

Microbiome Statistics: Compositional Data & Bias Correction — Hands-on

Build statistically rigorous, bias-aware microbiome analyses from the ground up. This module focuses on compositional data principles (Aitchison geometry), correct normalizations and transformations, robust differential abundance, and thorough handling of batch effects, zeros, confounders, and technical bias. You will implement analyses in R/Python/QIIME 2 and deliver a reproducible mini-report with checklists and interpretation notes.

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Session 1

Fee: Rs 8800 [Apply Now](#)

Compositional Foundations & Transforms

Aitchison geometry & pitfalls of rarefaction/TSS-only views

[closure & subcompositional coherence](#) [library-size confounding](#) [feature prevalence filtering](#)

Transforms & balances

[CLR/ALR/ILR](#) [SBP/phylogenetic ILR \(PhILR\)](#) [balance](#)

trees & interpretation

Zeros & limits of detection

multiplicative/Bayesian replacement **pseudo-count strategies** **sensitivity analyses**

Session 2

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Distances, Ordinations & Hypothesis Tests

Distance choices & ordination

Aitchison (Euclidean on CLR) **robust PCA**
(DEICODE/RPCA) **UniFrac vs composition-aware**

Group comparisons & covariates

PERMANOVA/permdisp caveats **AN(C)OVA on balances** **effect sizes & CIs**

Power/size for compositional analyses

simulation & Dirichlet-multinomial **sparsity & prevalence impacts** **multiple testing control**

Session 3

Fee: Rs 14800 Apply Now

Differential Abundance & Confounding

DA methods (strengths & caveats)

ANCOM-BC / ALDEx2 **corncob / Songbird (QLR)** **W-statistics & rankings**

Covariates & mixed models on balances

MaAsLin2 with CLR/ILR **random effects (subject/time)**
stratified/blocked analyses

Sensitivity & robustness checks

zero-handling variants rare taxa vs aggregates
simulation-based validation

Session 4

Fee: Rs 18800 Apply Now

Batch/Bias Correction & Reproducible Reporting

Batch & unwanted variation

ComBat/ComBat-Seq; RUV-III-NB removeBatchEffect
(limma) percentile normalization

Technical bias awareness

PCR/primer & lysis biases spike-ins & mock
communities contamination checks

Reporting, checklists & exports

Quarto notebooks & model cards tables/figures + env
files assumptions & limitations