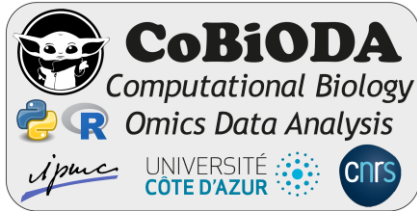


❑ Run on Carra/Bego server

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



Thanks for your attention !!



May the bioinformatics be with you