



HAL
open science

The challenge to produce robust data in UHPLC-HRMS/MS based metabolomics for molecular epidemiology studies

Quentin Vandoolaeghe, Claire Lopez-Piffet, Valérie Bouchart, Raphaël Delépée

► **To cite this version:**

Quentin Vandoolaeghe, Claire Lopez-Piffet, Valérie Bouchart, Raphaël Delépée. The challenge to produce robust data in UHPLC-HRMS/MS based metabolomics for molecular epidemiology studies. Congrès ANALYTICS, Sep 2022, Nantes, France. <hal-03846429>

HAL Id: hal-03846429

<https://normandie-univ.hal.science/hal-03846429v1>

Submitted on 10 Nov 2022

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



HAL Authorization

The challenge to produce robust data in UHPLC-HRMS/MS based metabolomics for molecular epidemiology studies

Quentin Vandoolaeghe^{1,2,3}, Claire Lopez-Piffet^{1,3,4}, Valérie Bouchart^{1,4,5}, Raphaël Delépée^{1,2,3,4}

*quentin.vandoolaeghe@unicaen.fr

¹Institut National de la Santé et de la Recherche Médicale (INSERM), Unité Mixte de Recherche (UMR) 1086 ANTICIPE, Caen, France; ²Centre de Lutte Contre le Cancer François Baclesse, Caen, France; ³Université de Caen Normandie, Caen, France; ⁴PRISMM platform, UNICAEN, CLCC François Baclesse, Caen, France; ⁵LABÉO, Pôle recherche développement et innovation, Caen, France

Context : Agricultural activity and cancer



Examples of agricultural tasks associated with exposure to pesticides

Link between occupational exposures and cancers demonstrated in farmers



Pesticides exposure effects?
Other determinants?

- Study cancer biological plausibility, early stages effects, lookout for predictive markers of cancer risks
- Holistic approach of cancers occurrence in farmers population

Utilisation of biobanks samples associated with exposure description and tasks listing for a metabolomic analysis

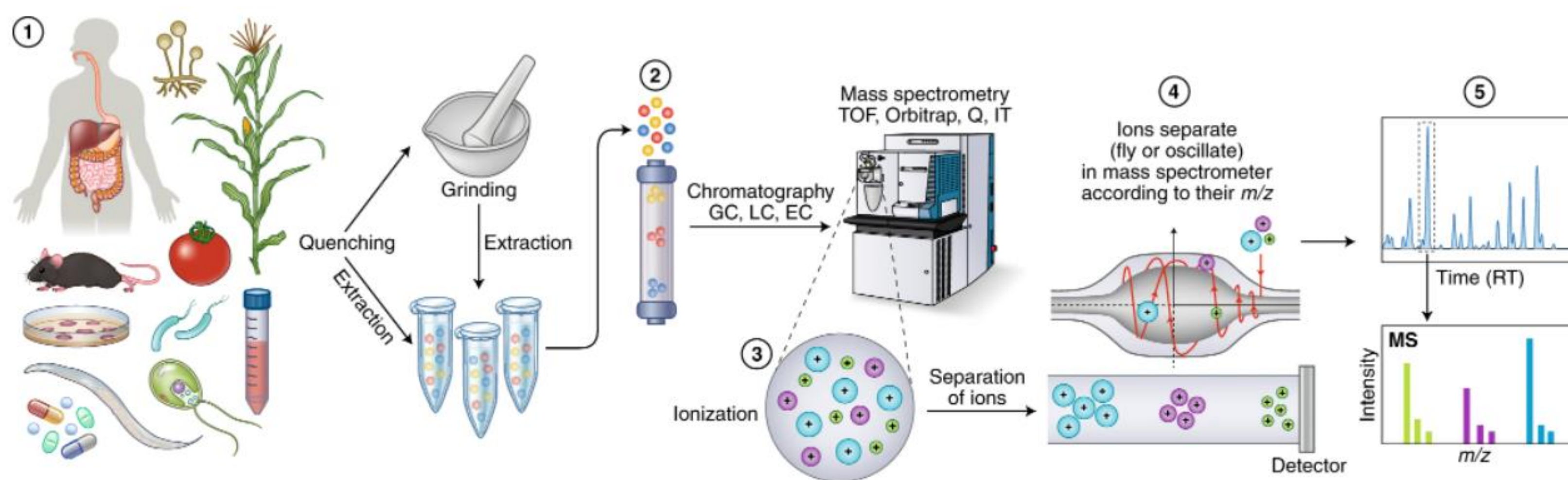


Potential available matrix

- Blood
- Urine
- Saliva
- Hair

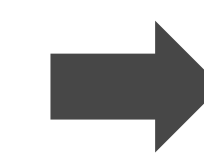
Metabolomic

General Workflow



- ❖ Experimental design
- ❖ Sample preparation
- ❖ Metabolites separation
- ❖ Ionisation
- ❖ Detection

