SIRIC MONTPELLIER CANCER · Inserm · IGF · ircm · IGH · igmm · UNIVERSITÉ DE MONTPELLIER · cnrs · GR-Ex

TRAINING

Unlocking Epigenomic Insights:
ATAC-seq Data Analysis in Practice

MAY 11-12-13, 2026

Montpellier Cancer Institute

Free 3-day training course

Up to **15 participants**

FACILITATED BY

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TRAINING PROGRAM

Requirements

Participants are expected to have basic proficiency in R and Unix command-line environments, along with foundational knowledge of statistics.
Participants must bring their own laptop.

11 MAY

From Experiment to Data: Epigenetics, ATAC-seq Fundamentals & Preprocessing

Objectives:
By the end of this day, participants will be able to explain key epigenetic concepts underlying chromatin accessibility, design a sound ATAC-seq experiment, assess raw data quality, and produce analysis-ready alignments and peak calls.

Topics covered: epigenetics & chromatin biology, experimental design principles, quality control, adapter trimming, read mapping, peak calling

12 MAY

Making Sense of Open Chromatin: Data Mining & Visualization

Objectives:
By the end of this day, participants will be able to identify differentially accessible regions, annotate them in a genomic context, and produce publication-ready visualizations.

Topics covered: peak annotation, differential accessibility analysis, functional enrichment, genome browser exploration, meta-profiles, heatmaps

13 MAY

Beyond Accessibility: Motifs, Footprinting & Multi-omic Integration

Objectives:
By the end of this day, participants will be able to apply advanced regulatory analysis methods and integrate ATAC-seq data with complementary omics layers to gain deeper biological insight.

Topics covered: motif enrichment analysis, transcription factor footprinting, multi-omic integration (e.g. RNA-seq, ChIP-seq)