



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. ECCB: 21st European Conference on Computational Biology, Sep 2022, Sitges, Spain. , 2022, 10.7490/f1000research.1119290.1 . hal-03890660

HAL Id: hal-03890660

<https://hal.inrae.fr/hal-03890660v1>

Submitted on 8 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.

Élise Maigné^{1,*}, Céline Noirot^{1,2,*}, Jérôme Mariette^{1,2}, Yaa Adu Kesewaah^{1,3}, Sébastien Déjean^{3,4},
Camille Guilmineau^{1,3}, Julien Henry^{1,3}, Arielle Krebs^{1,2}, Laurence Liaubet⁵, Fanny Mathevet^{1,3},
Hyphen-Stat⁶, Christine Gaspin^{1,2}, Nathalie Vialaneix^{1,3}

¹ Université de Toulouse, INRAE, UR MIAT, 31326, Castanet-Tolosan, France – ² Université Fédérale de Toulouse, INRAE, BioinfOmics, GenoToul Bioinformatics facility, 31326, Castanet-Tolosan, France – ³ Plateforme Biostatistique, Genotoul, Toulouse, France – ⁴ IMT, UMR5219, Université de Toulouse, CNRS, UPS, 31062, Toulouse, France – ⁵ GenPhySE, Université de Toulouse, INRAE, ENVT, F-31326, Castanet-Tolosan France – ⁶ Hyphen-stat, <https://hyphen-stat.com/>, Toulouse, France
* These authors contributed equally to the work.

ASTERICS web application

Explore, integrate and visualize your omics data.

