

NGS Data Handling & QC — Hands-on

Gain expertise in NGS data handling and quality control—FASTQ integrity, trimming and filtering, contamination screening, alignment QC, and reproducible reports.

NGS Data Handling & Quality Control

[Help Desk](#) · [WhatsApp](#)

Session Index

[Session 1 — FASTQ Integrity & Baseline QC](#) [Session 2 — Trimming, Filtering & Screening](#) [Session 3 — Alignment Metrics & Post-QC](#) [Session 4 — Mini Capstone: QC Pipeline](#)

Session 1

Fee: Rs 6300 [Apply Now](#)

FASTQ Integrity & Baseline QC

Directory layout, naming, checksums & metadata capture

[sha256sum](#) [MD5](#) [CSV/TSV manifests](#)

FASTQ structure: PHRED scores, barcodes & lanes

[Theory](#)

Baseline QC and multi-sample summaries

[FastQC](#) [MultiQC](#) [seqtk](#)

Session 2

Fee: Rs 8400 [Apply Now](#)

Trimming, Filtering & Screening

Adapter/quality trimming & length/complexity filters

Cutadapt **Trimmomatic** **fastp**

Contamination screening & host read removal

FastQ Screen **Kraken2** **BBDMap**

Deduplication, downsampling & QC re-evaluation

clumpify **seqtk sample**

Session 3

Fee: Rs 11200 Apply Now

Alignment Metrics & Post-QC

Short/long-read alignment & primary metrics

BWA-MEM2 **Bowtie2** **STAR**

SAM/BAM QC, duplicates, insert size & coverage stats

samtools stats/flagstat **Picard metrics** **mosdepth**

Spike-in checks, strandedness & library complexity

RSeQC **preseq**

Session 4

Fee: Rs 14000 Apply Now

Mini Capstone: QC Pipeline

Design reproducible QC workflow from raw reads to report

Theory

Automate FastQC→trim→screen→align→metrics with provenance

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

Deliver dashboards, artifacts & submission-ready metadata

`pandas` `JupyterLab` `Quarto`