



**HAL**  
open science

## **ASTERICS: A Tool for the ExploRation and Integration of omiCS data**

Élise Maigné, Céline Noirot, Jérôme J. Mariette, Yaa Adu Kesewaah, Sébastien Dejean, Camille Guilmineau, Julien Henry, Arielle Krebs, Laurence Liaubet, Fanny Mathevet, et al.

### ► To cite this version:

Élise Maigné, Céline Noirot, Jérôme J. Mariette, Yaa Adu Kesewaah, Sébastien Dejean, et al.. ASTERICS: A Tool for the ExploRation and Integration of omiCS data. Journée Régional Bioinfo/Biostat, Dec 2022, Toulouse, France. hal-03882998

**HAL Id: hal-03882998**

**<https://hal.science/hal-03882998v1>**

Submitted on 2 Dec 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.

# ASTERICS: A Tool for the ExploRation and Integration of omiCS data

Élise MAIGNÉ<sup>1,\*</sup>, Céline NOIROT<sup>1,2,\*</sup>, Jérôme MARIETTE<sup>1,2</sup>, Yaa ADU KESEWAAH<sup>1,3</sup>, Sébastien DÉJEAN<sup>3,4</sup>,  
Camille GUILMINEAU<sup>1,3</sup>, Julien HENRY<sup>1,3,†</sup>, Arielle KREBS<sup>1,2</sup>, Laurence LIAUBET<sup>5</sup>, Fanny MATHEVET<sup>1,3</sup>,  
Hyphen-Stat<sup>6</sup>, Christine GASPIN<sup>1,2</sup>, and Nathalie Vialaneix<sup>1</sup>

<sup>1</sup> Université de Toulouse, INRAE, UR MIAT, 31326, Castanet-Tolosan, France

{prenom.nom}@inrae.fr

<sup>2</sup> Université Fédérale de Toulouse, INRAE, BioinfOmics, GenoToul Bioinformatics facility, 31326,  
Castanet-Tolosan, France

<sup>3</sup> Plateforme Biostatistique, Genotoul, Toulouse, France

<sup>4</sup> IMT, UMR5219, Université de Toulouse, CNRS, UPS, 31062, Toulouse, France

sebastien.dejean@math.univ-toulouse.fr

<sup>5</sup> GenPhySE, Université de Toulouse, INRAE, ENVT, F-31326, Castanet-Tolosan, France

laurence.liaubet@inrae.fr

<sup>6</sup> Hyphen-stat, <https://hyphen-stat.com/>, Toulouse, France

david.colongo@hyphen-stat.com

\* These authors contributed equally to the work. – † Presenting author.

## 1 Introduction

The rapid development of omics acquisition techniques has induced the production of a large volume of heterogeneous and multi-level omics datasets measured on the same individuals. Complex information of biological interest is obtained from so-called *integration methods*, which have been increasingly developed in the past few years. Some of these methods are already available in R packages (like **mixOmics** [1] or **mixKernel** [2] to which our team has contributed). However, the use of these packages still requires to learn a programming language and to have access to sufficient statistical knowledge to choose method parameters and interpret outputs.

## 2 ASTERICS

### 2.1 Features

ASTERICS is a web application that aims at making complex exploratory and integration analysis workflows easily available to biologists. Data edition, exploration and integration menus organize the interface to perform

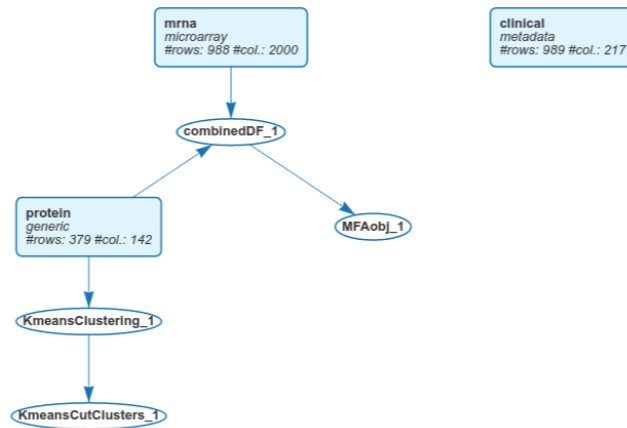
1. data edition, missing value imputation, and normalization,
2. data exploration with interactive plots, numerical summaries, PCA, tests, clustering, and self-organizing maps,
3. data integration with differential analysis, MFA, or PLS-based methods.

Analyses are adapted to the most standard omics datasets (RNA-seq or count data from sequencing technologies, microarray, metabolomics, metagenomics or other compositional data).

ASTERICS is also designed to make the analysis flow understandable with a navigable workspace that displays uploaded or obtained datasets and performed analyses in a graph (see Figure 1). Finally, it also comes with a documentation for beginners that helps interpret the results, choose proper options or the next analysis to perform.

### 2.2 Technical information

ASTERICS is based on Rserve, pyRserve, and flask. R package versions are controlled using **renv**. Frontend is developed in Vue.js and uses the CSS framework Bulma.



**Figure 1.** Example of a workspace as displayed in ASTERICS.

ASTERICS is available online at <https://asterics.miat.inrae.fr/> and will also be released as a docker image for local usage.

## Acknowledgements

This work is funded by Région Occitanie (Grant 20008788 – ASTERICS).

## References

- [1] F. Rohart, B. Gautier, A. Singh, and K.-A. Le Cao, “mixomics: an R package for ’omics feature selection and multiple data integration,” *PLoS Computational Biology*, vol. 13, no. 11, p. e1005752, 2017.
- [2] J. Mariette and N. Villa-Vialaneix, “Unsupervised multiple kernel learning for heterogeneous data integration,” *Bioinformatics*, vol. 34, no. 6, pp. 1009–1015, 2018.