backend

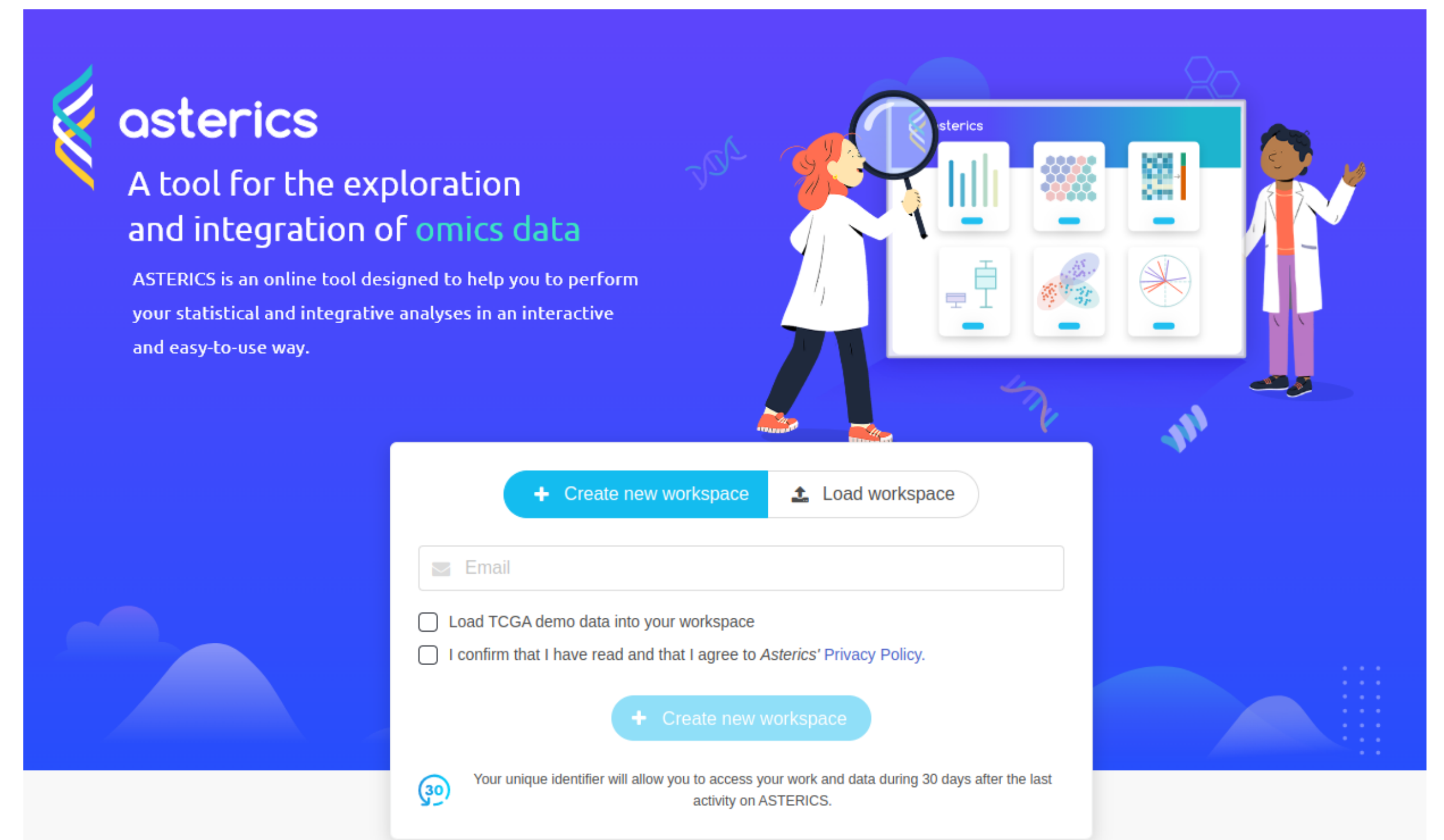


PyRserve
Flask

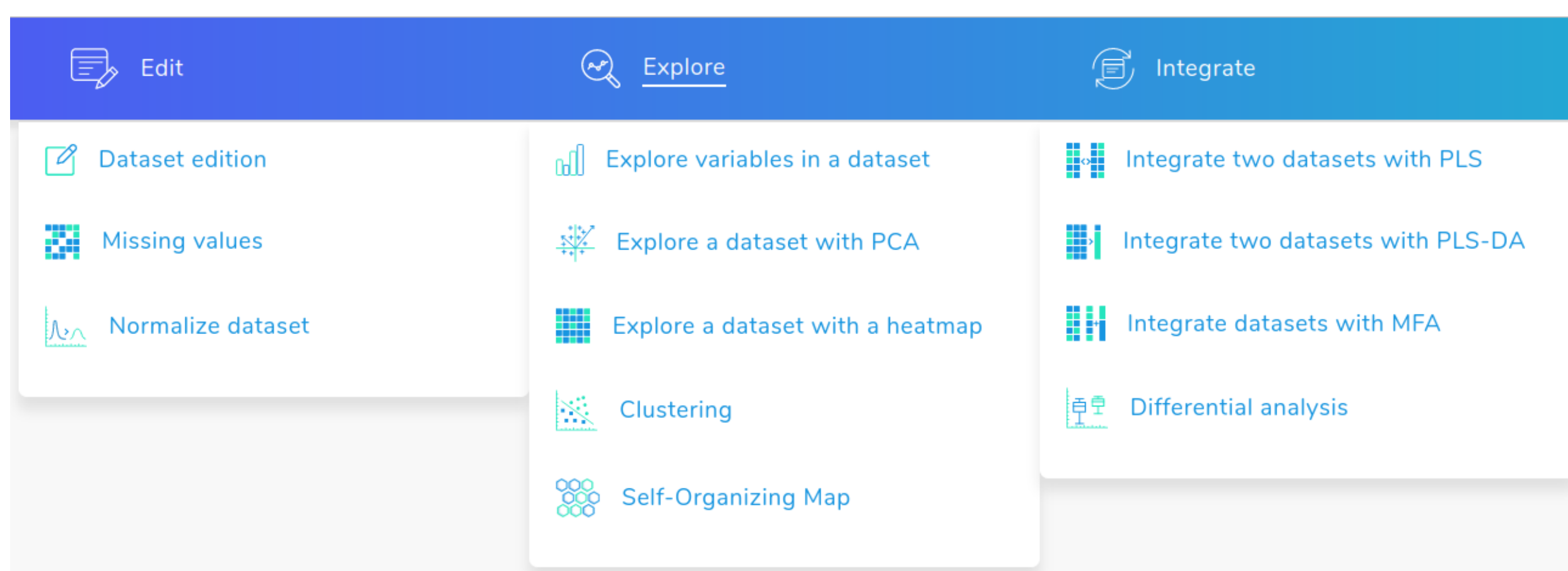
