MetaboHUB: Innovation, development and training dedicated to metabolomics and fluxomics

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Metabolomics and fluxomics require several complementary analytical and computational approaches such as nuclear magnetic resonance (NMR), mass spectrometry (MS) and bioinformatics.

To meet the metabolomics community needs involving large-scale programs, MetaboHUB is developing:

- **Robotic workflows** enabling high-throughput cell culture and sample preparation
- **Analytical procedures** for metabolic profiling, and methods for absolute quantitation

Many training sessions and workshops are organized on these technologies: [http://www.metabohub.fr/next-trainings.html](http://www.metabohub.fr/next-trainings.html)

Bioinformatics resources are of prime importance for analyzing and handling the large amount of data generated in such studies:

- **A web portal “MAMA”** gives the entire community access to these developments and facilities
- **Three long-term sustained e-MetaboHUB platforms** offer online data processing, analysis, and interpretation

**MAMA**

MetaboHUB Analyst MAnager

Analytical request centralisation and management for MetaboHUB users
Create your account and enter your analytical request
mama-webapp.metabohub.fr

**NetExplore**

*In silico global analysis of metabolism*

- Import/export networks
- Collaborative curation
- Pathway enrichment
- Omics data mapping
- Chemical library mapping
- Flux computations
- Network visualization
- www.metexplore.fr

**Workflow4metabolomics**

4 > 40 modules for data processing, statistical analysis, and annotation
- LC-MS, FIA-MS, GC-MS, and NMR
- Galaxy environment
- Referencing of workflows (DOI)
- > 800 users
- Trainings with tutoring on your own data
- In partnership with the French Institute of Bioinformatics (IFB)
- workflow4metabolomics.org

- Examples of **two proofs of concept projects** designed to apply the MetaboHUB high-value service in health and disease fields:

- An investigation of the links between nutrition and chronic metabolic diseases within the Canadian NuAge cohort:
  - Lipidomic and metabolic phenotyping
  - Statistical methods for longitudinal studies and data integration
  - Metadata and data management, data analysis workflows

- Metabolomic and fluxomic studies on acute myeloid leukemia (AML) cells to highlight new therapeutic targets and strategies:
  - Quantitative metabolomics by LC-MS/MS of acute myeloid leukemia (AML) cells
  - Reconstitution of metabolic fluxes in AML cells
  - Integrative omics and *in silico* modelling

**References**

Farge et al., Cancer Discov. 2017, 7:713-725.
Giacomoni et al., Bioinformatics, 2015, 31:1493-1495.

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