

Workshop

Bioinformatics analysis of ATAC-seq data

Organizer

CUBiDA (Core Unit Bioinformatik, Datenintegration und Analyse) at the Universitätsklinikum Erlangen

Instructors

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Outline

This workshop will provide an overview of Assay for Transposase-Accessible Chromatin with sequencing (ATAC-seq) technology, covering its biological and technical principles. Participants will learn about the steps involved in ATAC-seq data analysis, from initial data processing to downstream analyses. The workshop will include hands-on sessions where participants will have the opportunity to independently explore and execute key stages of the analysis.

Outcome

Upon successful completion of this workshop, participants will be able to:

- Understand the principles of ATAC-seq and its applications in chromatin accessibility studies.
- Perform quality control checks on raw ATAC-seq data.
- Map reads to the reference genome using appropriate tools.
- Identify and remove potential biases in ATAC-seq data.
- Call peaks and identify differentially accessible regions.
- Perform downstream analyses such as motif enrichment analysis and gene ontology analysis.
- Visualize and interpret ATAC-seq data using various tools.
- Understand the limitations and challenges of ATAC-seq data analysis.

Number of participants

15

Target audience

This workshop is designed for biomedical researchers with a foundational interest in ATAC-seq.

Prerequisites

While beginner-friendly in its approach to ATAC-seq analysis, the workshop assumes basic proficiency in working with the command line, scripting languages (such as Bash), and the R statistical environment.

Teaching format

This workshop will combine interactive lectures with hands-on exercises. All participants will have access to dedicated workstations equipped with the necessary software and datasets.

We will also provide you with all teaching materials, including presentations, scripts, and data files, for your future reference.

Provisional workshop schedule

DAY 1	
8:30-16:30	Introduction to chromatin accessibility and ATAC-seq technology. Quality control checks on raw ATAC-seq data using FastQC. Read mapping to the reference genome using Bowtie2/BWA. Introduction to peak calling algorithms. Peak calling and filtering using MACS2. Introduction to data visualization with IGV. Signal Visualization with deepTools.
DAY 2	
8:30-16:30	Introduction to differential accessibility analysis. Differential accessibility analysis of replicate samples with DiffBind. Introduction to motif enrichment analysis. Motif enrichment analysis using HOMER. Gene ontology analysis using clusterProfiler. Aggregation of reports with interactive plots for multiple bioinformatics analyses with MultiQC.

At least one break will be provided each morning and afternoon.

Questions

Please, contact us at mik-cubida@uk-erlangen.de.