Metatranscriptomics Community RNA Seq Workflows — Hands-on

Learn how to profile active gene expression in microbiomes using metatranscriptomic community RNA sequencing. You will plan metatranscriptomics experiments, configure read QC and mapping workflows, quantify transcripts, perform differential expression and generate functional pathway reports for clinical, environmental and industrial cohorts.

Metatranscriptomics Community RNA Seq Workflows

Help Desk · WhatsApp

Session Index

Session 1

Fee: Rs 8800 Apply Now

Study Design & Wet Lab Considerations

Metatranscriptomics in microbiome projects

RNA vs DNA based views · activity vs potential · links to environment and host

Sample collection, stabilization & RNA extraction concepts

preserving RNA integrity · matrix specific challenges · co extracted inhibitors mindset rRNA depletion, library prep & sequencing design

polyA vs rRNA depletion ideas | paired end vs single end | depth and replication planning

Session 2

Fee: Rs 11800 Apply Now

Read QC, Mapping & Quantification

Read QC for community RNA Seq data

adapter and quality trimming logic | host read removal thinking | rRNA depletion efficiency checks

Mapping strategies for metatranscriptomes

mapping to MAGs or reference catalogs | handling multi mapped reads | strand specific considerations

Quantification units and normalization concepts

counts vs TPM style units | library size and compositionality | batch and technical effect checks

Session 3

Fee: Rs 14800 Apply Now

Differential Expression & Pathway Views

Differential expression frameworks for metatranscriptomes

design matrices and contrasts | multiple testing thinking | effect sizes and shrinkage ideas

Functional and pathway level summaries of activity

mapping transcripts to gene families | pathway enrichment mindsets | linking to metagenomic potential

Visualization of active pathways and transcripts volcano and MA style plots heat maps and bubble plots condition wise pathway panels

Session 4

Fee: Rs 18800 Apply Now

Mini Capstone: Community RNA Seq Report

End to end metatranscriptomics workflow on a cohort

Theory plus guided practical

Interpreting active pathways with metadata and outcomes

linking expression to interventions clinical and environmental case styles caveats in causal interpretation

Deliverables: count matrices, plots & methods block

normalized count and DE tables pathway / activity figures reusable metatranscriptomics methods text