

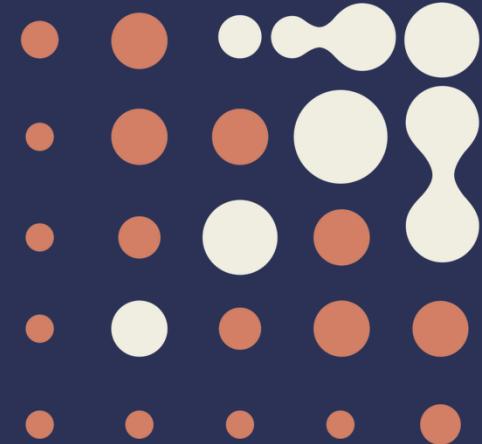
Medical Genomics course

N. Alcala & M. Foll

Computational Cancer Genomics Team

2025

International Agency
for Research on Cancer



Philosophy

Hands-on course with a focus on real-world medical problems

- >to know if you want to dedicate your professional career to medical genomics research, you need to **experience what working on a typical medical genomic project is like**
- > We will see just enough theory to grasp the main concepts and then **code and do actual data analysis**, and do **team work**

General information

Venue: IARC – WHO: the world's cancer agency <https://www.iarc.who.int>

Attendees: INSA students + CanBioS doctoral school students + IARC early career scientists (normally ~20 students in total)



CanBioS
CANCÉROLOGIE
BIOLOGIE
SANTÉ
UNIVERSITÉ DE LYON

International Agency for Research on Cancer



IARC nouveau centre in the Gerland biodistrict



Nicolas Alcalá
Computational
Cancer
Genomics team,
cancer ecology
and evolution
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Matthieu Foll
Computational
Cancers
Genomics team
leader, head of
bioinformatics
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IARC's Mission: research on cancer prevention

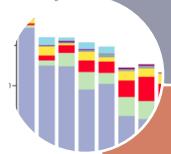
- ◆ .. is the specialized cancer agency of the World Health Organization (WHO).
- ◆ .. promotes international collaboration in cancer research.
- ◆ .. identifies the causes of cancer so that preventive measures may be adopted.
- ◆ .. conducts research in LMICs through partnerships and collaborations with researchers in these regions.



27 Participating States
+2 who recently joined

Main areas of IARC's research

Pillar 1 Data
for action



Cancer
Surveillance

Pillar 2
Understanding
the causes



Nutrition &
Metabolism



Genomic
Epidemiology



Laboratory Support
& Biobanking

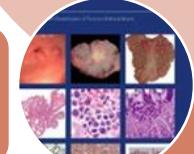
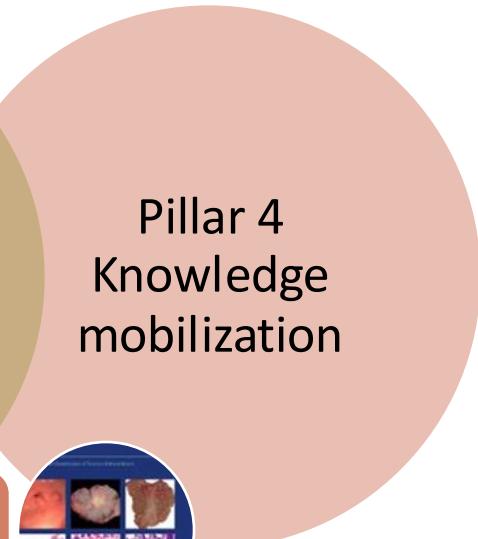
Pillar 3 From
understanding
to prevention



Early Detection,
Infections &
Prevention



Environment &
Lifestyle



Evidence Synthesis
& Classification



Learning &
Capacity Building

The Computational Cancer Genomics team

Multi-omics characterization of tumors. Identify aggressive phenotypes.

