Amplicon (16S/ITS/18S) Analysis & Compositional Data Principles — Hands-on

Learn how to take raw 16S/ITS/18S reads through quality control, denoising, feature table construction, taxonomy and phylogeny, while respecting the compositional nature of microbiome data. This module focuses on practical amplicon workflows with QIIME 2 and related tools, plus the statistical mindset needed for downstream analyses.

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Session Index

Session 1

Fee: Rs 8800 Apply Now

From Raw Reads to Quality Filtered Data

Understanding amplicon read structure and metadata linkage

- barcodes and primers
- paired end overlap
- sample and run metadata

Quality profiles and trimming strategies

- Phred quality curves
- adapter and primer removal
- cutadapt and other tools

Demultiplexing and initial quality control in QIIME 2

import and manifest files per sample sequence counts QC summaries and reports

Session 2

Fee: Rs 11800 Apply Now

Denoising, Feature Tables & Taxonomy

Denoising with DADA2 or Deblur

ASVs versus OTUs error models chimera handling

Feature table construction and filtering

samples versus features matrix prevalence and abundance filters rare features and noise

Taxonomic assignment and phylogeny building

reference databases (SILVA, Greengenes, UNITE) naive Bayes classifiers phylogenetic trees for diversity metrics

Session 3

Fee: Rs 14800 Apply Now

Compositional Data & Normalization Strategies

Why microbiome data are compositional

library size and relative scale closure and spurious correlations Aitchison geometry intuition

Normalization and transformation options

rarefaction and its limits relative abundance CLR, ALR and ILR transforms

Preparing feature tables for downstream diversity and differential analyses filtering low depth samples handling zeros exporting to R and Python

Session 4

Fee: Rs 18800 Apply Now

Mini Capstone: End-to-End Amplicon Workflow

Designing and running a small 16S workflow

guided theory plus practical

Quality reports, feature tables and taxonomy summaries

QIIME 2 visualizations **exported tables** **basic diversity preview**

Compositional checklist and documentation for next modules

pipeline and parameter log **data export and backup** **FAIR and reproducibility notes**