Shotgun Metagenomics Library Prep & Platforms — Hands-on

Learn how to take microbiome and environmental DNA from extraction to high quality shotgun metagenomics libraries. You will plan fragmentation, library construction, host depletion and platform selection, and interpret run level QC so that downstream assembly, profiling and MAG workflows are reliable.

Shotgun Metagenomics Library Prep and Platforms

Help Desk · WhatsApp

Session Index

Session 1

Fee: Rs 8800 Apply Now

Shotgun Metagenomics Concepts & Use Cases

What shotgun metagenomics measures vs amplicon

taxonomic + functional profiling **MAGs and strain resolution** **resistome and mobilome**

When to choose shotgun designs

clinical and AMR studies **environmental and wastewater** **industrial and bioprocess monitoring**

Input requirements and complexity considerations

DNA yield and integrity **community complexity** **host background load**

Session 2
Fee: Rs 11800 Apply Now

DNA QC, Fragmentation & Library Construction

Input DNA QC and contamination checks

spectrophotometry and fluorometry **fragment analysis** **host DNA estimation**

Fragmentation and end repair workflows

enzymatic vs mechanical **target insert size** **over fragmentation pitfalls**

Library construction chemistries and indexing

ligation and tagmentation kits **single vs dual index adapter dimer control**

Session 3
Fee: Rs 14800 Apply Now

Host Depletion, Size Selection & Platform Choice

Host depletion strategies and trade offs

physical and enzymatic depletion **capture based approaches** **impact on community structure**

Size selection and pooling for metagenomes

bead ratios and cleanup **insert distribution checks** **equimolar pooling approaches**

Platform and run configuration selection

short read Illumina platforms **long read options (ONT**

/ PacBio) depth and coverage planning

Session 4

Fee: Rs 18800 Apply Now

Run Metrics, QC & Handoff to Bioinformatics

Run metrics and troubleshooting

Theory + guided practical

Base calling, demultiplexing and data delivery

BCL to FASTQ pipelines sample sheet verification data integrity checksums

Deliverables: run QC pack and bioinformatics handoff spec

run reports and plots library and sample manifest metadata + FASTQ packaging guidelines