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Maxime Chazalviel, Adrien Rohan, Nathalie Poupin, Florence Vinson, Clément Frainay, et al.. MetExplore: Omics data analysis in the context of metabolic networks. European RFMF Metabomeeting 2020, Jan 2020, Toulouse, France. . hal-02948391

HAL Id: hal-02948391

<https://hal.inrae.fr/hal-02948391>

Submitted on 24 Sep 2020

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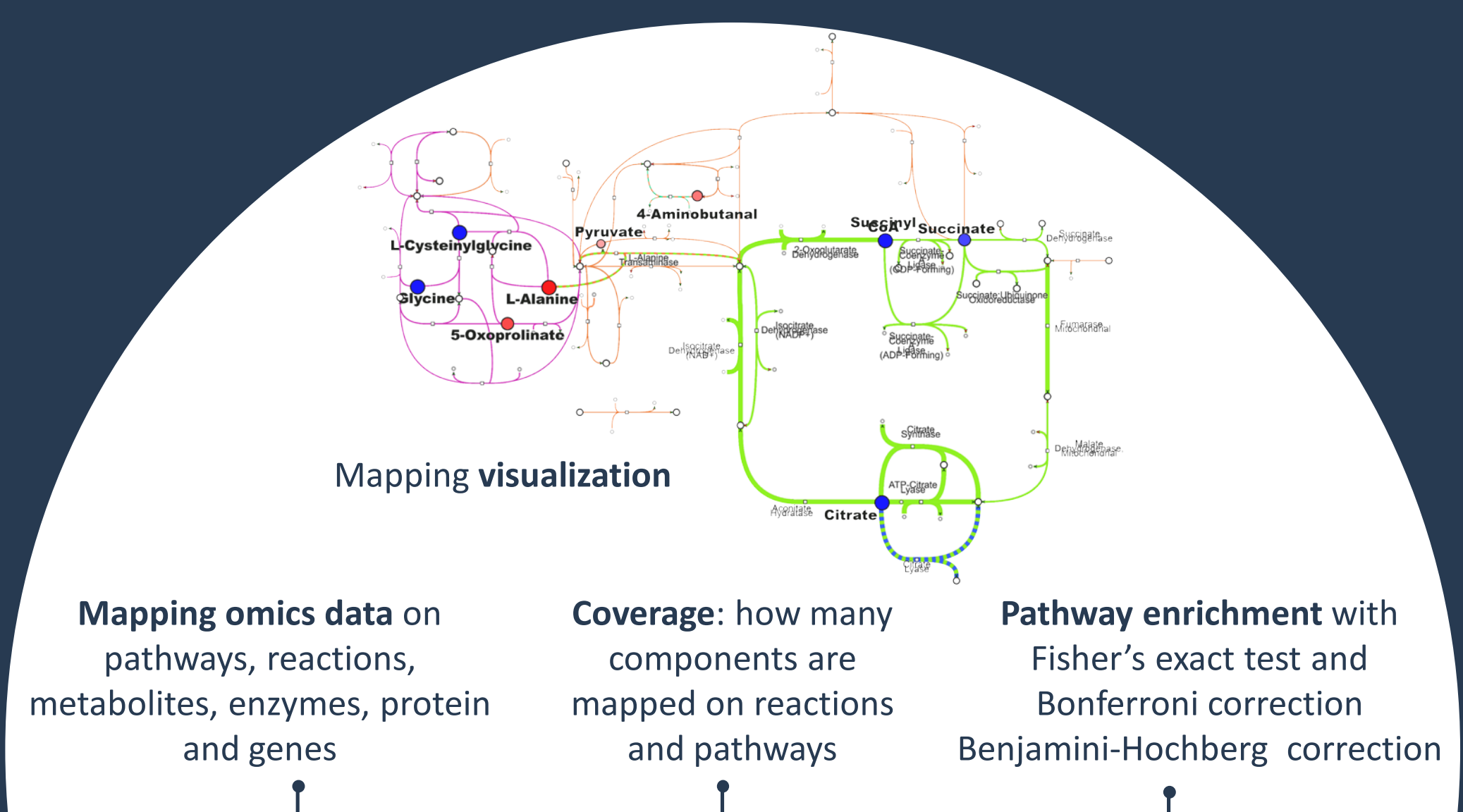
Omics data analysis in the context of metabolic networks

