Glycoproteomics Quantification — Label-Free & Isobaric — Hands-on

Learn how to plan, run and interpret quantitative glycoproteomics studies using both label-free and isobaric workflows. This module walks through experimental design, LFQ and iBAQ style label-free quantification, TMT/iTRAQ based multiplexing, normalization, batch correction and data visualization for confident biological conclusions.

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Session 1

Fee: Rs 8800 Apply Now

Quantitative Glycoproteomics Designs & Controls

Study designs for quantitative glycoproteomics

case vs control and time course **biological vs technical replicates** **blocking and randomization**

Choosing between label-free and isobaric approaches

sample numbers and depth **instrument time constraints** **precision vs flexibility**

Controls, standards and reference channels

QC pools and references | spike in glycoprotein standards | bridging across batches

Session 2

Fee: Rs 11800 Apply Now

Label-Free Quantification (LFQ/iBAQ)

MS1 intensity based label-free concepts

peak picking and integration | feature alignment across runs | match between runs ideas

LFQ and iBAQ type metrics for glycopeptides

relative vs approximate absolute | handling charge states and isotopes | intensity transforms (log2)

Normalization and missing value strategies

global vs local scaling | median/quantile approaches | imputation options for glyco data

Session 3

Fee: Rs 14800 Apply Now

Isobaric Quantification (TMT/iTRAQ)

Designing TMT/iTRAQ based glycoproteomics experiments

channel layouts and multiplexing | reference channels and bridging | batching large cohorts

Reporter ion based quantification and ratio compression

reporter extraction windows | coisolation and interference | MS3 and SPS concepts

Normalization and batch correction for isobaric data

within and between run scaling | using reference

channels visual QC of channel performance

Session 4

Fee: Rs 18800 Apply Now

Mini Capstone: Quantitative Glycoproteomics Comparison

Build a small quantitative workflow on example glyco datasets

label-free and/or TMT style data

Generate differential glycoprotein and glycoform summaries

log2 fold changes and p values volcano and heatmap plots linking results to biology or CQAs

Deliverables and documentation set

processed quant tables plots for a short report notes on normalization and batch handling