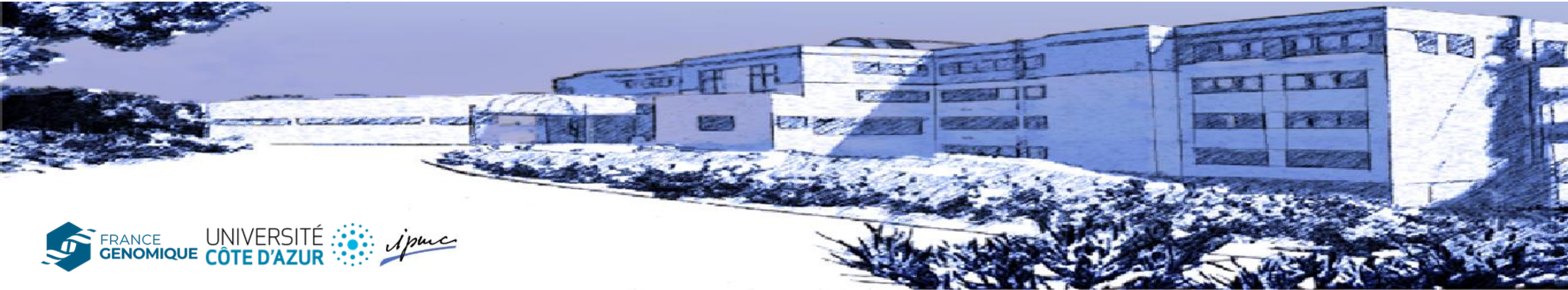
IPMC Bioinformatics Hub

CoBiODA
Computational Biology
Omics Data Analysis

Kévin Lebrigand
Computational Biology and Omics Data Analysis
https://cobioda.github.io
IPMC, CNRS, Côte d’Azur University, France
lebrigand@ipmc.cnrs.fr
@kevinlebrigand



Institute of Molecular and Cellular Pharmacology (IPMC)

Sophia-Antipolis

20 research teams composed of > 220 members

- Ion channels (pain, perception, epilepsy)
- Molecular signaling (molecular trafficking, lipidomics)
- Neurodegenerative disorders (Alzheimer, Parkinson)
- Neuropsychiatric disorders (nervous breakdown, mental retardation)
- Functional genomics and bioinformatics

15 Engineers running 5 technological platforms

- MICA, Imaging and Flow Cytometry
- CAPABIO, Proteomics and Metabolomics
- ANIPRO, animal care and behavior facility
- CoBiODA, Bioinformatics Hub
- UniCA GenomiX, Functional Genomics platform

FRANCE GENOMIQUE

Core member of the "France Génomique" network (2008, 60M€) > 500 academics

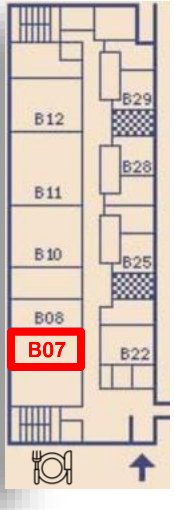
2015 2016 2018 2022 2024

IPMC Bioinformatics Hub

A dedicated open space for bioinformatics (sept. 2023)

IPMC2 R-1 B07, an optimal working environment

☐ 10 desks open space for IPMC engineers
☐ group bioinformaticians recruited by teams and facilities
☐ train and mentor people around common methods
☐ share knowledge, ideas, and resources
☐ secure methodological developments
☐ discuss about IPMC projects and results

