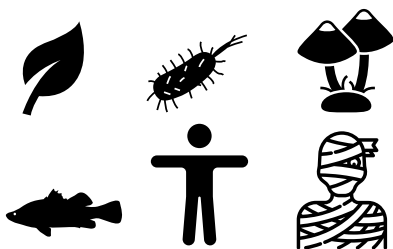




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What do we analyze ?



Any biological matrices !

This ranges from plants to bacteria, fungi, model animals and human biofluids ... we even shoot 5000 years old mummy samples !

We assist you in determining the appropriate conditions for sample preparation or realize it in house.

Data management

Your data is safe !

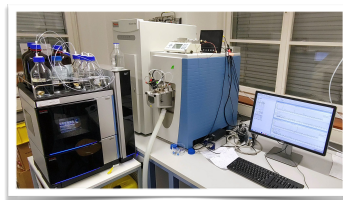
Raw spectral data is saved on the producing platforms and duplicated in a regularly backed-up server.

All users get a dedicated Github repository ensuring FAIRness of the data generated on the platform and secure versioning of the obtained results.



```
(base) bioinformatics@violeta-vogler-group voletco$ copier update --trust
Updating to template version 0.2.4
not doing anything ...
? What is your email?
  pierre-marie.allard@unifr.ch
? The name of the repository on GitHub. Should be lowercase and dash-separated.
  john-doe-group
? What is your GitHub username?
  mapp-metabolomics-unit
? The path to the repository containing the templated repo on your local system.
  /Users/voletco/git_repos/mapp-metabolomics-unit
? The name of the project in the MAPP Metabolomics Unit.
  mapp_project_00001
? The name of the batch in the MAPP Metabolomics Unit.
  mapp_batch_00001
? The description of the batch in the MAPP Metabolomics Unit.
  positive
? What is the ionization mode of the study?
  Should the gap filling be performed?
  Yes
? What is the noise level for the analysis?
  500000.0
? The OMS job ID (optional).
  10ba90b0d0c440b9e2b06a8936c12f
? The Job ID of the stats job to be used for automated report (optional).
? The common filename pattern for the files in the batch.
  source_batch
? The target variable for the analysis (optional)
  source_batch
```

Instrumentation



UHPLC-HRMS

Vanquish Transcend - QExactive HF-X
Applications: *Untargeted and targeted metabolomics, Lipidomics*

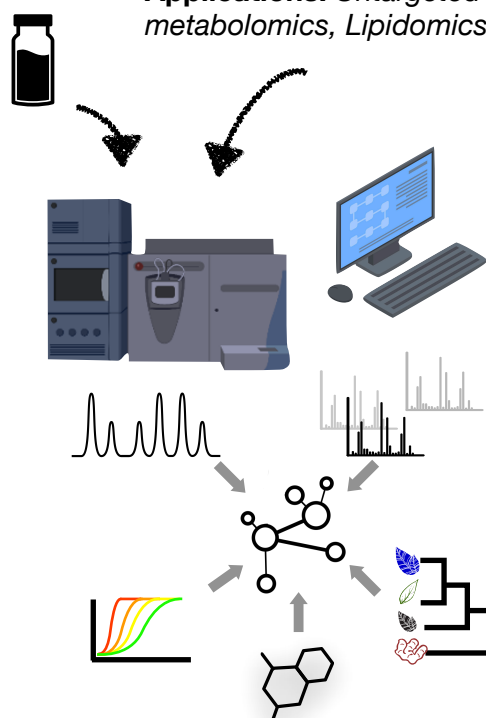


GC-HRMS

Agilent 7200 QToF
Applications: *Untargeted and targeted volatiles analysis*

GC-FID

Agilent 7890
Applications: *FAME, BAME analysis*



... and tracked !

Samples are systematically relabelled and tracked in a Postgres relational database.

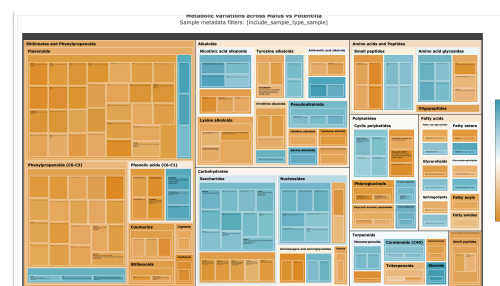


Data exploration

State-of-the-art computational metabolomics

We use in house and publicly available open-source software to *annotate, organize and visualize* complex datasets.

We notably establish **molecular networks** to organize spectral data acquired on your samples and map additional information coming from **metabolite annotation** pipelines or supervised and unsupervised **biostatistics**.



MAPP website

MAPP Metabolomics platform

mapp-metabolomics@unifr.ch



[https://github.com/
mapp-metabolomics-unit](https://github.com/mapp-metabolomics-unit)

This poster in pdf

<https://doi.org/10.5281/zenodo.17293302>

