

Fluxomics Modeling from Tracer Data — EMU & COBRA — Hands-on

Learn how to move from stable isotope labeling data to quantitative intracellular flux maps. This module focuses on the EMU framework, ¹³C metabolic flux analysis workflows, building reaction and atom mapping models, fitting fluxes to tracer data and interpreting flux distributions together with COBRA-style constraint-based models for systems-level insight.

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Session 1

Fee: Rs 8800 [Apply Now](#)

Fluxomics Concepts & EMU Framework

From tracer experiments to fluxomics questions

[pool sizes vs fluxes](#) [steady state vs non steady state](#)
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EMU (Elementary Metabolite Unit) framework basics

[isotopomers, isotopologues and EMUs](#) [atom](#)
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full isotopomer models

Inputs, assumptions and data requirements

reaction network and reversibility **measured labeling patterns and flux bounds** **identifiability and experimental design links**

Session 2

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Building EMU / Isotopomer Models

Defining the metabolic network for ¹³C MFA

choosing reactions and compartments **irreversible vs reversible splits** **linking to genome scale models**

Atom mapping and EMU decomposition

carbon atom mapping for key reactions **automatic vs manual EMU generation** **reducing model size without losing identifiability**

Software workflows and file formats

model specification tables/spreadsheets **exchange with COBRA style models** **export/import to flux analysis tools**

Session 3

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Fitting Fluxes & Assessing Uncertainty

Objective functions and optimization strategies

least squares cost functions **constraints and bounds on fluxes** **global vs local optimization approaches**

Goodness of fit and residual diagnostics

chi square and residual plots **detecting model**

misspecification **sensitivity to individual measurements**

Confidence intervals and identifiability analysis

profile likelihoods and confidence ranges **flux coupling and unidentifiable directions** **using results to improve experimental design**

Session 4

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Mini Capstone: Flux Map & Report

End to end ¹³C MFA on a teaching dataset

from labeling data to fitted fluxes

Visualizing and interpreting the flux map

graphical flux diagrams **comparing conditions or genotypes** **linking fluxes to phenotypes and pathways**

Deliverables: model files, flux tables & methods text

reaction and atom mapping specification **flux estimates with confidence ranges** **ready to edit methods/results template**