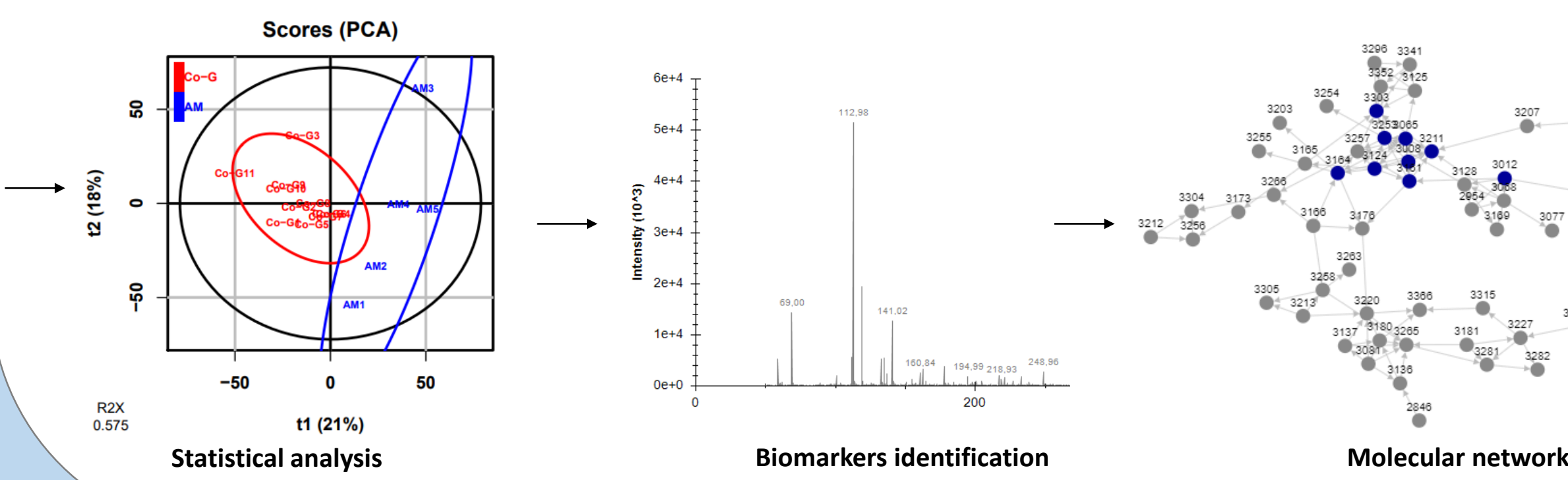
- ❖ Data treatment
- ❖ Statistical analysis
- ❖ Metabolites identification
- ❖ Biological interpretation



Many steps to be optimized

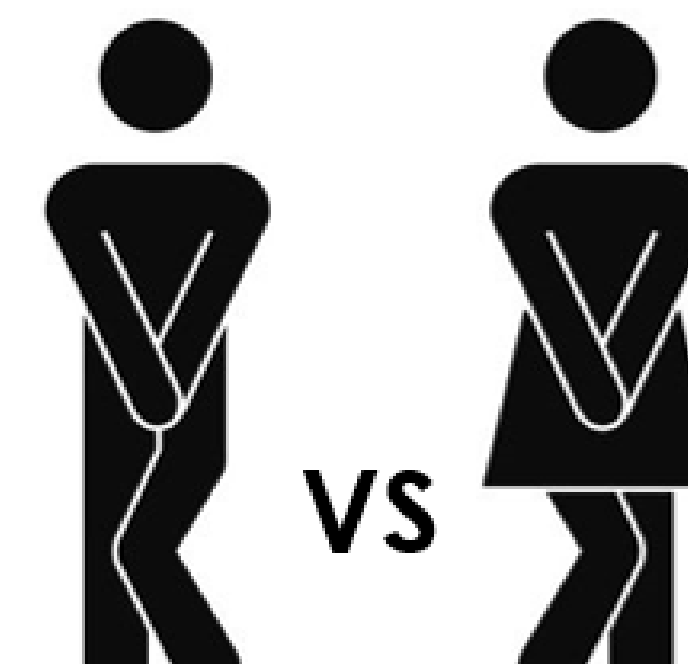
No general method for metabolomic analysis of human urine samples in the literature

