



Register  
by 30 Aug 2024



18-22 Nov 2024



Human Technopole  
Milano

# BrainOmics 2.0

Computational approaches  
to single-cell multi-omics  
in neuroscience





# FACULTY

## HT SCIENTIFIC ORGANISERS

### PIERO CARNINCI

Head of Functional Genomics Research Centre  
& Group Leader

### CRISTINA CHERONI

Senior Manager - Cell Reference Brain Atlas  
Scientific Service Unit, Neurogenomics

### IVANO LEGNINI

Group Leader, Functional Genomics

### ELENA TAVERNA

Group Leader, Neurogenomics

### GIUSEPPE TESTA

Head of Neurogenomics & Group Leader

*Image credits: Aurelio Ortale, Oliviero Leonardi (Testa Group, HT)*

# FACULTY

## SPEAKERS AND INSTRUCTORS

### NICOLÒ CAPORALE

Postdoctoral Associate, HT - Instructor

### DAVIDE CASTALDI

Postdoc, HT - Instructor

### CRISTINA CHERONI

Senior Manager, HT - Organiser & Instructor

### REBECCA HODGE

Assistant Investigator, Allen Institute for Brain Science (US) - Speaker

### CHUNG CHAU HON

Group Leader, RIKEN Centre for Integrative Medical Sciences (JP) - Speaker + Instructor

### JOSHUA LEVIN

Group Leader, Broad Institute of MIT & Harvard (US) - Speaker

### CHONG LI

Postdoc, Institute of Molecular Biotechnology (AT) - Speaker & Instructor

### STEN LINNARSSON

Professor, Karolinska Institutes (SE) - Speaker

### JOAKIM LUNDBERG

Professor, SciLifeLab (SE) - Speaker

### AHMED MAHFOUZ

Assistant Professor, Leiden University Medical Center (NL) - Speaker & Instructor

### VALERIYA MALYSHEVA

Group Leader, VIB-UAntwerp Center for Molecular Neurology (BE) - Speaker

### BENEDETTA MANZATO

PhD Student, Leiden University Medical Center (NL) - Instructor

### GAJA MATASSA

PhD Student, HT - Instructor

### NIKOLAUS RAJEWSKY

Scientific Director, Berlin Institute for Medical Systems Biology, and Group Leader, Max Delbrück Center for Molecular Medicine (DE) - Speaker

### NENAD SESTAN

Professor & Executive Director of the Genome Editing Center, Yale School of Medicine (US) - Speaker

### GENEVIEVE LAUREN STEIN-O'BRIEN

Assistant Professor, Johns Hopkins University - School of Medicine (US) - Speaker

### ALESSIA VALENTI

PhD Student, HT - Instructor

### EMANUELE VILLA

Senior Staff Scientist, HT - Instructor

### ALESSANDRO VITRIOLO

Postdoctoral Associate, HT - Instructor

# CONCEPT

## COURSE OVERVIEW

**BrainOmics 2.0** represents a **unique interdisciplinary hands-on course on single-cell multi-omics computational analysis with a focus on the brain and its disorders** and builds on the experience of the [2022 edition](#), with the addition of **integrative sessions on functional genomics**.

Single-cell omics technologies are breaking new ground in neurobiology by substantially increasing the precision and resolution with which the complex cell populations of the nervous system can be characterised. Approaches that profile several layers of information (genome, epigenome, transcriptome, proteome, spatial location) allow to generate data of unprecedented depth on the molecular state of the diversity of cells composing the nervous system.

This increase in data volume and complexity generates as many opportunities as new analytical challenges.

This compact **course aims at empowering participants in mastering key computational tools for the analysis of single-cell omics datasets**, starting from individual molecular layers to then tackle their integration, alongside providing a theoretical overview of the impact of these technologies at the leading edge of neurobiology.

## TARGET AUDIENCE

This course is aimed at bioinformaticians and computational biologists with expertise or interest in neurobiology and (at least) a basic knowledge of omics techniques.

The core of the course will be centred around **hands-on data analysis sessions**. A basic understanding of **Unix command line, Python** and/or **R** is required. Previous experience with single-cell analytical workflows will be considered as an added value to harness the most from the course training sessions.

## MAIN TOPICS

**Lectures:** impact of multimodal approaches on neurobiology research; spatial transcriptomics; single-cell omics; long noncoding RNAs; innovative computational approaches for multi-omics data analysis; integrative biology; spatial transcriptomics approaches in neuroscience; CRISPR-based approaches for perturbation experiments.

