

Epigenomics: ATAC-Seq & Methylation — Hands-on

Gain expertise in epigenomics using ATAC-Seq and DNA methylation workflows, from QC and peak calling to footprinting, DMR analysis, and reproducible reporting.

Epigenomics (ATAC-Seq, Methylation)

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Session 1

Fee: Rs 6300 [Apply Now](#)

Library QC & Read Processing

Experimental design, controls and metadata capture

Theory

FASTQ QC, trimming and adapter removal

[FastQC](#) [MultiQC](#) [Cutadapt](#) [fastp](#)

Alignment and duplicate handling for chromatin assays

[Bowtie2](#) [BWA-MEM2](#) [Picard](#) [samtools](#)

Session 2

Fee: Rs 8400 [Apply Now](#)

ATAC-Seq Peaks & Footprinting

Peak calling, TSS enrichment and FRiP metrics

MACS2 **deepTools** **ATACseqQC**

Motif analysis and transcription factor footprints

HOMER **HINT-ATAC** **TOBIAS**

Peak annotation and regulatory context

ChIPseeker **GREAT** **bedtools**

Session 3

Fee: Rs 11200 Apply Now

Bisulfite Mapping & DMRs

WGBS and RRBS library concepts and QC checks

Theory

Bisulfite aware alignment and methylation extraction

Bismark **BS-Seeker2** **Methyldackel**

Differential methylation regions and annotation

methyKit **DSS** **annotatr**

Session 4

Fee: Rs 14000 Apply Now

Mini Capstone: Epigenomics Pipeline

Design an end to end ATAC and methylation workflow with provenance

Theory

Automate QC to peaks or DMRs with unified reports

Snakemake **Conda/Mamba** **MultiQC**

Publish ready figures and tables for regulatory interpretation

`pandas` `ggplot2` `R Markdown/Quarto`