Glyco-Bioinformatics — Search Engines & File Formats — Hands-on

Build practical glyco-bioinformatics pipelines from raw LC-MS data to standardized, shareable outputs. This module focuses on glycan encodings, search engines, scoring schemes and open file formats such as mzML, mzIdentML and mzTab, together with guidelines for MIRAGE and FAIR-compliant export that plugs into downstream statistics and visualization.

Glyco-Bioinformatics — Search Engines & File Formats

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Session Index

Session 1

Fee: Rs 8800 Apply Now

Glycan Encodings, IDs & Data Structures

Representing glycans in software tools and databases

- composition vs structure encodings
- SNFG linkage notation recap
- tree and graph like data models

Glycan identifier systems and notations

- database accession styles
- text encodings overview
- mapping between ID systems

Core tables for glyco analysis projects

sample, run and file metadata | feature and identification tables | linking to experimental factors

Session 2
Fee: Rs 11800 Apply Now

Glyco Search Engines & Scoring Workflows

Overview of released glycan and glycopeptide search tools

searches for released glycans | intact glycopeptide engines | vendor integrated workflows

Configuring searches and score models for glycans

search space and modification lists | mass tolerances and adduct rules | fragment ion and oxonium support

Practical search engine output handling

export to tabular formats | joining IDs with quant tables | basic R / Python parsing templates

Session 3
Fee: Rs 14800 Apply Now

File Formats, Standards & Converters

MS data and identification file formats in glycomics

raw vendor formats and mzML | mzIdentML for IDs | mzTab style summary tables

MIRAGE, MSI levels and reporting expectations

minimum information concepts | capture of instrument and method details | linking IDs to evidence and spectra

Using converters and validation tools

converting vendor to open formats checking file integrity and metadata troubleshooting common issues

Session 4

Fee: Rs 18800 Apply Now

Mini Capstone: Glyco-Bioinformatics Analysis Report

Assemble a small glyco-bioinformatics workflow on example data

from raw file to standardized ID and quant tables

Create export ready files for statistics and repositories

curated identification spreadsheet annotated mzML and mzTab metadata summary pages

Deliverables and documentation set

FAIR oriented data package short glyco-bioinformatics report checklist for MIRAGE style reporting