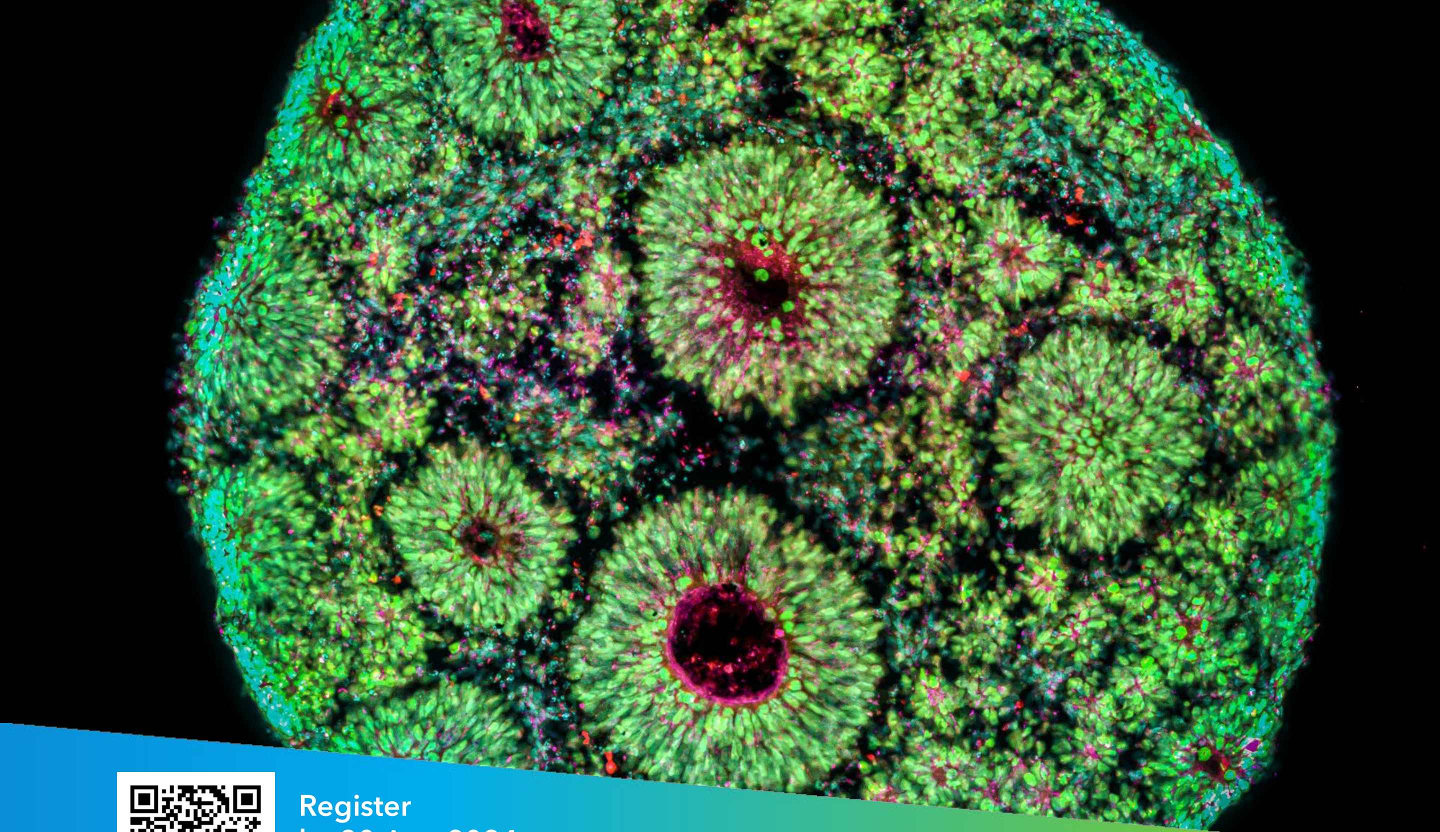


Register
by 30 Aug 2024

18-22 Nov 2024

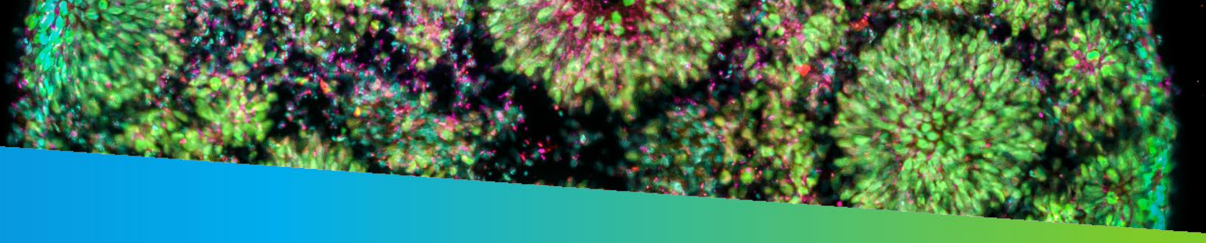
Human Technopole
Milano

BrainOmics 2.0

Computational approaches to single-cell multi-omics in neuroscience

HUMAN
TECHNOPOLE

course



FACULTY

HT SCIENTIFIC ORGANISERS

PIERO CARNINCI
Head of Functional Genomics Research Centre
& Group Leader

