



IPMC Bioinformatics Hub

Kévin Lebrigand and Marin Truchi

Computational Biology and Omics Data Analysis

IPMC, CNRS, Côte d'Azur University, France

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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



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 (BM/GV)



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

Communicate
and animate

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

Expertise
transfert

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

Analyse
datasets

- Develop and maintain 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

- Set-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/>

IPMC Bioinformatics

Projects Guidelines IT Research Grants Talks Teaching People Blog



- 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.



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 data analysis workflows (Nextflow or method. developments)



Exploratory analysis

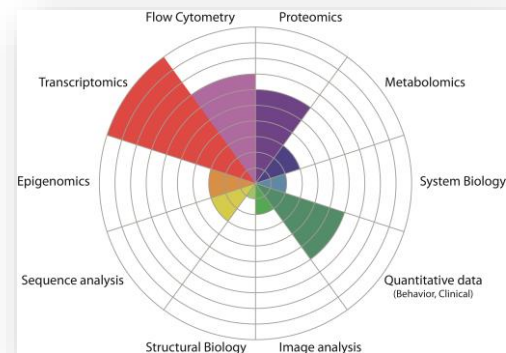
- Regular milestone meetings about project evolution
- Definition of secondary biological questions to be addressed
- Requires a close collaboration between the team and the bioinformatics hub



Conclusion of the project, publication of results

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

Current expertise  



Institute priority technological areas

Spatial transcriptomics and proteomics

Methodological developments



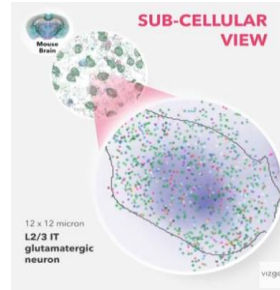
Vizgen Merscope



Nanostring CosMx



10x Genomics Xenium



- Spatial transcriptomics (multiplexed FISH)
- 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



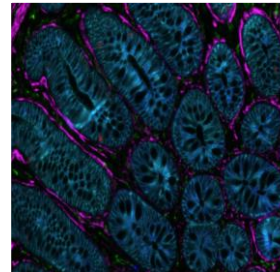
Akoya phenocycler



Fluidigm Hyperion



Rarecyte Orion



- Spatial proteomics (IMC, multiplexed antibody staining)
- 40 (hyperion) - 100 targets (phenocycler)
- semi-quantitative measurement
- large imaging area: 1 cm²
- sub-cellular resolution: 500 nm
- 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



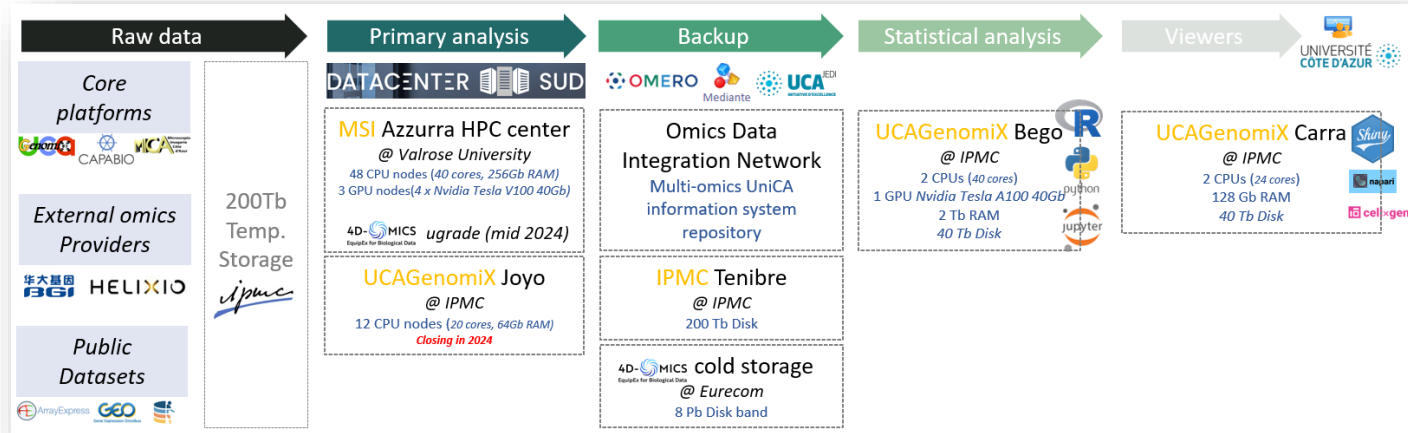
- ❑ Olfactory epithelium development (HuDeCa, Paolo Giacobini, Lille)
- ❑ Pulmonary Arterial Hypertension (Christophe Guignabert, Paris)
- ❑ Non small Lung Cancer (IHU RespirERA, Paul Hofman, Nice)
- ❑ Epileptic mouse (Massimo Mantegazza, IPMC)