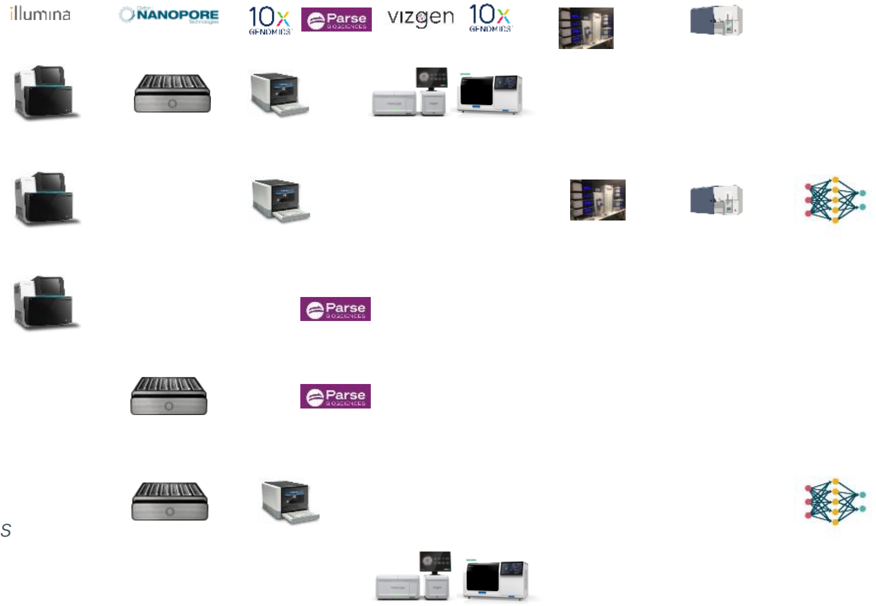


IPMC Bioinformatics Hub

People expertise's

Committed to support bioinformatics of IPMC research teams and core facilities

Short-read Long-read Single-cell Spatial Proteomics Cytometry IA




Kevin Lebrigand, IRHC CNRS
Single-cell and Spatial transcriptomics, Nanopore long-read


Marin Truchi, IR UniCA
Bulk and single-cell transcriptomics, proteomics, cytometry
O.D.I.N project Engineer (July 24 - October 25)


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


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

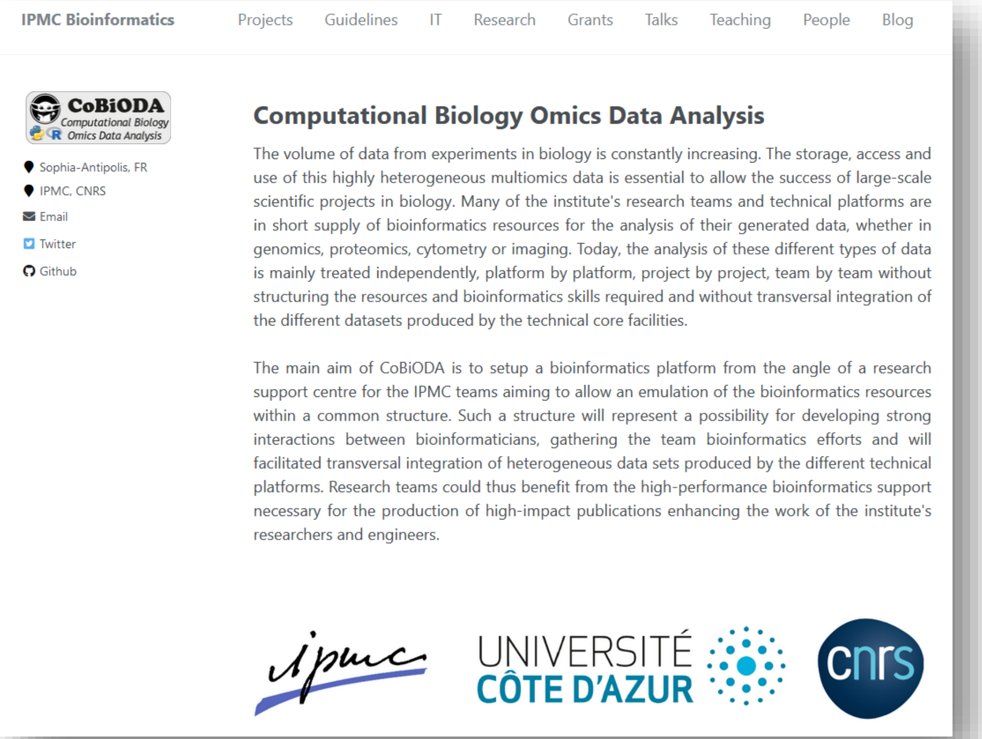

Eamon Mcandrew, Phd Student (PB/KL)
Single-cell long-read functional exploration using deep learning approaches


Morgane Fierville, Phd Student (PB/KL)
Spatial transcriptomics

Bioinformatics @ IPMC

web site, blog post, workshops, seminars

https://cobioda.github.io/



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.