Maxime Chazalviel¹, Adrien Rohan², Nathalie Poupin², Florence Vinson², Clément Frainay², Ludovic Cottret³ and Fabien Jourdan²

1 MedDay Pharmaceuticals, Paris, France

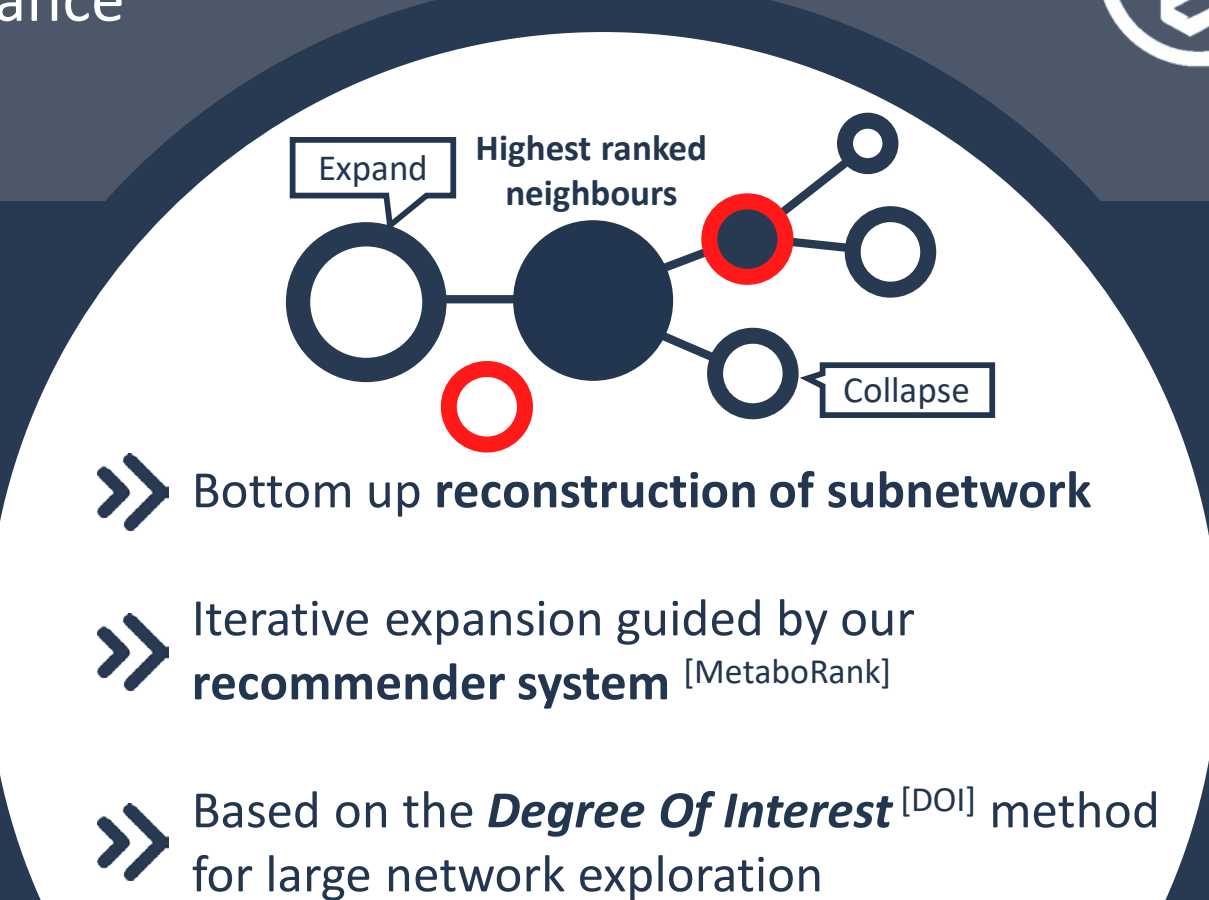
2 Toxalim, Université de Toulouse, INRAE, ENVT, INP-Purpan, UPS, Toulouse, France

