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

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-requisite: 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 problematic

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

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