Data Standards and Repositories — PRIDE mzIdentML mzTab — Hands-on

Understand how modern proteomics datasets are structured, annotated and shared through community standards and repositories. This module introduces mzIdentML and mzTab concepts, PRIDE and ProteomeXchange style submissions at a high level, and how to design studies and metadata so that data are reusable and compliant with FAIR principles.

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Session Index

Session 1

Fee: Rs 8800 Apply Now

FAIR Proteomics & Data Standards Foundations

Why proteomics needs standards and repositories

large multi sample LC–MS/MS studies · complex workflows and parameters · reproducibility and reuse motivations

FAIR principles applied to proteomics datasets

findable and accessible concepts · interoperable formats and vocabularies reusable through rich metadata

Overview of key proteomics formats and repositories

raw vendor files vs open formats identification and quant layers PRIDE and ProteomeXchange landscape

Session 2

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mzIdentML, mzTab & Related File Concepts

Thinking in terms of identification result formats

search engine output structure ideas PSM, peptide and protein levels scores, FDR and metadata fields

Conceptual view of mzIdentML and its building blocks

spectra, peptide and protein sections controlled vocabulary usage idea linkages to raw data references

mzTab style tabular summaries for sharing results

small molecule and proteomics sections table like view of IDs and quant using mzTab for downstream tools

Session 3

Fee: Rs 14800 Apply Now

PRIDE Style Submissions & Metadata Thinking

What a typical PRIDE submission contains conceptually

raw files and peak lists identification and quant outputs study metadata and protocols

Designing metadata and sample descriptions on paper

sample groups and experimental factors instrument and method descriptors controlled vocabulary term usage

Public vs private access and embargo concepts

embargo during manuscript review accession numbers and citations releasing data for community reuse

Session 4

Fee: Rs 18800 Apply Now

Data Management Plans, Reuse & Reporting

Sketching a proteomics data management plan

theory plus planning worksheet

Thinking about reuse and secondary analyses

re mining public PRIDE datasets benchmarking and method development integrating with other omics layers

Reporting data standards and deposition in manuscripts

accession numbers and links methods text for formats and repos checklists for reviewers and readers