Alesek S et al. Mass spectrometry-based metabolomics: a guide for annotation, quantification and best reporting practices. Nat Methods. 2021



Setting up of a test study on healthy volunteers

Men urine samples



Women urine samples



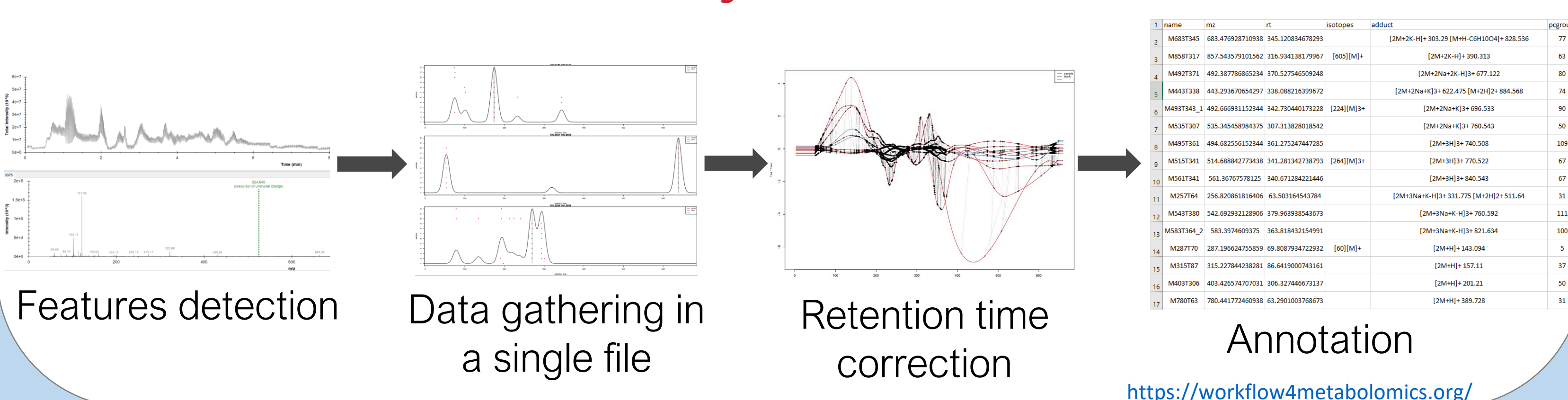
Methodology

Chromatographic parameters and HRMS detection

	ESI Positif	ESI Negatif
Separation of low polarity molecules C18 Waters Acquity® BEH C18 (1x100mm; 1,7 µm)	✓	✓
Separation of high polarity molecules HILIC Waters Acquity® BEH amide (1x100mm; 1,7 µm)	✓	✓