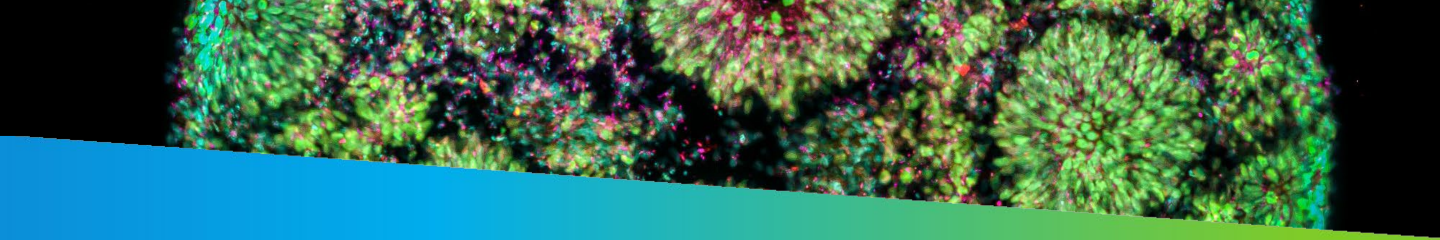
CRISTINA CHERONI
Senior Manager – Cell Reference Brain Atlas
Scientific Service Unit, Neurogenomics

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
Group Leader, Max Delbrück Center (DE) – Speaker

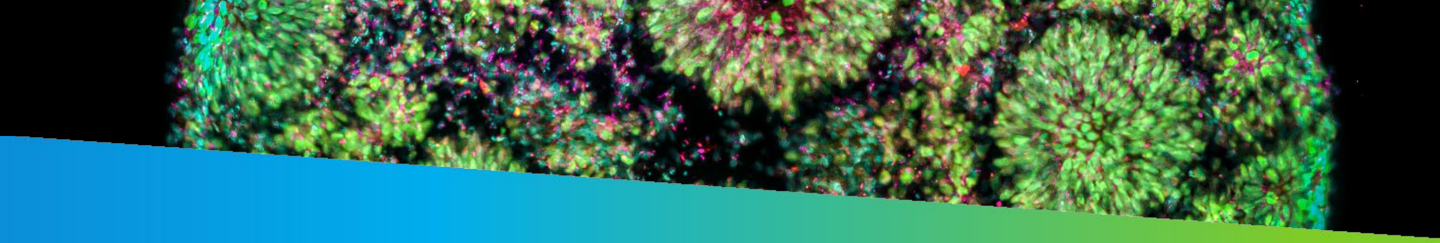
NENAD SESTAN
Professor & Executive Director of the Genome Editing Center, Yale School of Medicine (US) – Speaker

