GC–MS Workflows — Derivatization & Deconvolution — Hands-on

Build end-to-end GC–MS metabolomics competence, from choosing columns and temperature programs to optimizing derivatization reactions and performing deconvolution of complex chromatograms. This module focuses on volatile and semi-volatile metabolites, derivatization strategies, practical acquisition setups and data quality checks that feed into downstream annotation and quantitation pipelines.

GC–MS Workflows — Derivatization & Deconvolution

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Session 1 — GC–MS Principles & Hardware for Metabolomics
Session 2 — Derivatization Chemistry & Workflows
Session 3 — Acquisition, Deconvolution & Data Quality
Session 4 — Mini Capstone: GC–MS Method & Deconvolution Plan

Session 1

Fee: Rs 8800 Apply Now

GC–MS Principles & Hardware for Metabolomics

Gas chromatography fundamentals for metabolomics

volatility and thermal stability **capillary columns and stationary phases** **temperature programs and ramps**

Mass spectrometry and EI ionization basics

electron ionization (EI) **quadrupole / TOF analyzers**

scan speed and mass range

GC–MS system setup and maintenance

inlet liners and syringes | leak checks and tuning | source cleaning and performance logs

Session 2

Fee: Rs 11800 Apply Now

Derivatization Chemistry & Workflows

Why derivatization is needed in metabolomics

increasing volatility and stability | improved peak shape and response | functional group targeting

Common derivatization chemistries

oximation and methoximation | silylation (MSTFA / BSTFA) | alkylation and acylation examples

Optimizing derivatization workflows

reaction time and temperature | solvent and reagent stability | minimizing artefacts and degradation

Session 3

Fee: Rs 14800 Apply Now

Acquisition, Deconvolution & Data Quality

Acquisition methods and injection strategies

split vs splitless injection | full scan, SIM and MS/MS options | retention time locking concepts

Peak detection and deconvolution concepts

co-elution and overlapping peaks | mass spectral deconvolution | library matching (NIST etc.)

QC metrics and troubleshooting GC–MS data

retention time drift | sensitivity loss and contamination | blank and QC chromatogram review

Session 4

Fee: Rs 18800 Apply Now

Mini Capstone: GC–MS Method & Deconvolution Plan

Designing a GC–MS method for a metabolomics use case

clinical, nutrition or microbial study

Injection order, QC layout and derivatization schedule

blank, QC and calibration placement | batching and drift control | sample stability planning

Deliverables: GC–MS method, derivatization SOP & QC checklist

temperature and timing program | reagent and column details | deconvolution and review workflow