Taxonomic Profiling & Strain-Level Analytics — Hands-on

Build practical skills for converting shotgun metagenomics reads into robust taxonomic profiles and strain level insights. This module covers marker gene and k mer based profilers, reference database strategy, benchmarking with mock communities, and strain aware workflows for clinical, environmental and AMR focused microbiome projects.

Taxonomic Profiling & Strain-Level Analytics

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Session Index

Session 1

Fee: Rs 8800 Apply Now

Taxonomic Profiling Fundamentals

Concepts in read based taxonomic profiling

- marker gene versus whole genome
- k mer and alignment based
- relative versus absolute views

Mainstream profiling tools and workflows

- Kraken2 / Bracken
- MetaPhlAn / HUMAnN context
- Centrifuge and alternatives

Inputs, outputs and basic QC for profiles

- clean host depleted reads
- taxon count and relative

tables read assignment statistics

Session 2

Fee: Rs 11800 Apply Now

Databases, Benchmarks & Performance

Reference database choices and trade offs

NCBI RefSeq and GTDB curated marker sets custom and host filtered builds

Building and updating profiler databases

Kraken2 database builds MetaPhlAn reference updates storage and reproducibility notes

Benchmarking with mock communities and metrics

precision, recall and F1 L1 distance and correlation runtime and memory considerations

Session 3

Fee: Rs 14800 Apply Now

Strain-Level & Subspecies Analytics

Moving from species to strain level views

SNVs, haplotypes and microdiversity coverage depth and breadth clonality and mixtures

Strain aware tools and workflows

StrainPhlAn and related tools inStrain and mapping based approaches MAG based strain comparison overview

Use cases: transmission, persistence and AMR context

patient and household transmission longitudinal carriage and relapse linking to resistome modules

Session 4

Fee: Rs 18800 Apply Now

Mini Capstone: Comparative & Strain Aware Profiling

Designing a comparative taxonomic profiling analysis

guided theory plus practical

Running one profiler and one strain level workflow

from clean reads to taxon tables | basic strain comparison | visual summaries for reporting

Deliverables: profiles, strain summaries and metadata

taxon abundance tables | strain distance or tree outputs | analysis notes for downstream modules