

Info Sheet:

LC-MS based metabolite and lipid profiling

General description

Metabolite analysis: TCA intermediates, glycolysis, pentose phosphate pathway metabolites, amino acids, nucleotides, CoA-esters and other metabolites

Lipid analysis: free fatty acids, bile acids, phospholipids including (lyso-) phosphatidylcholines, phosphatidylethanolamines and phosphatidylglycerols, triglycerides, sterols, oxylipids and other lipids

Deliverables

- LC-MS/MSMS raw files, two peaklists (csv files) with all possible identifications for each compound ion and with relative abundance values of each compound ion in each sample
- A merged matrix with identification and abundance of each compound ion and sample
- Multivariate data analysis: supervised Between Group Analysis (BGA)
- Visualizations of data analysis: BGA biplot, heat map, boxplot and volcano plot
- Lists or tables ready for Pathway Analysis by MetaboAnalyst or other software suites

Requirements

The extraction with 80% Methanol is recommended as the most used extraction method. The delivery of ready to analyse extracts is requested. The extracts have to be prepared from:

- > 1 to 10mio cells
- > 10mio bacterial cells
- > 25mg plant or animal tissue (wet weight)
- > 200uL body fluid (serum, plasma, urine, csf, saliva)

Experimental design

- 12 or multiples of 12 samples
- Up to 4 conditions
- Up to 3 comparisons