Read QC, Host Depletion & Contaminant Screening — Hands-on

Learn how to move from raw FASTQs to clean, analysis ready microbiome and metagenomic datasets. You will design read QC, trimming and filtering workflows, implement host depletion and systematically screen for contaminants, with clear run level reports for downstream taxonomic, functional and MAG analytics.

Read QC, Host Depletion & Contaminant Screening

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Session Index

Session 1

Fee: Rs 8800 Apply Now

Raw Reads, FASTQ Structure & Basic QC

FASTQ format and sequencing error profiles

- read layout and quality scores
- per base quality patterns
- adapter and primer remnants

QC reports and run health interpretation

- per sequence GC and length
- overrepresented sequences
- duplication, N content

Toolchain overview for read QC

FastQC / MultiQC concepts command line basics project folder organization

Session 2

Fee: Rs 11800 Apply Now

Trimming, Filtering & Read Retention

Adapter and quality trimming strategies

sliding window vs fixed trim paired end constraints minimum length thresholds

Filtering for complexity, Ns and artifacts

low complexity filters N rich reads duplicate and optical duplicates

Balancing stringency and data retention

yield vs quality trade offs amplicon vs shotgun needs documenting parameter choices

Session 3

Fee: Rs 14800 Apply Now

Host Depletion & Decontamination Pipelines

Host read removal strategies post sequencing

read mapping to host genome choice of reference builds alignment vs k mer approaches

Contaminant screening and background catalogs

kit and lab contaminants blank and negative controls statistical contaminant calling

End to end decontamination workflow design

workflow managers and scripts intermediate file management logging and provenance capture

Session 4

Fee: Rs 18800 Apply Now

Mini Capstone: Clean FASTQs for Analysis

Designing and running a complete QC pipeline

Theory plus hands on

Comparing pre and post QC, host and contaminant removal

read retention summaries QC dashboards decision logs for reviewers

Deliverables: QC report pack and reusable workflow

MultiQC style summaries configurable pipeline scripts documentation for collaborators