Learn how to turn shotgun metagenomics reads into interpretable functional profiles and pathways. This module focuses on gene family abundance (KOs, ECs, UniRef), HUMAnN-style workflows, KEGG/MetaCyc pathway reconstruction, normalization strategies, and differential functional analysis in microbiome and AMR contexts.

Functional Profiling & Pathway Reconstruction

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Session 1
Fee: Rs 8800   Apply Now
Functional Profiling Concepts & Gene Families

From taxonomic to functional views of microbiomes

genes, pathways and modules   taxon contribution to function   context for AMR and metabolism

Gene family concepts and annotation spaces

KEGG Orthology (KOs), EC numbers   UniRef90/50, eggNOG, COGs   GO terms and functional categories

Read alignment and translated search basics

pangenome and protein databases Bowtie2 / DIAMOND style workflows sensitivity vs runtime trade offs

Session 2
Fee: Rs 11800 Apply Now

HUMAnN Workflows & Pathway Reconstruction

HUMAnN style pipelines: overview and logic

taxonomic prescreening pangenome versus unaligned reads gene families to pathways

Pathway reconstruction with KEGG/MetaCyc style resources

pathway definitions and modules presence/absence vs abundance completeness thresholds

Outputs: gene family, pathway and contribution tables

stratified vs unstratified outputs linking to taxonomic profiles export for R and Python analysis

Session 3
Fee: Rs 14800 Apply Now

Normalization & Differential Functional Analysis

Units, scaling and compositionality in functional data

RPK, RPKM, CPM and relative abundance copies per million vs coverage link to compositional thinking

Normalization and transformation strategies

library size and length corrections CLR/log transforms for functions batch and covariate adjustment overview

Differential pathway and gene family analysis

DESeq2 / edgeR style workflows multiple testing and effect sizes visualizations: volcano, heatmaps

Session 4
Fee: Rs 18800 Apply Now

Mini Capstone: Taxon-to-Function Story

Designing a small functional profiling analysis

guided theory plus practical

Running a HUMAnN style workflow on a teaching dataset

gene family and pathway tables basic differential functions link to taxon profiles from earlier modules

Deliverables: figures, tables and narrative for a microbiome question

functional heatmaps and barplots pathway summary tables short report tying taxa to functions