3 LIPM, Université de Toulouse, INRAE, CNRS, Castanet-Tolosan, France



Name	No. Reactions	Coverage	No. of Mapped	p-value	Bonferroni corrected p-value	BH-corrected p-value
Citric acid cycle	14	16.67	5	1.84e-9	*** (7.17e-8)	*** (2.17e-8)
Glutamine metabolism	10	22.22	4	3.25e-8	*** (1.27e-6)	*** (5.34e-7)
Glutamate metabolism	16	14.29	4	2.15e-7	*** (8.40e-6)	*** (2.72e-6)
Urea cycle	47	6.33	5	2.79e-7	*** (1.09e-5)	*** (2.72e-6)
Pyruvate and aspartate metabolism	13	12.5	4	3.77e-7	*** (1.47e-5)	*** (2.94e-6)
Pyruvate metabolism	297	1.4	7	1.11e-5	*** (4.32e-4)	*** (7.20e-5)
Alanine, aspartate, and threonine metabolism	46	5	4	1.98e-5	*** (8.16e-4)	*** (8.81e-5)

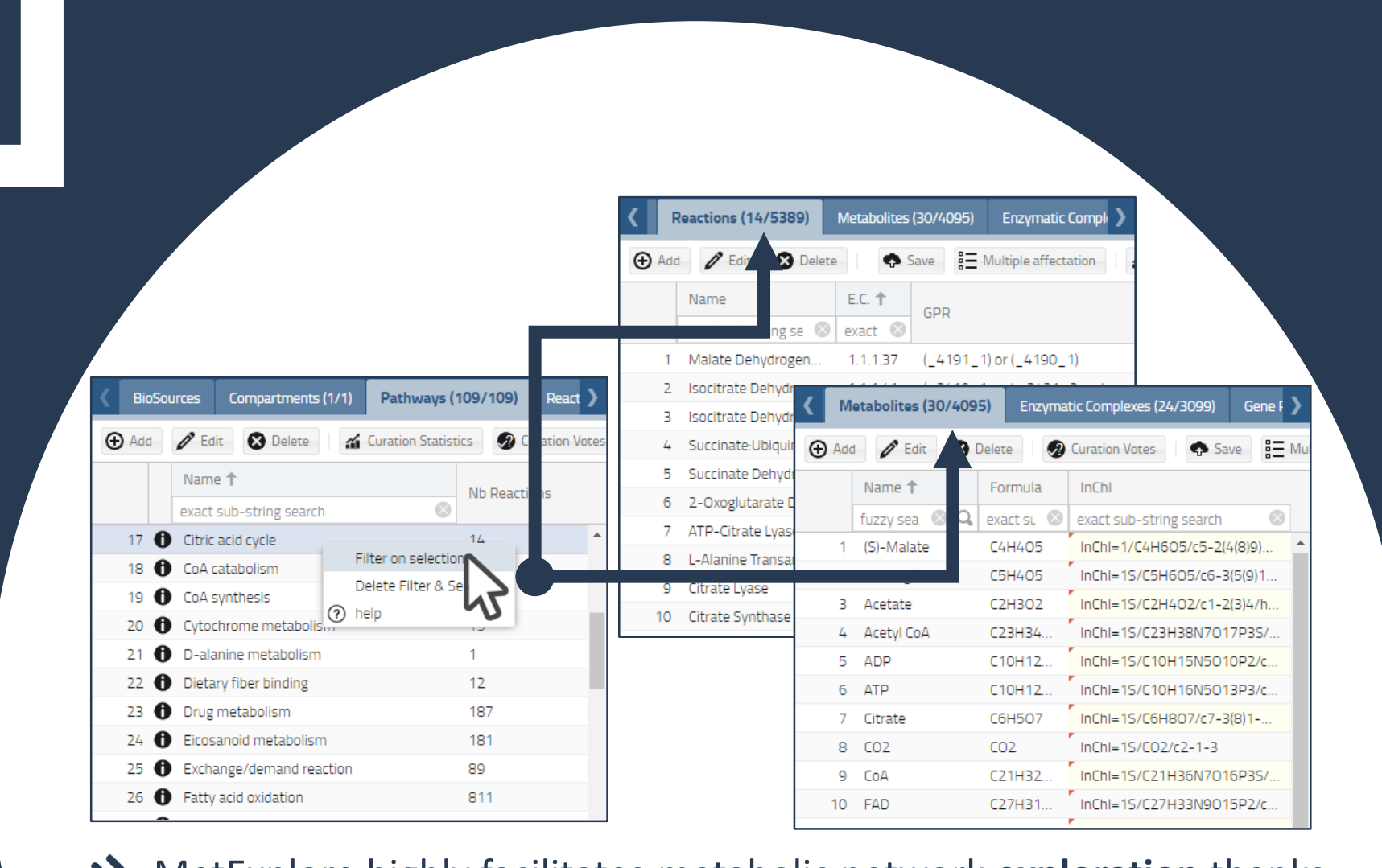
Multi omics mapping



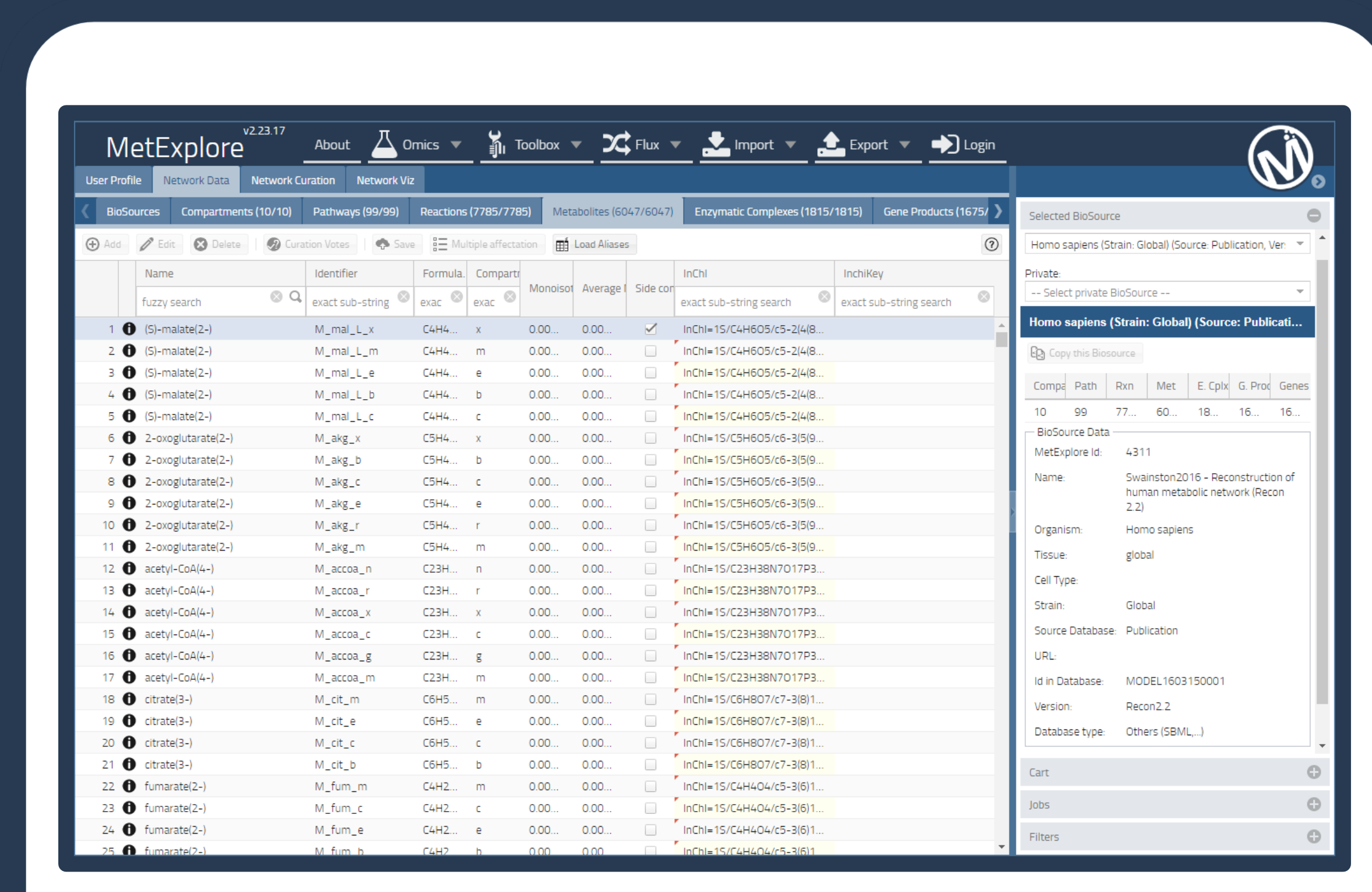
Computer assisted exploration

MetExplore is a well-established sustainable web server dedicated to the analysis of genome scale metabolic networks