Masse detection : QTOF Agilent 6540, 1 scan/sec, 50-1000 m/z

Data treatment : Galaxy W4M & mixOmics

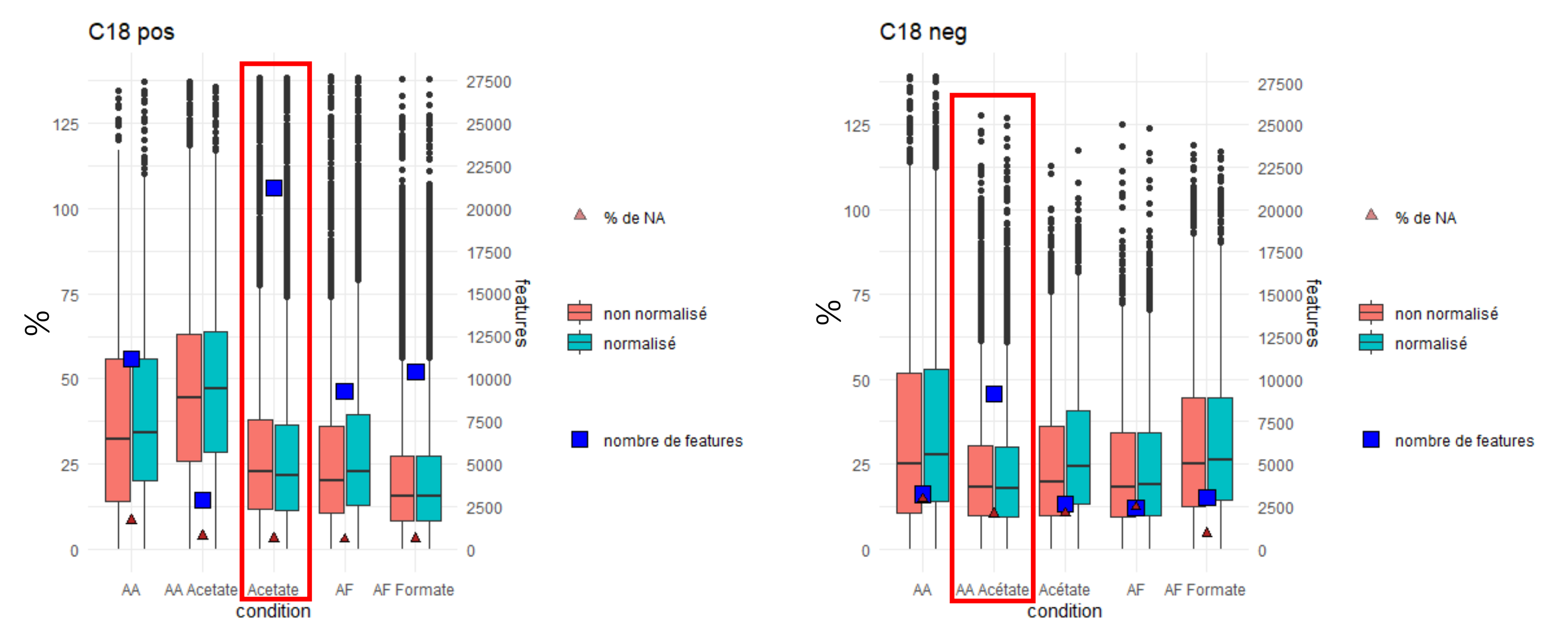


Perspectives

- Ion annotation tool optimisation
- Biobank samples analysis
- Study on blood, hair or saliva
- Use of new statistical tools

Results

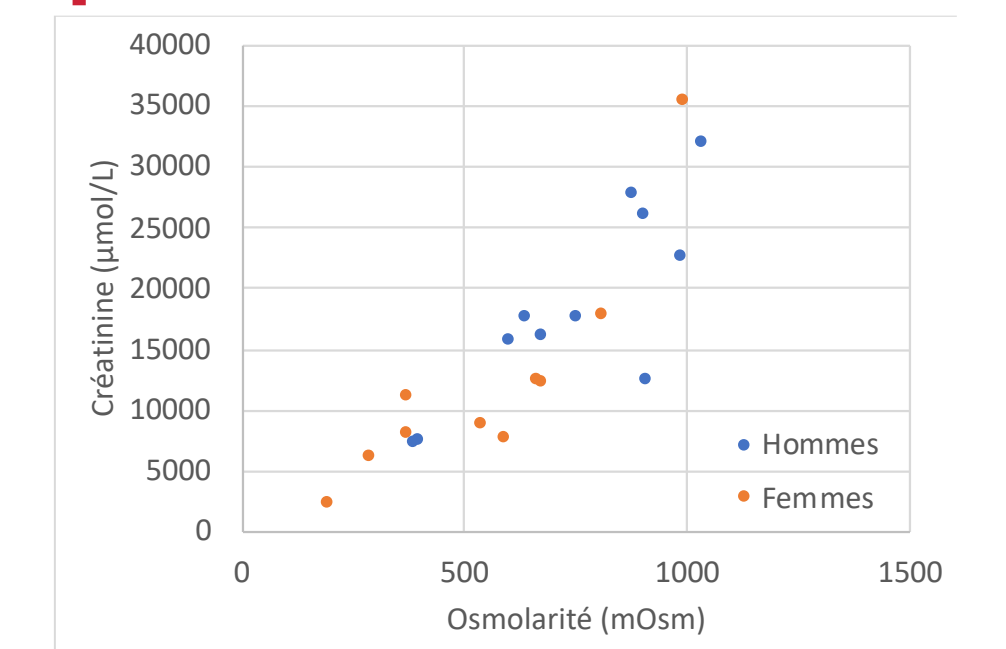
5 mobile phases comparison



Signal normalisation comparison

- Osmolarity
- Creatinine
- Total MS signal

Gagnebin et al., Analytica chimica Acta, 2017
Warack et al., Journal of chromatography B, 2009



Groups separation and markers highlighted