frontend



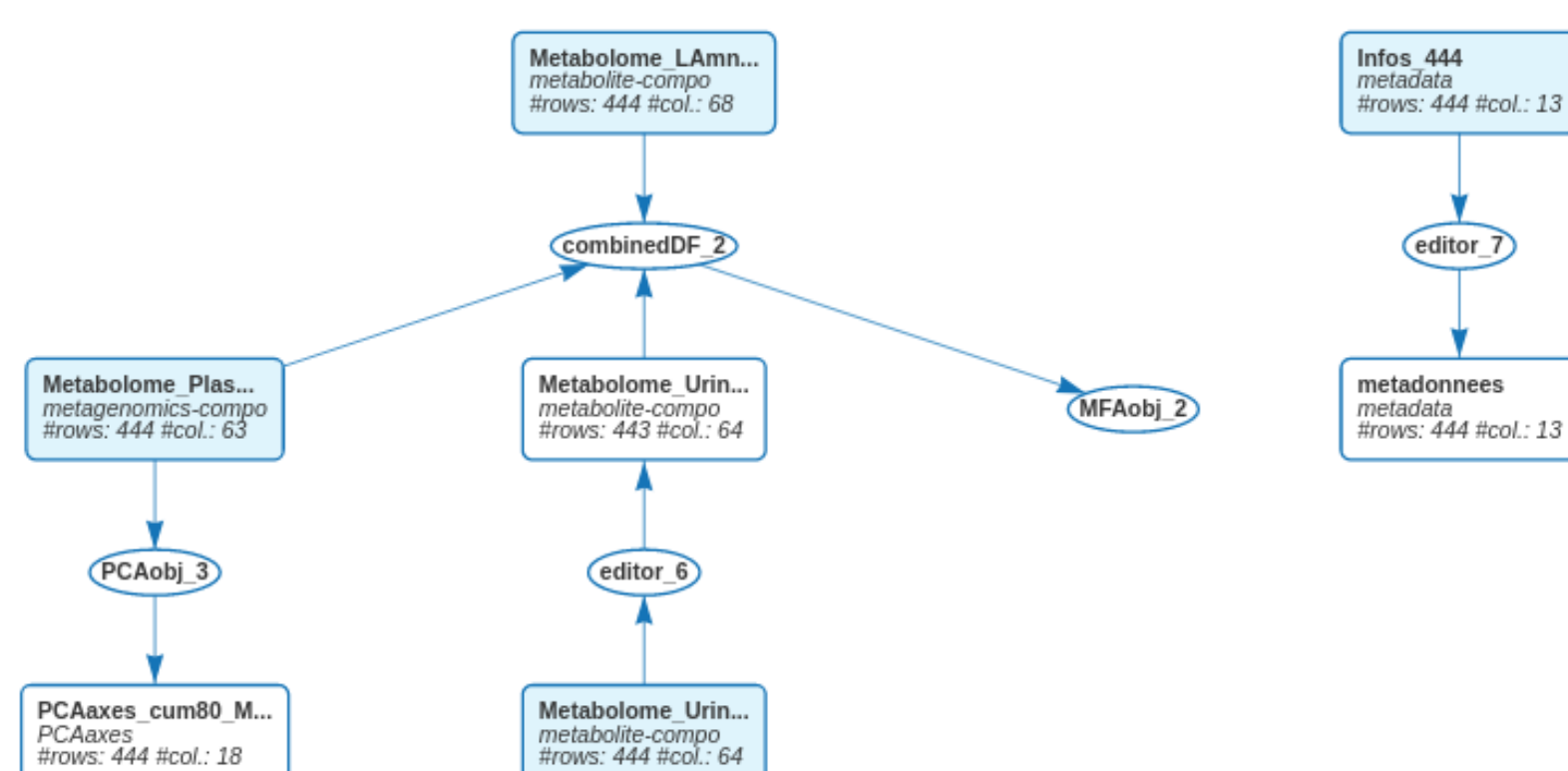
- Available at: <http://asterics.miat.inrae.fr>
- Source code (GPLv2): <https://forgemia.inra.fr/asterics/asterics>



