Toxalim
RESEARCH CENTRE IN FOOD TOXICOLOGY

RÉPUBLIQUE FRANÇAISE
Liberté
Égalité
Fraternité

INRAE

Genotoul
Metatoul

ANALYSIS CATALOGUE

Axiom platform

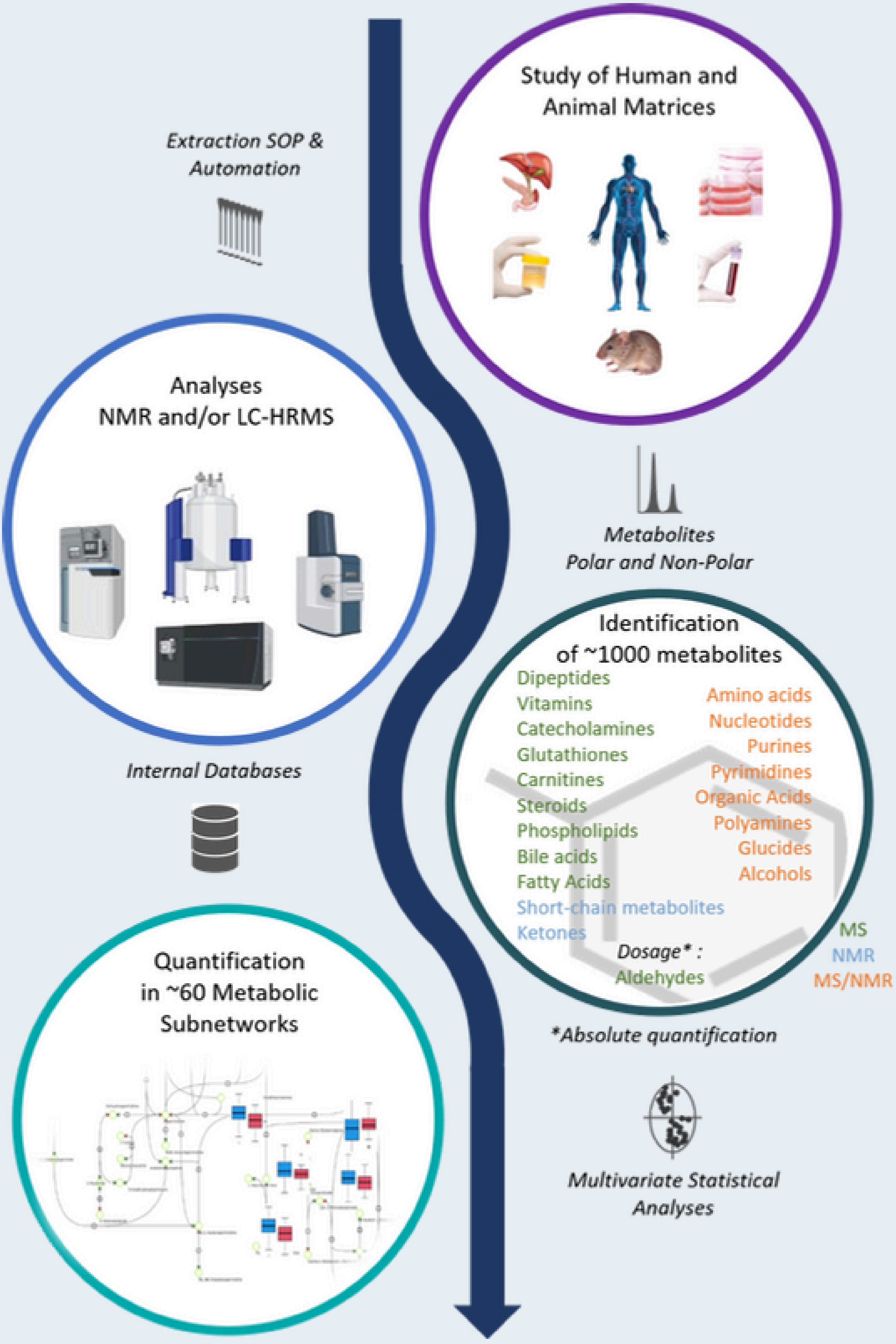
MetaToul-MetaboHUB platform

METABOHUB

MetaToul is co-funder of National Infstructure MetaboHUB

LRQA
CERTIFIED
ISO 9001 · NFX 50-900

UNTARGETED METABOLOMICS



Study of Human and Animal Matrices

Extraction SOP & Automation

Metabolites Polar and Non-Polar

Analyses NMR and/or LC-HRMS

Identification of ~1000 metabolites

Dipeptides
Vitamins
Catecholamines
Glutathiones
Carnitines
Steroids
Phospholipids
Bile acids
Fatty Acids
Short-chain metabolites
Ketones

