

# 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

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### **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

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### **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

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### **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)*