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

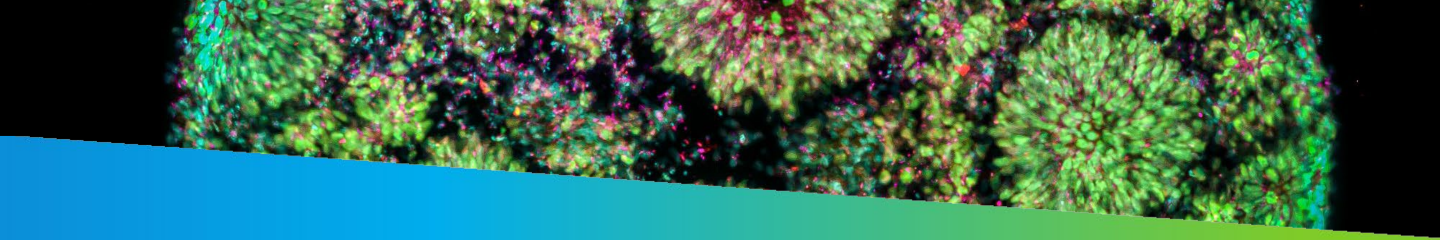
WHAT FEES INCLUDE

- 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.

HUMAN TECHNOPOLE

course

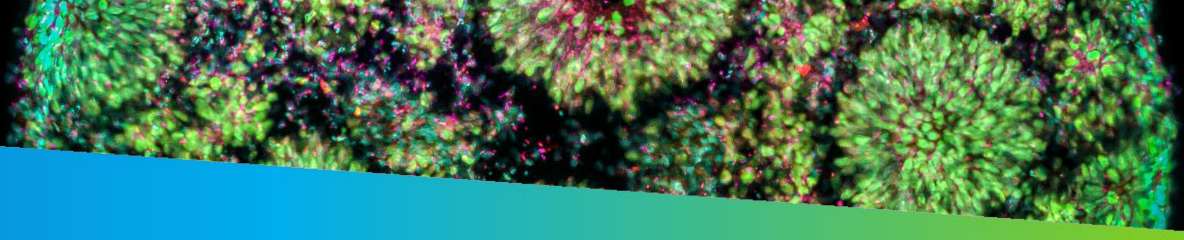


PROGRAMME

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, Max Delbrück Center, 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***

11:45-13:00 **Hands-on – Advanced approaches to single-cell RNA-seq data @ Mezzanine Room**
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 Lundeberg, 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

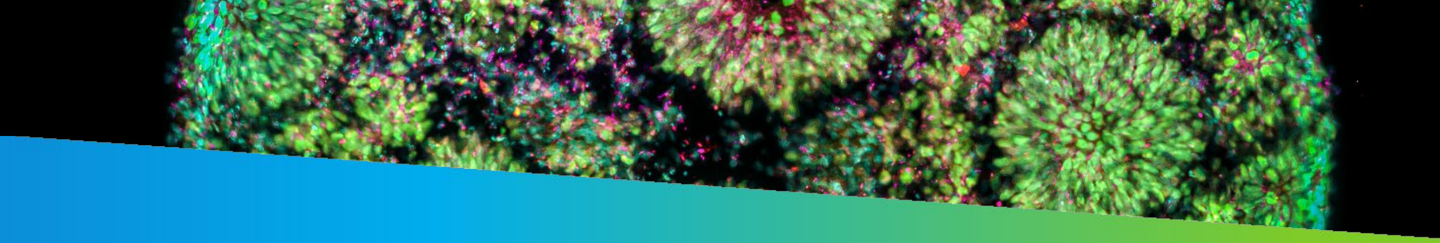
13:00-14:30 ***Lunch***

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

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

HUMAN TECHNOPOLE

course



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***

HUMAN TECHNOPOLE

course