Amino acids
Nucleotides
Purines
Pyrimidines
Organic Acids
Polyamines
Glucides
Alcohols

*Dosage** :
Aldehydes

MS
NMR
MS/NMR

**Absolute quantification*

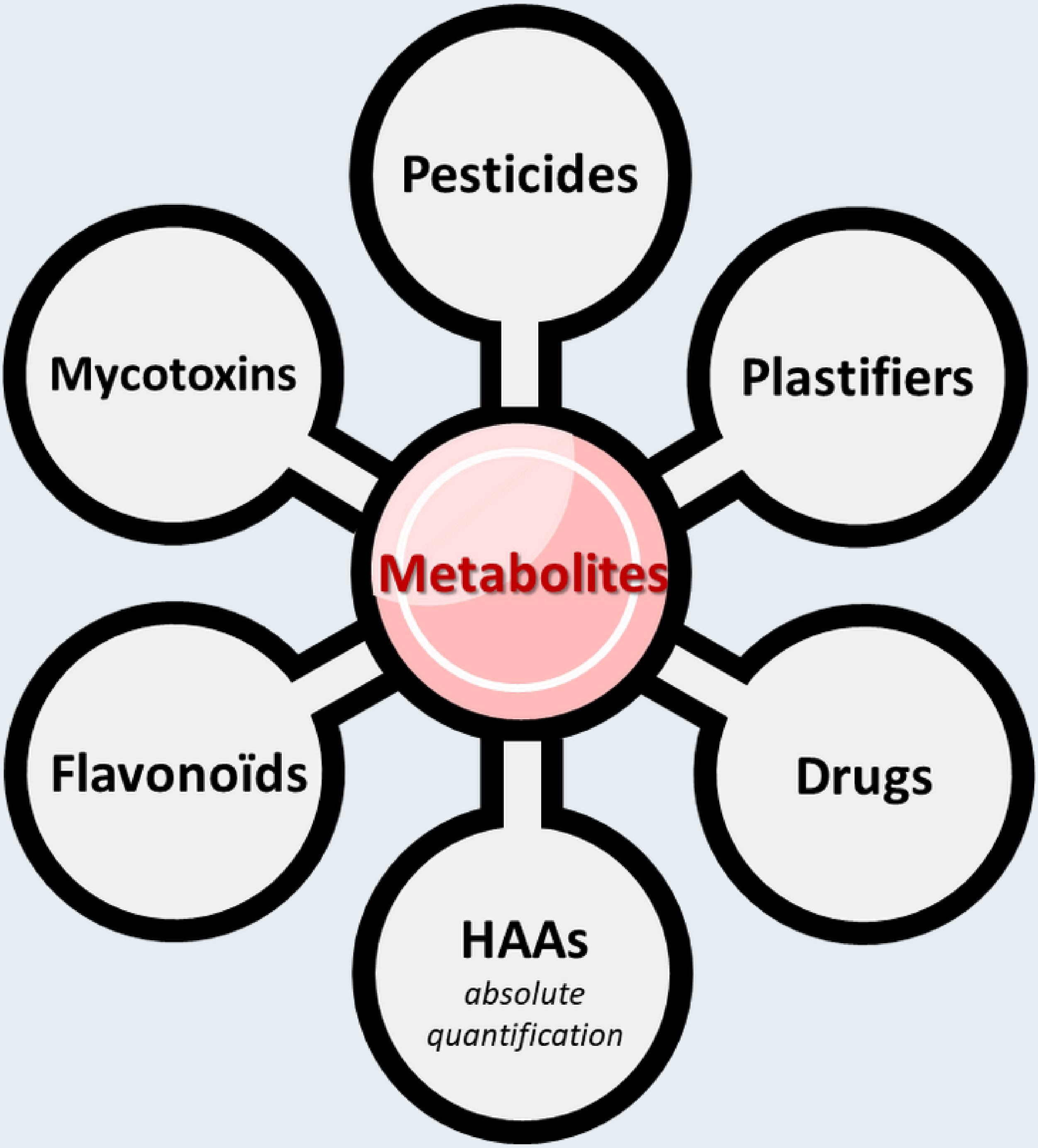
Internal Databases

Quantification in ~60 Metabolic Subnetworks

Multivariate Statistical Analyses

Submit a project here

XENOBIOTICS SCREENING



LC-MS or GC-MS analysis of xenobiotics and/or their metabolites following their extraction from biological matrices.

