Multi-Omics Integration for Systems Models — Hands-on

Learn how to move beyond single omics analysis and build integrated, systems level views of biology. This module covers study design for multi omics, data harmonization and batch handling, statistical and latent factor integration (e.g., mixOmics, MOFA), and network or model centric integration to constrain GRNs, signaling pathways and GEMs. You will implement reproducible workflows in R and Python that turn multi omics layers into mechanistic insight and model ready inputs.

Multi-Omics Integration for Systems Models

Help Desk · WhatsApp

Session Index

Session 1

Fee: Rs 8800 Apply Now

Omics Modalities, QC & Harmonization

Omics layers & experimental design for integration

genomics / epigenomics **transcriptomics / proteomics** **metabolomics / phenotypes**

Preprocessing, normalization & batch effects

platform specific QC **cross cohort harmonization** **batch correction (Combat, limma)**

Common identifiers and feature mapping

gene, protein & metabolite IDs mapping to pathways and networks feature selection for integration

Session 2

Fee: Rs 11800 Apply Now

Statistical & Matrix Based Integration

Unsupervised integration methods

PCA / MFA / CCA MOFA style latent factor models (overview) clustering and sample stratification

Supervised and discriminant integration

partial least squares (PLS / sPLS) DIABLO multi omics integration (overview) feature importance and stability

Toolchain implementation

R: mixOmics, MOFA2 (overview) Python: scikit learn pipelines reproducible notebooks and reports

Session 3

Fee: Rs 14800 Apply Now

Network, Pathway & Model Centric Integration

Network based integration approaches

similarity network fusion (SNF overview) multi layer networks module and community detection

Pathway and systems model overlays

multi omics pathway enrichment mapping to GRNs and signaling models linking to GEMs and flux constraints

Tools and visualization

Cytoscape, igraph, graph tools | KEGG / Reactome overlays | linking outputs to modeling platforms

Session 4

Fee: Rs 18800 Apply Now

Mini Capstone: From Multi-Omics to a Systems Model

Case study: integrate at least two omics layers into a systems model context

Theory + Practical

From integration outputs to model constraints and validation

deriving network or pathway signatures | feeding constraints into GRN, signaling or GEM | checking consistency with experimental phenotypes

Deliverables

PDF/HTML multi omics integration report | R/Python notebook and scripts | environment.yml / requirements.txt