**Computational hand-on sessions:** key steps and troubleshooting in the analysis of single-cell transcriptomics data; advanced computational approaches to single-cell RNA-seq data; analysis of spatial transcriptomics data; analytical workflow for single cell ATACSeq and multi-omics data integration; analytical approaches to CRISPR perturbation data

## WHAT FEES INCLUDE

- Participation in all lectures, practical sessions, tutorials, and seminars
  - Personal working station
  - All meals provided during the course, including dinners if scheduled in the programme
  - Onsite transport
- Fees do not include accommodation and travel.

# PROGRAMME

DAY 1

18/11/2024

(time in CET, UTC +1)

**9:00-9:30** Registration & welcome coffee

**09:30-09:50** **OPENING**

09:50-10:20 10 X Participants' presentations (3' each)

**Lectures - Multi-omics approaches in neurobiology  
@ Auditorium**

10:20-11:10 Nikolaus Rajewsky, Berlin Institute for Medical Systems Biology,  
and Max Delbrück Center for Molecular Medicine (DE)

11:10-12:00 Genevieve Stein-O'Brien, John Hopkins University, US

12:00-12:50 Sten Linnarsson, Karolinska Institutet, SE

**12:50-14:00** **Lunch**

14:00-14:30 10 X Participants' presentations (3' each)

**Hands-on - Essential workflow for single-cell RNA-seq  
computational analyses @ Mezzanine Room**

14:30-18:30 C. Cheroni, G. Matassa, N. Caporale, HT

**18:30-21:00** **Dinner**

# PROGRAMME

DAY 2 19/11/2024

## Lectures - Stem cell and organoid disease modelling @ Auditorium

09:30-10:20 Rebecca Hodge, Allen Institute for Brain Science, US  
10:20-11:10 Nenad Sestan, Yale school of medicine, US

### 11:10-11:45 *Coffee*

## Hands-on - Advanced approaches to single-cell RNA-seq data @ Mezzanine Room

11:45-13:00 E. Villa, D. Castaldi, A. Valenti, HT, IT

### 13:00-14:30 *Lunch*

14:30-17:00 E. Villa, D. Castaldi, A. Valenti, HT, IT  
17:00-18:30 **Grouping and assignment of projects**

### 18:30-21:00 *Dinner*

DAY 3 20/11/2024

## Lectures - Spatial transcriptomics in neuroscience @ Auditorium

09:30-10:20 Ahmed Mahfouz, Leiden University Medical Center, NL  
10:20-11:10 Joakim Lundberg, SciLifeLab, SE

### 11:10-11:45 *Coffee*

11:45-13:00 **Hands-on - Computational analysis of spatial transcriptomics data  
@ Mezzanine Room**

D. Castaldi, A. Valenti HT, IT; Ahmed Mafouz, Benedetta Manzato  
LUMC, NL

### 13:00-14:30 *Lunch*

14:30-18:30 D. Castaldi, A. Valenti HT, IT; Ahmed Mafouz, Benedetta Manzato  
LUMC, NL

### 18:30-21:00 *Dinner*

# PROGRAMME

DAY 4 21/11/2024

## Lectures - Genome and transcriptome regulation in neurobiology @ Auditorium

09:30-10:20 Chung Chau Hon, RIKEN, JP  
10:20-11:10 Valeriya Malysheva, VIB Center for Molecular Neurology, BE

**11:10-11:45** *Coffee*

11:45-13:00 **Hands-on - noncoding RNAs, ATACSeq @ Mezzanine Room**  
Chung Chau Hon, RIKEN, JP; A. Vitriolo, HT

**13:00-14:30** *Lunch*

14:30-18:30 Chung Chau Hon, RIKEN, JP; A. Vitriolo, HT

**18:30-21:00** *Dinner*

DAY 5 22/11/2024

## Lectures - Genetic screening and CRISPR perturbation @ Auditorium

09:30-10:20 Chong Li, Institute of Molecular Biotechnology, AT  
10:20-11:10 Joshua Levin, Broad Institute of MIT and Harvard, US

**11:10-11:45** *Coffee*

11:45-13:30 **Hands-on - Computational analysis of CRISPR perturbation data @ Mezzanine Room**  
Chong Li, Institute of Molecular Biotechnology, AT

**13:30-14:30** *Lunch*

14:30-17:00 **Project presentations**

**17:00** **CLOSING REMARKS & DEPARTURE**