Relative quantification by HRMS and identification by MS/MS. Absolute quantification by LC-tQMS in the particular case of HAAs in meat.

Mass-Spectrometry Imaging

Human
Retina
Mouse
Liver
Rat
Colon

Samples

Human
Animals

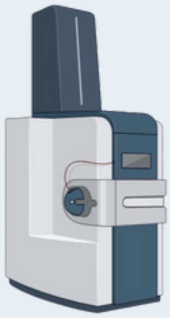
Sample preparation

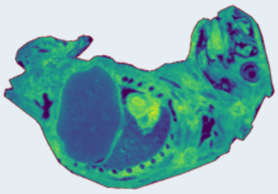
Sectioning

Matrix deposition

Spatial resolution
10 µm (or more)

MALDI-HRMS analysis





Data-processing

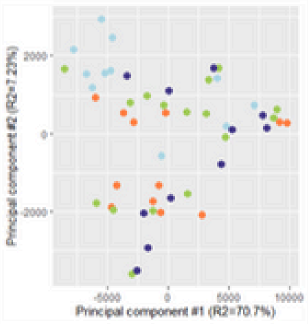
Visualization
Statistical analysis
Metabolite identification

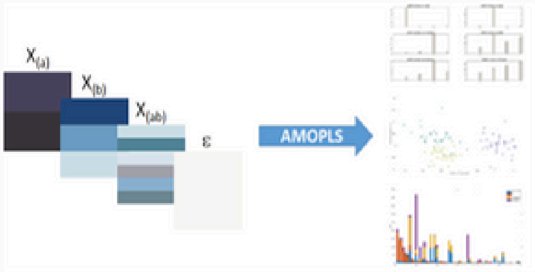
Submit a project here

STATISTICS

Multivariate analysis

- *PCA*
- *PLS-DA*
- *Repeated measures (A-SCA, AMOPLS)*



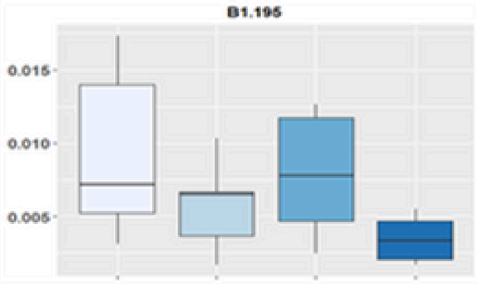


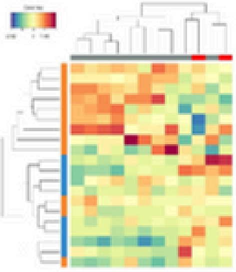
Single block analysis

Individual analysis of each metabolomics data

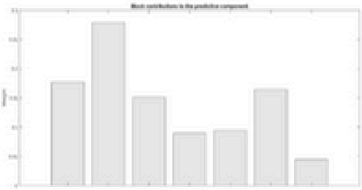
Univariate analysis

- *Hypothesis testing*
- *Variable selection (ongoing)*





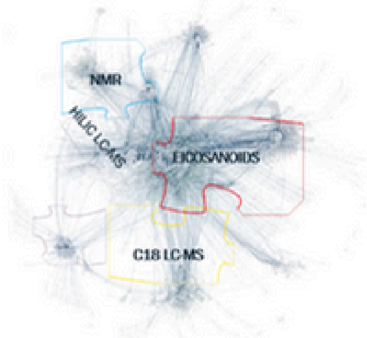
Discrimination of individuals with a metabolic signature



Block contribution to factor prediction

Multi-block analysis

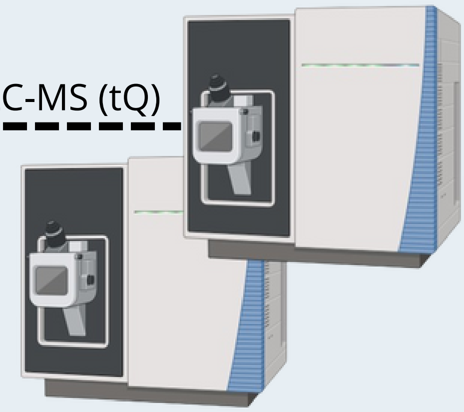
Combination of different analytical metabolomics data to adjust predictive models thanks to a deeper metabolic coverage



