

Genomic Analysis in Neuroscience (GAIN 2026)

Course Overview

This course provides an introduction to the analysis of high-throughput genomic data in neuroscience. Participants will gain practical experience in the processing, analysis, and interpretation of bulk and single-cell sequencing datasets, with a particular focus on transcriptomic and epigenomic approaches. Through a combination of lectures, interactive discussions, and hands-on computational sessions, attendees will learn key bioinformatics concepts and apply statistical methods using widely adopted analysis tools and workflows.

This course will cover the following topics:

- Bulk transcriptomics (RNA-seq)
- Epigenomic profiling (ATAC-seq, CUT&Tag)
- Chromatin architecture and gene regulation (4C, Hi-C, HiChIP)
- Single-cell genomics (scRNA-seq, scATAC-seq, Multiome)
- Spatial transcriptomics (sequencing-based and imaging-based approaches)

The course is intended for PhD students interested in applying high-throughput sequencing and single-cell technologies to neuroscience research.

GAIN 2026 is part of the training activities of the UMH PhD Programme in Neuroscience at the Instituto de Neurociencias (IN, UMH-CSIC):

<https://in.umh-csic.es/en/formation/programa-de-doctorado-en-neurociencias-2/>

Course Director:

Jose P López-Atalaya

Guest Lecturers:

Mario F. Fraga – CINN, CSIC, El Entrego, Spain

Ana B. Muñoz Manchado – Univ. Cádiz, Cádiz, Spain

Keynote Lecture:

Angel Barco

Course Lecturers:

Rafael Alcalá Vida

Violeta Durán Laforet

José P. López-Atalaya

José V. Sánchez Mut

Expert Instructors

Carmen Escolar (Bioinformatics facility IN)
Marina Guillot (J.P. López-Atalaya lab)
Lara López (V. Borrell lab)
Roser Montañana (S. Jurado lab)
Nitin Narwade (A. Nieto lab)
Sergio Niñerola (A. Barco lab)
Lorenzo Puche (G. López-Bendito lab)

Systems administrator

Angel Márquez (IN, UMH-CSIC)

Dates and schedule

The course will take place from October 19 – 23, 2026.

Venue

Instituto de Neurociencias, Universidad Miguel Hernández - Consejo Superior de Investigaciones Científicas, Avenida Santiago Ramon Y Cajal, S/N, 03550, Sant Joan d'Alacant, Alicante, Spain.

Registration

The course is limited to 20 participants.

Local students: Register before July 15, 2026, by writing a mail to gaincourse2026@gmail.com (with your PhD supervisor in copy) and stating "GAIN2026" as subject.

International students: FENS (<https://www.fens.org/>) and IBRO-PERC (<https://ibro.org/>) provide stipends of up to 750 EUR for Master and/or PhD students located in Europe interested in attending this course. Through these stipends FENS and IBRO-PERC aim to encourage and promote international experience of students; hence, students that are currently residing or studying in Portugal are not eligible for a FENS and IBRO-PERC stipend for this course. Apply for GAIN 2026 (deadline July 15, 2026):

<https://fens.jotform.com/260571016349354>

Programme

	Monday	Tuesday	Wednesday	Thursday	Friday
9:00-10:00	Lecture Jose V Sanchez-Mut	Keynote lecture Angel Barco	Guest lecture Ana B. Muñoz Manchado	Guest lecture Mario F. Fraga	Lecture Jose P Lopez-Atalaya
10:00-10:30h	break				
10:30h-11:30h	Expert talk Carmen Escolar <i>Bulk transcriptomics and epigenomics</i>	Lecture Rafael Alcala Vida	Expert talk Lorenzo Puche - Marina Guillot <i>Single-cell transcriptomics and epigenomics</i>	Expert talk Lara López - Roser Montañana <i>Sequencing-based spatial transcriptomics</i>	Lecture Violeta Duran
11:30h-11:40h	break				
11:40-12:40h	Hands-on session Carmen Escolar	Expert talk Sergio Niñerola <i>3D chromatin architecture and gene regulation</i>	Hands-on session Marina Guillot - Lorenzo Puche	Hands-on session Lara López - Roser Montañana	Expert talk Nitin Narwade <i>Imaging-based spatial transcriptomics</i>
12:40-13:30h		Hands-on session Sergio Niñerola			Hands-on session Nitin Narwade
13:30h-14:30h	break - lunch -				
14:45h-17:00h	Hands-on session Carmen Escolar	Hands-on session Sergio Niñerola	Hands-on session Marina Guillot - Lorenzo Puche	Hands-on session Lara López - Roser Montañana	Hands-on session Nitin Narwade
Hands-on topic	Bulk transcriptomics and epigenomics	3D chromatin architecture and gene regulation	Single-cell genomics	Sequencing-based Spatial Transcriptomics	Imaging-based Spatial Transcriptomics
Methods	RNA-seq, ATAC-seq, ChIP-seq, CUT&Tag	4C, Hi-C, HiChip	scRNAseq, scATACseq, scMultiome	Visium, Seeker, Treeker	MERFISH, Xenium