Label Free & Isobaric Quantitative Proteomics — Hands-on

Design and execute robust quantitative proteomics studies using both label free and isobaric strategies. Learn how to plan channels and replicates, control inter batch variation, handle missingness, normalize and transform data, and apply sound statistics for differential protein abundance with publication ready outputs.

Label Free & Isobaric Quantitative Proteomics

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Session Index

Session 1

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Quantitation Strategies & Study Design

Choosing label free vs isobaric designs

discovery vs targeted goals **depth vs throughput** **budget and instrument time**

Replicates, blocking and channel planning

biological vs technical replicates **balanced groups** **pooled reference channels**

Sources of variability in quantitation

sample prep and load | LC MS drift | batch and instrument effects

Session 2

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Label Free Quantitation Workflows

Intensity and spectral counting approaches

MS1 feature based LFQ | spectral counts | match between runs concepts

Feature detection and alignment

RT alignment | peak integration | handling shared peptides

Export formats and QC for LFQ data

protein groups tables | CVs within groups | missingness patterns

Session 3

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Isobaric (TMT/iTRAQ) Design & Analysis

TMT and iTRAQ chemistry and multiplexing

channel layout | bridge channels | reference designs

Ratio compression and interference handling

co isolation effects | MS3 and SPS ideas | filtering high interference PSMs

Reporter ion extraction and QC

reporter S/N | missing channels | channel balance checks

Session 4

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Normalization, Batch Correction & Statistics

Normalization strategies for protein intensities

global scaling | median and quantile | log transforms

Batch correction and missing value handling

combat like correction ideas | missing not at random scenarios | imputation strategies

Differential abundance and reporting

moderated t tests | FDR controlled hit lists | volcano plots and heatmaps