Available analyses

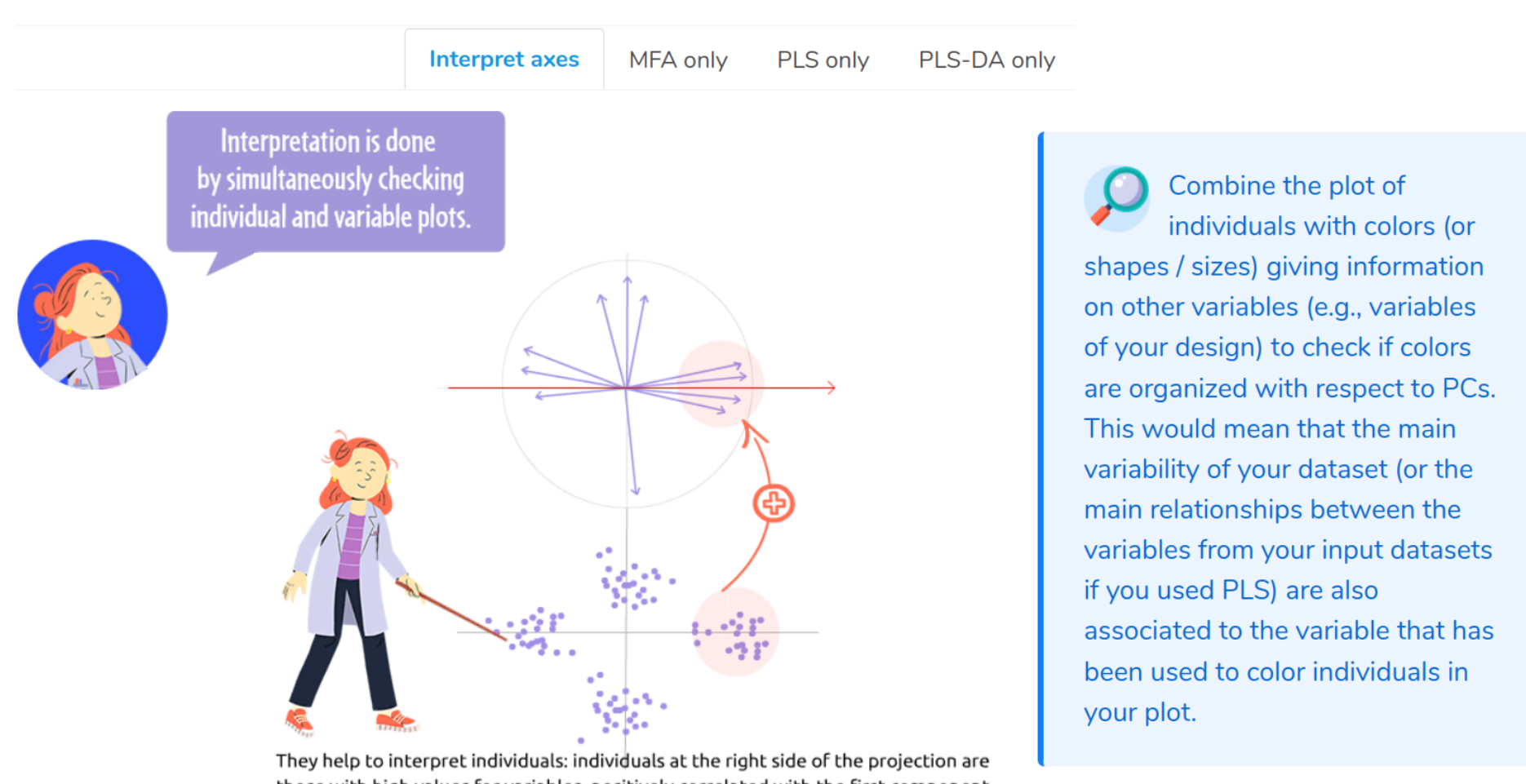
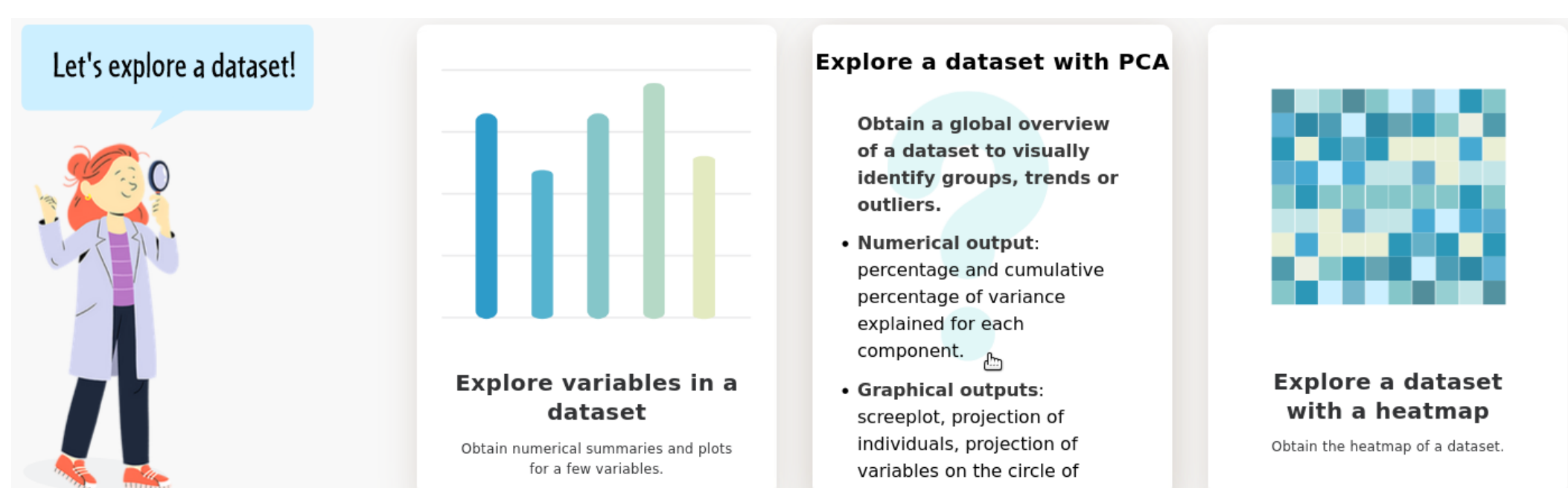


Generated datasets and analyses are navigable using a DAG:



Help pages

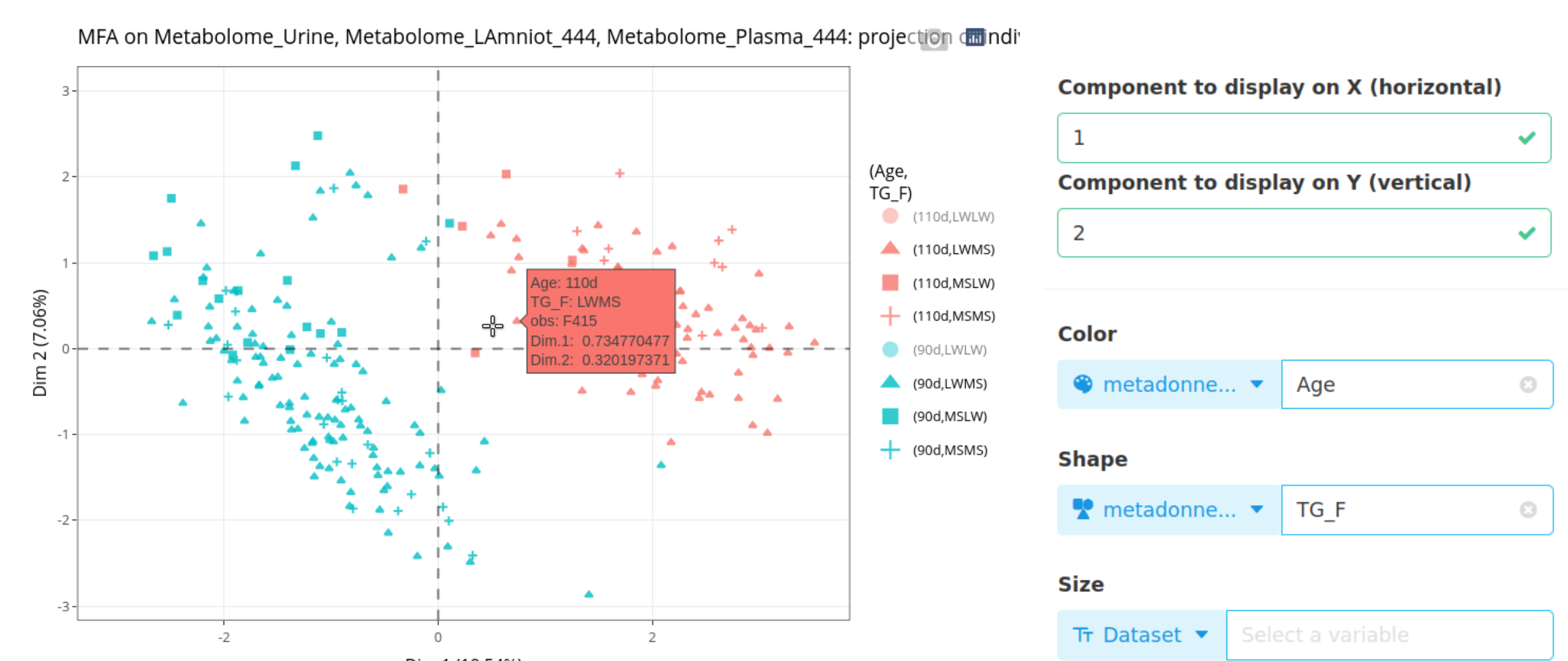
On each analysis page, **focused help pages** are available to help the user choose analysis settings or interpret the results. These pages include images and GIF animations.



Full documentation:
https://asterics.pages.mia.inra.fr/user_documentation/

Outputs of analyses

• Interactive and easily customizable plots:



• Sortable and filterable tables:

Post-hoc test results for protein vs clinical. (Wilcoxon tests, corrected with 'BH')

Variables	Conditions	p-values	Adj. p-values	Signs
	left lower			
14.3.3_epsilon	left lower inner quadrant-left	0.6071	1	-1
14.3.3_epsilon	left lower outer quadrant-left	0.5617	1	-1
14.3.3_epsilon	left lower outer quadrant-left lower inner quadrant	0.9426	1	1
14.3.3_epsilon	left upper inner quadrant-left lower inner quadrant	0.563	1	1

Additional features

- Use your **UUID** to come back later to your analyses.
- Export the results of your analysis in **HTML reports** (using Rmarkdown).
- **Export** complex objects as RDS data or data.frame as CSV files.
- Use the online tool or use **Docker** for a local use or for deployment.

Contributors

Partners



Funding