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
INSTITUT DE BIOLOGIE VAIROSE

Omics Data Integration Network (ODIN)

Bioinformatics Platforms (UniCA)

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

Take-lab message

- ❑ Bioinformatics can be quite complex for biologists, but is easy for bioinformaticians, come to see and discuss about your projects
 - CoBiODA website updates,
 - Bioinformatics monthly newsletter
 - « Open Desk » discussion (thursday 9-12h, B07)

- ❑ Bioinformatics needs accurate datasets, bench biology is crucial

- ❑ Generating datasets cost money, providing data analysis too, grants need to also secure for the bioinformatics support
 - Bioinformatics resources is limited
 - Project's team exclusive support or co-financed contract across IPMC teams
 - Recurrent IPMC contract for a shared research engineer on the Hub

- ❑ [Marin Truchi: IPMC bioinformatics projects](#)

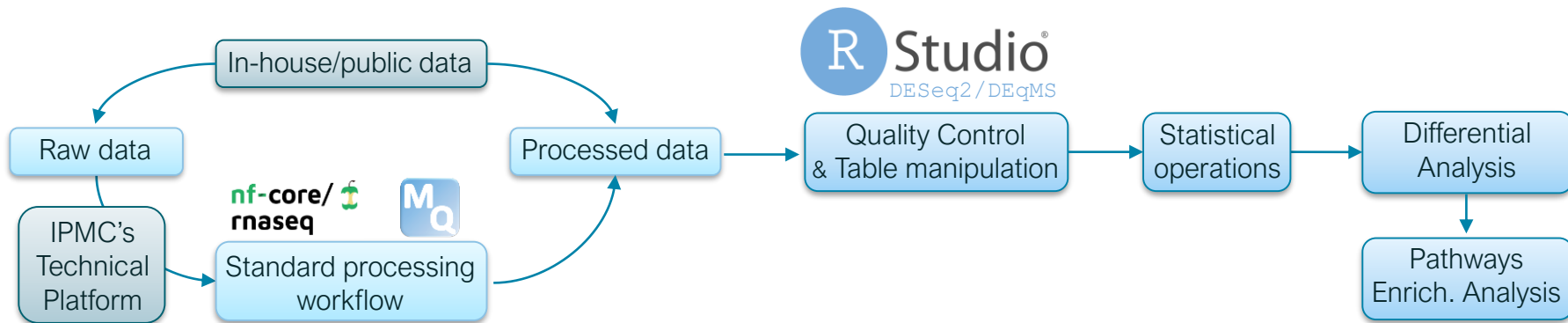
CoBiODA involvements summary

Already running and coming soon projects

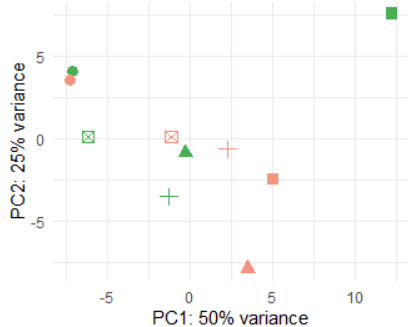
Structuration	Core platform	Research teams projects		Developments
Architecture Logiciel ODIN	Animalerie Eq. Davidovic Live Mouse Tracker	Eq. Honoré Gregor / Malika Extern RNA-seq oxLDL	Eq. Lesage Nicolas G. Extern scRNA-seq	Eq. Barrès MC. Dumargne Epigenomics
Architecture Informatique 4D-Omics	Cytometrie Eq. Simon multiorgan time serie	Eq. Marie RNA-seq MISEPA2	Eq. Mari Bernard scRNA-seq Fibrose	Eq. Barbry Spatial Merfish PAH
Structuration Bioinformatique Labex Signalife	Proteomique Eq. Bardoni FMRP	Eq. Bardoni Carole / Wassila FMRP	Eq. Mantegazza Spatial Merfish Epileptic mice	Eq. Roux Smart-seq Live cell imaging
	Imagerie Eq. Davidovic ClearMap	Eq. Lambeau Franck Bihl Kidney GEM clinical data	Eq. Anjueres Spatial Hyperion Breast Cancer	
	CrispR Eq. Mari		Eq. Lambeau Spatial Merfish Mouse brain Pla2	