- > **Cancers of interest:** mesothelioma, neuroendocrine neoplasms (focus on lung), rare cancers (<https://rarecancersgenomics.com>)
- > **Approaches:** bioinformatics, computational biology, deep-learning, modeling, evolution and ecosystems
- > **Techniques:** genome, transcriptome, epigenome, single-cell and spatial omics, images



Matthieu Foll
Team leader - Computational Biolo



Lynnette Fernandez-
Cuesta
Team leader - Biology/Biochemistry



Nicolas Alcalá
Scientist - Statistics



Laurane Mangé
PhD student - Computational Biology



Alexandra Sexton-Oates
Scientist - Biology/Biochemistry



Catherine Voegele
Data analyst - Bioinformatics



Lisa Bonheme
Postdoc - Machine learning/AI



Gabrielle Drevet
PhD student - Surgery



Lipika Kalson
PhD student



Yuliya Lim
PhD student - Computational Biology

Program

- Monday November 24th
 - 11-12:00 welcome and general introduction
 - 13-15:00 genomics lecture
- Tuesday November 25th
 - 9-10:00 single-cell RNA-seq lecture
 - 10-12:00 single-cell practical part I
 - 12-13:00 spatial RNA-seq lecture
 - Lunch break
 - 14-16:00 single-cell practical part II
 - 16-18:00 epigenomics and multi-omic integration lecture
- Wednesday November 26th
 - 9-10:00 AI for digital pathology
 - 10-12:00 AI for digital pathology practical part I
 - 12-13:00 AI for multi-modal integration
 - Lunch break
 - 14-16:00 AI for digital pathology practical part II
 - 16-18:00 projects
- Friday November 28th
 - 9-12:00 projects
- Tuesday December 16th
 - 14-16:00 project presentations
 - 16-18:00 networking event





OnDemand provides an integrated, single access point for all of your HPC resources.

Pinned Apps A featured subset of [all available apps](#)

 JupyterLab System Installed App	 RStudio System Installed App	 QuPath System Installed App	 igv IGV System Installed App
 Fiji System Installed App	 NextFlow Tower System Installed App	 Visual Studio Code System Installed App	 Mega System Installed App

Practical information

Computing resources

Scientific IT platform: dedicated portal for data analysis

<http://portal.sit.iarc.fr> / HPC: `osiris.iarc.lan`

Training-MG folder on Osiris

Accounts and gateway created for **external participants**:

<https://ovd-esg.iarc.who.int/ovd/>

login: `firstname.lastname@iarc.who.int`

password: received by email

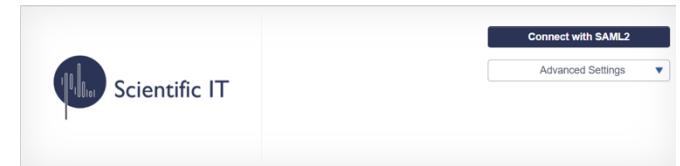
Connection instruction were sent your (insa) email address

Teams channel: [IARC-Medical genomics course | General | Microsoft Teams](#)

GitHub page: https://github.com/IARCBioinfo/medical_genomics_course

Lunch / coffee break

Cafeteria on ground floor



Practicals

1. Single-cell and spatial transcriptomic analyses
2. Deep learning analysis of whole-slide pathological images

Data on IARC's HPC Osiris

Launch jupyterlab from the IARC SIT platform (web browser)

Both using python, use links sent if needed (in particular the R to Python tutorial)

Group projects

5 projects based on actual research done at the agency

- ranging from more bioinformatics oriented to more data analysis oriented
- Groups of 3 students

Group presentation on December 16th (10 min + 10 min of questions per group).

Note the cafeteria will be unavailable this day for external participants.

Evaluation for INSA students

- grade is 50% supervisor evaluation and 50% presentation evaluation
- Criteria are: understanding of subject, clarity of explanations, organization and structure of the presentation, visuals, engagement, and answer to questions
- All group members should present something

Practical setup

- Log in to Inuvika using the login information sent to you on Friday
- Once in Inuvika, follow the steps listed in
/data/Training-MG/files/scripts/Practical1/2025/TODO_BEFORE_PRACTICAL1.txt
to setup your environment for the first practical.
- If you have some time left, follow the steps listed in
/data/Training-MG/files/data/AI_practicals_2025/practical_setup.md
to setup your environment for the second practical.
- If you encounter any issues during the installation of your environments, let us know!