



Institute of Biotechnology and Biochemical Engineering Petersgasse 12/I, 8010 Graz

# **Master's Thesis**

# **Metabolomics**

#### **Outline**

Analysis of intracellular metabolites (metabolomics) represents an essential tool in human- and bio- sciences to study cellular properties at molecular level and identify process-relevant metabolic bottlenecks or health-associated biomarkers. Typically, mass spectrometry-based techniques are applied and hundreds of compounds can be addressed in one sample run.

Because metabolite-specific ion suppression, losses throughout the complex procedure of sample preparation as well as strong matrix effects impair strongly the quality and therefore reliability of acquired mass-spec data compound-specific internal standardization is indispensable.

To this end, samples are spiked with a <sup>13</sup>C-labeled metabolite extract (<sup>13</sup>CME). However, applicability of current <sup>13</sup>CMEs is largely limited by their insufficient metabolite coverage, interfering matrix, and because commercial products are extremely expensive.

The objective of this work is to identify and optimize targets in the production process of <sup>13</sup>CME to extend its applicability and to reduce production costs.

This is a joint project of the IBB together with the HEALTH Institute, Joanneum Research.

## Methods involved

Cultivation of yeasts, monitoring of yeast growth, downstream processing, LC-MS analytics and corresponding data analysis, uni and multivariate statistics of experimental data

## Start of the Thesis

ASAP

#### Contact

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