Functional genomic analysis: Integrating sequencing data from Transcriptomics and Epigenomics:

RNA-seq and ChIP-Seq Analysis

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Effectives: 20

Language: English

Prerequisites:
none

Where?
Université Paris Cité
Moulin Campus

When?

Evaluation:
Oral exam on friday

Questions:
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Number ECTS: 3
Total numbers of hours:
30h
Teaching format:
lectures, practical

Teaching objectives

Learn to process, analyze and integrate RNA-seq data and ChIP-Seq data

Develop the skills to integrate transcriptomics and epigenomics data for a comprehensive functional genomic analysis.

Teaching outline

We will use **Galaxy** and **R** tools to analyze RNA-seq and ChIP-Seq data in understanding gene regulation.

RNA-seq Data Analysis
Introduction to RNA-seq: Experimental setup
Quality control, alignment, and quantification.
Graphical representations of data

ChIP-Seq Data Analysis

Introduction to ChIP-Seq: Experimental setup and histone mark profiling.
Quality control, mapping, peak calling, and annotation.(e.g., promoters, enhancers).
Graphical representations of data

Integrative Genomic Analysis

Combining RNA-seq and ChIP-Seq data to link expression profiles with epigenetic modifications.
Visualization of integrated data using genome browsers (IGV, UCSC) and bioinformatics tools (R packages).