ChIP-seq, RNA-seq and Hi-C: treatment, analysis and data visualization

Scientific and technical environment of the training course

INSTITUT DE GÉNÉTIQUE MOLÉCULAIRE DE MONTPELLIER

Institut de génétique moléculaire de Montpellier
http://www.igmm.cnrs.fr

COURSE DIRECTORS

Jean-Christophe ANDRAU
Senior researcher
UMR 5535
Amal MAKRINI
Research engineer
UMR 5535
Cyril ESNAULT
Researcher
UMR 5535

LOCATION

MONTPELLIER (34)

ORGANISATION

4,5 days: from Monday 02:00 p.m. to Friday 05:00 p.m.
Training course in English
From 8 à 12 attendees

TEACHING METHODS

- Lectures (5h) and practical courses (27h)
- Practical courses are supervised by 1 teacher for 4 attendees

Along the course, corrected exercises will allow the attendees to evaluate their knowledge acquisition.

TRAINING FEES

1950 Euros

AT THE END OF THE TRAINING COURSE

- Satisfaction survey from trainees
- A certificate of training is delivered

COURSE DATE

Ref. 23 028 : from Monday 22/05/23 to Friday 26/05/23

OBJECTIVES

- Learn how to plan a simple experiment of ChIP-seq or RNA-seq
- Acquire the skills to evaluate data quality for transcriptome and gene regulation experiments
- Understand and apply the principal methods and analysis tools for RNA-seq and ChIP-seq
- Be able to visualize data in a genome browser and extract enriched regions
- Learn how to manipulate and annotate enriched regions files using bedtools
- Become acquainted with the principal methods of analysis for long-distance genomic interactions (Hi-C) and generate chromosomal interaction maps

AUDIENCE

Engineers and researchers in biology

Pre-requirement : knowledge of basic command lines under Linux can be useful but is not absolutely required. A recall of basic knowledge will be proposed.

TRAINING PROGRAMME

Day 1: ChIP-seq and RNA-seq data pre-processing

- Initiation to Linux command lines (3 h)
- Basic notions of ChIP-seq, RNA-seq and Hi-C and their analysis pipeline, principle of spike-in normalization
- Pre-treatment of data (quality of raw data, alignments, sequencing artifacts)
- Exploration of aligned data (fragments size estimation, alignment quality)

Days 2 and 3: ChIP-seq analysis

- Generation of signal files (.wig) using the R-PASHA package
- Visualization of .wig files and isolation of enriched regions adapting detection parameters (MACS2 or using a genome browser option)
- Initiation to meta-profiling around regions of interest (genes, TSS, TES, enhancers)
- Enrichment of functional annotations (gene ontology)
- Motif search in enriched regions
- External spike-in normalization

Day 4: RNA-seq analysis

- Quantification of gene expression in RNA-seq data (RPKM)
- Spike-in normalization principle
- Differential gene expression analysis for transcripts and exons

Day 5: Hi-C analysis

- Quality controls, alignment and filtering of Hi-C data
- Generation of a chromosomal interaction map
- Visualization and interpretation of the interaction matrix
- Identification of subnuclear compartments
- Identification of Topologically Associating Domains (TADs) and loops
- Presentation of few databases and visualization tools for Hi-C
- Discussion (1 h) around participants questions and own problematics

EQUIPMENT

Each participant will access a working station under Linux with pre-installed softwares required for the training.