☐ Bioinformatics monthly newsletter

CoBiODA website updates

☐ «Open Desk» morning discussion

Thursday morning 9-12h, B07

☐ Bioinformatics internal seminars

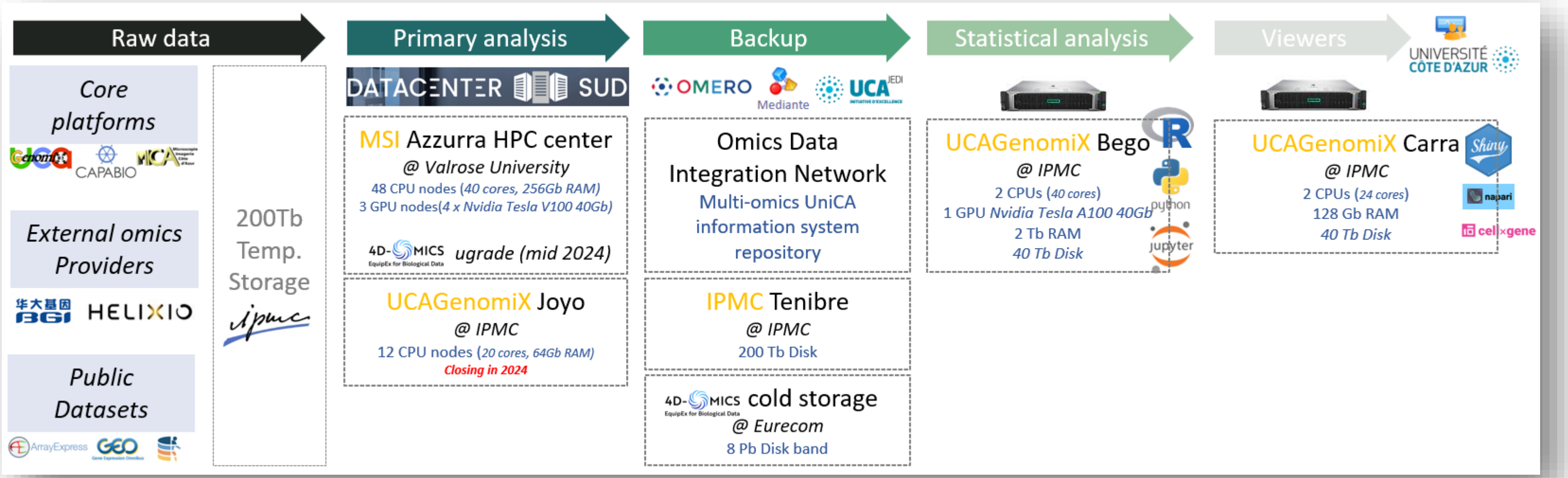
External speaker invitation and journal clubs

☐ Bioinformatics workshops

- Public dataset re-analysis(Marin Truchi)
- Spatial Transcriptomics (Kévin Lebrigand)
- AI in biological research (Eamon Mcandrew)

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

@ IPMC and UniCA level



Raw data → Primary analysis → Backup → Statistical analysis → Viewers

Core platforms

External omics Providers

Public Datasets

200Tb Temp. Storage

DATACENTER SUD

MSI Azzurra HPC center
@ Valrose University
48 CPU nodes (*40 cores, 256Gb RAM)*
3 GPU nodes(*4 x Nvidia Tesla V100 40Gb)*
ugrade (mid 2024)

UCAGenomiX Joyo
@ IPMC
12 CPU nodes (*20 cores, 64Gb RAM)*
Closing in 2024

Omics Data Integration Network
Multi-omics UniCA information system repository

IPMC Tenibre
@ IPMC
200 Tb Disk

cold storage
@ Eurecom
8 Pb Disk band

UCAGenomiX Bego
@ IPMC
2 CPUs (*40 cores*)
1 GPU *Nvidia Tesla A100 40Gb*
2 Tb RAM
40 Tb Disk

UCAGenomiX Carra
@ IPMC
2 CPUs (*24 cores*)
128 Gb RAM
40 Tb Disk

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

Structurer la composante biologique de DATASUD

Pascal Barbry (UniCA, AMU)

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

Omics Data Integration Network (ODIN)

Bioinformatics Platforms (UniCA)

- ❑ User-oriented multiomics research project manager
- ❑ Académie 4 (CDD 16 months)

IPMC, 660 route des Lucioles, 06560 Valbonne - Sophia-Antipolis
https://www.ipmc.cnrs.fr

May the bioinformatics be with you

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