Bulk RNA-seq or Proteomics workflow

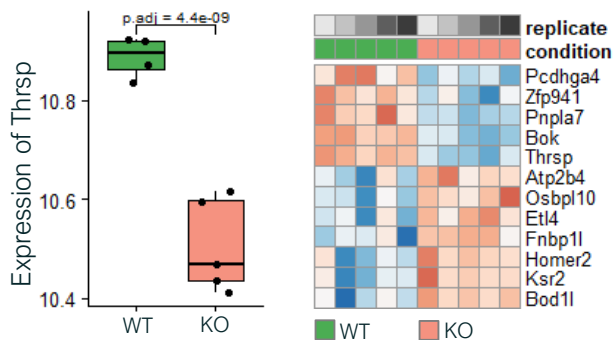
Compare gene expression or protein levels between 2 experimental conditions



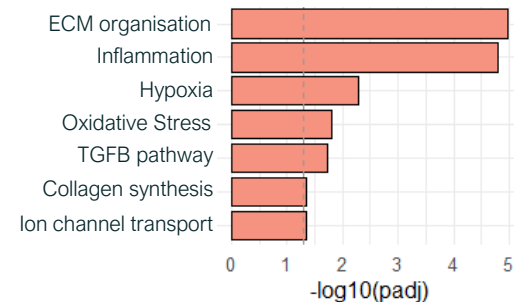
☐ Assess data quality, detect outlier samples & bias (technical, experimental)



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



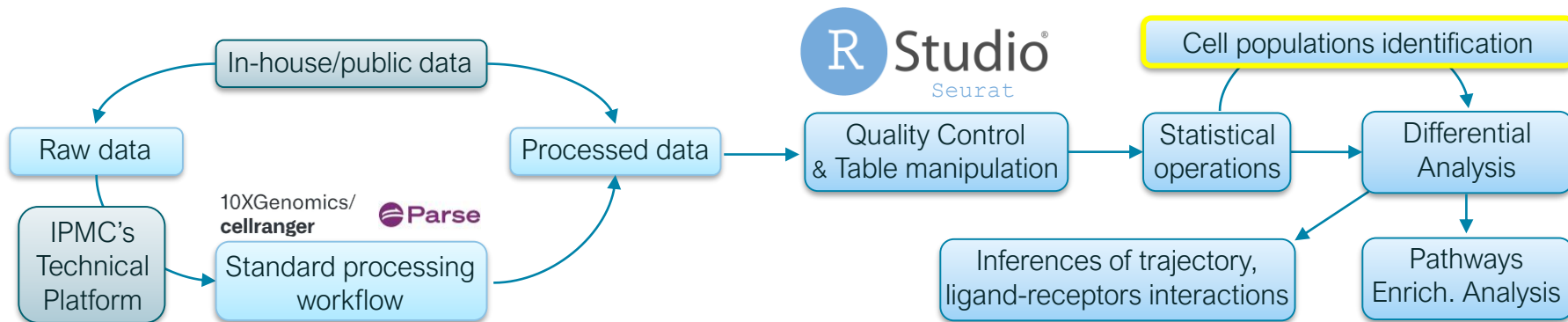
☐ Infer functional hypothesis



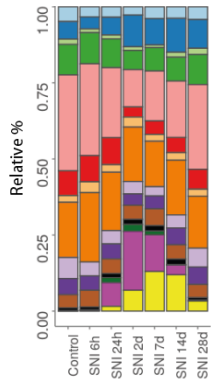
☐ Run on a laptop

Single-cell RNA-seq workflow

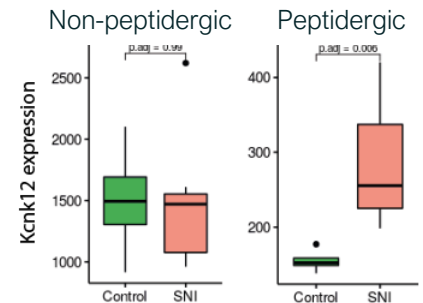
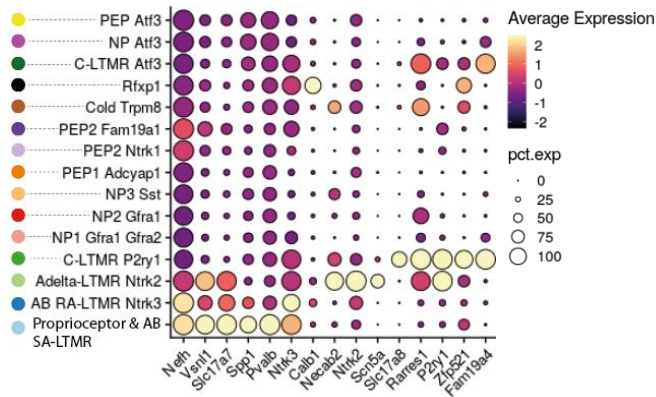
Identify cell populations, explore gene expression, compare population abundances and gene expression between samples



