

# JuFLUX

## Tutorial: Introduction to $^{13}\text{C}$ Metabolic Flux Analysis with the JuFlux platform

### Metabolic Flux Analysis: What is this?

Cellular metabolism is manifested by enzymatic reactions. Their operation rates, referred to as metabolic fluxes, are the ultimate representation of a cellular phenotype. Metabolic flux analysis with isotope labeling experiments ( $^{13}\text{C}$  MFA) is the state-of-the-art approach to determine these reaction rates within living cells.

### Fluxes: Why do we want them?

Knowledge of the fluxes helps you to test the effectiveness of genetic manipulations, study intracellular responses to changes by external cues or to understand the mode of action of drugs. This renders  $^{13}\text{C}$  MFA a want-to-have technique with a wide range of biotechnological and medical applications.

### How do we get the fluxes?

To determine the fluxes from the measured intracellular labeling patterns by means of metabolic models requires the use of several computational tools operated in multi-step evaluation workflows. Here, domain knowledge from bio(tech)logy, analytical chemistry, mathematical modeling, and computer science is adopted.

### JuFLUX: Our way of doing it!

Our new JuFlux platform is designed to lower the initial hurdles of  $^{13}\text{C}$  MFA for newcomers and, at the same time, to raise convenience for expert users. JuFlux provides an easy to use graphical user interface and a powerful workflow engine for fast assembly of custom analysis pipelines. Computational performance is guaranteed by operating the high performance simulator 13CFLUX2 as calculation kernel.

### What the tutorial is about:

- Introduction to the basic steps and terminology of  $^{13}\text{C}$  MFA
- Hands-on exercises featuring the complete lifecycle of an isotope labeling data set
  - Model set-up, validation and simulation
  - Formulation and incorporation of data
  - Flux fitting and statistical assessment

Participants are welcome to bring their own research questions, data sets and models to discuss their implementation onsite.

**Target audience:**

- Experimentalists and modelers with interest in analyzing fluxes with isotope labeling experiments
- Background knowledge on the basics of metabolic network modeling is helpful

**Suggested literature:**

- Wiechert, Niefenführ, Nöh (2015)  
A Primer to <sup>13</sup>C Metabolic Flux Analysis.  
Fundamental Bioengineering, pp. 97–142  
DOI: [10.1002/9783527697441.ch05](https://doi.org/10.1002/9783527697441.ch05)

**Requirements:**

- Participants are expected to bring their own computers with Oracle Java 8 running.

**Duration & Attendance:**

- 4 - 5 h
- The number of participants is limited to 20.

**How to register?**

- Send an email with your contact details to [info@13cflux.net](mailto:info@13cflux.net).

**Tutors:**

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