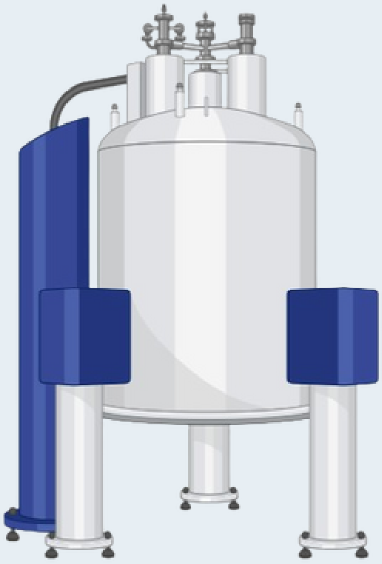
DIABLO (mixOmics)
Consensus OPLSDA (Boccard et al.)
Regularized Consensus OPLSDA (ongoing)

The axiom core facility develop and apply analytical chemistry methods by NMR and MS, for analysis of metabolome, xenobiotics and their metabolites, and exposome in toxicology, human and animal health.

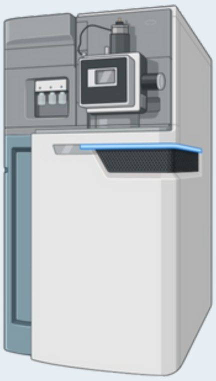
Our resources include 17 scientists, 1 NMR, 6 mass spectrometers and 1 robot for sample preparation



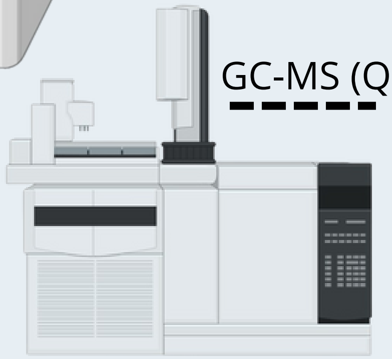
2 x LC-MS (tQ)



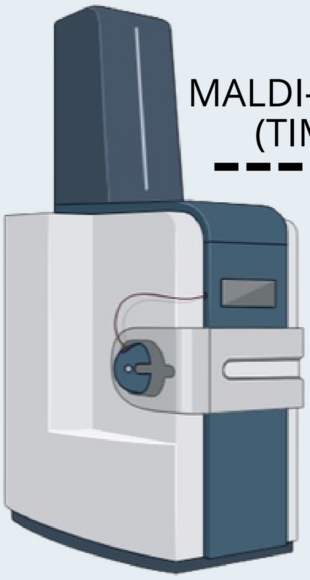
600 MHz NMR



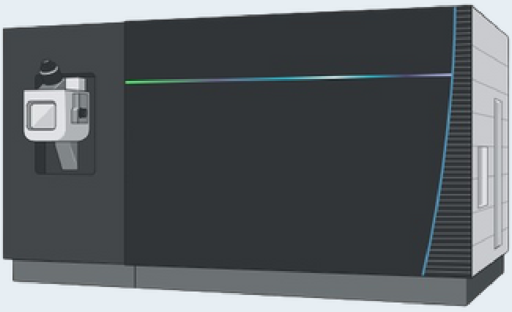
LC-HRMS (QToF)



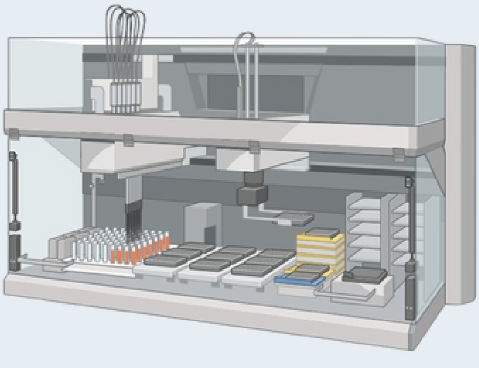
GC-MS (Q)



MALDI-LC-IM-HRMS (TIMS-QToF)



LC-HRMS (IQ-X)



Sample preparation robot

Spectrometer images : BioRender