☐ Explore public datasets to increase your knowledge of your model



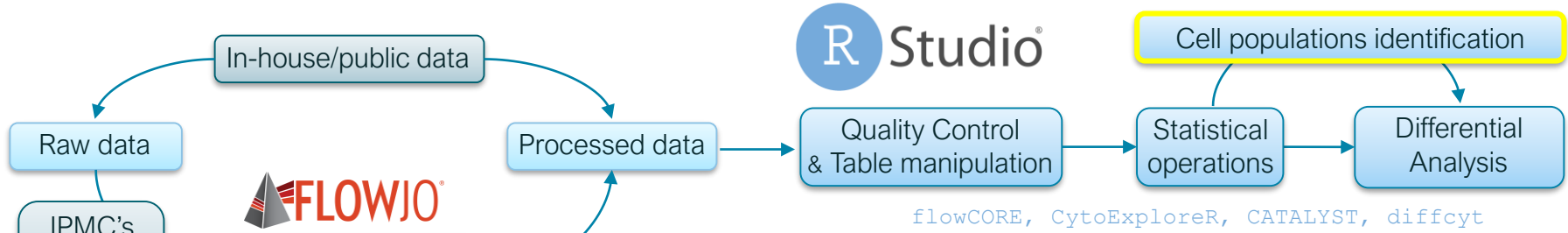
☐ Characterize the expression of your favorite gene between populations & conditions



☐ Run on Carra/Bego server

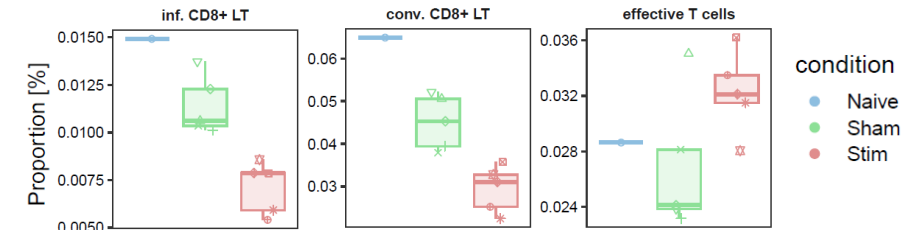
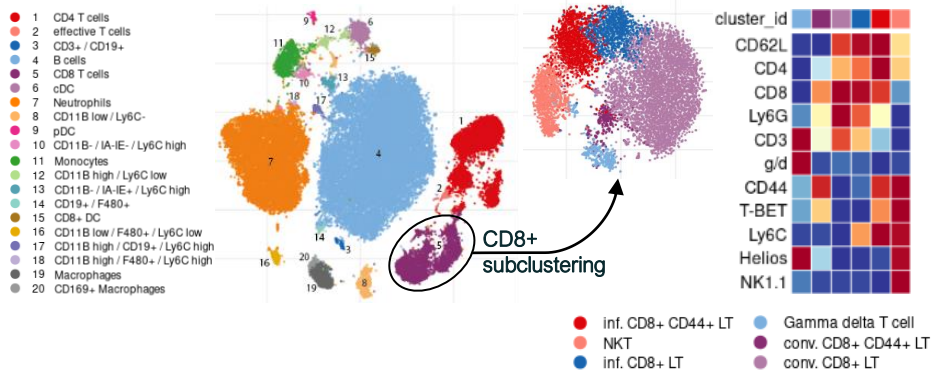
Flow and Mass Cytometry workflow

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



Perform semi-supervised annotation of subpopulations

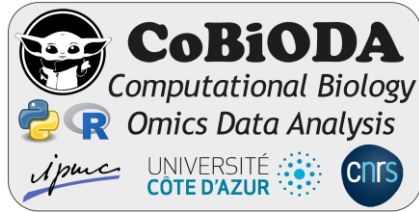
Compare population abundances between samples



Better resolution, scalability, reproducibility and adaptability compared to commercial tools

Run on Carra/Bego server

Thanks for your attention !!



May the bioinformatics be with you