- » Freely available project maintained since 2010
- » Certified within Elixir Service Delivery Plan
- » Using 3 VMs to build, test and release the application
- » Cluster based high performance computing



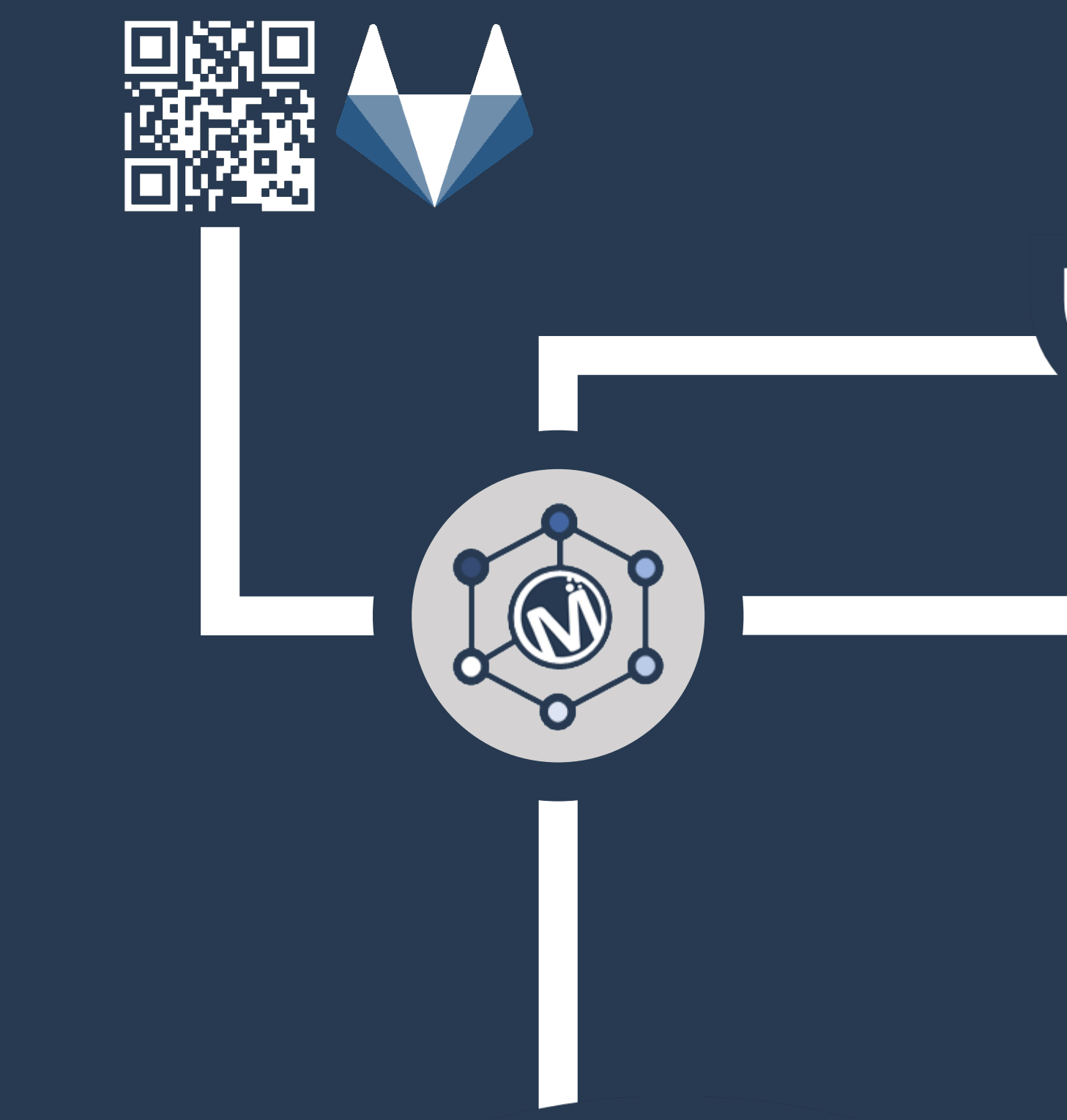
Interactive browsing of metabolic network content



www.metexplore.fr

Other features

- Flux computation
- MetaboRank computation on human network
- Metabolic network annotation
- » Import/export
- » Curation
- » Collaboration

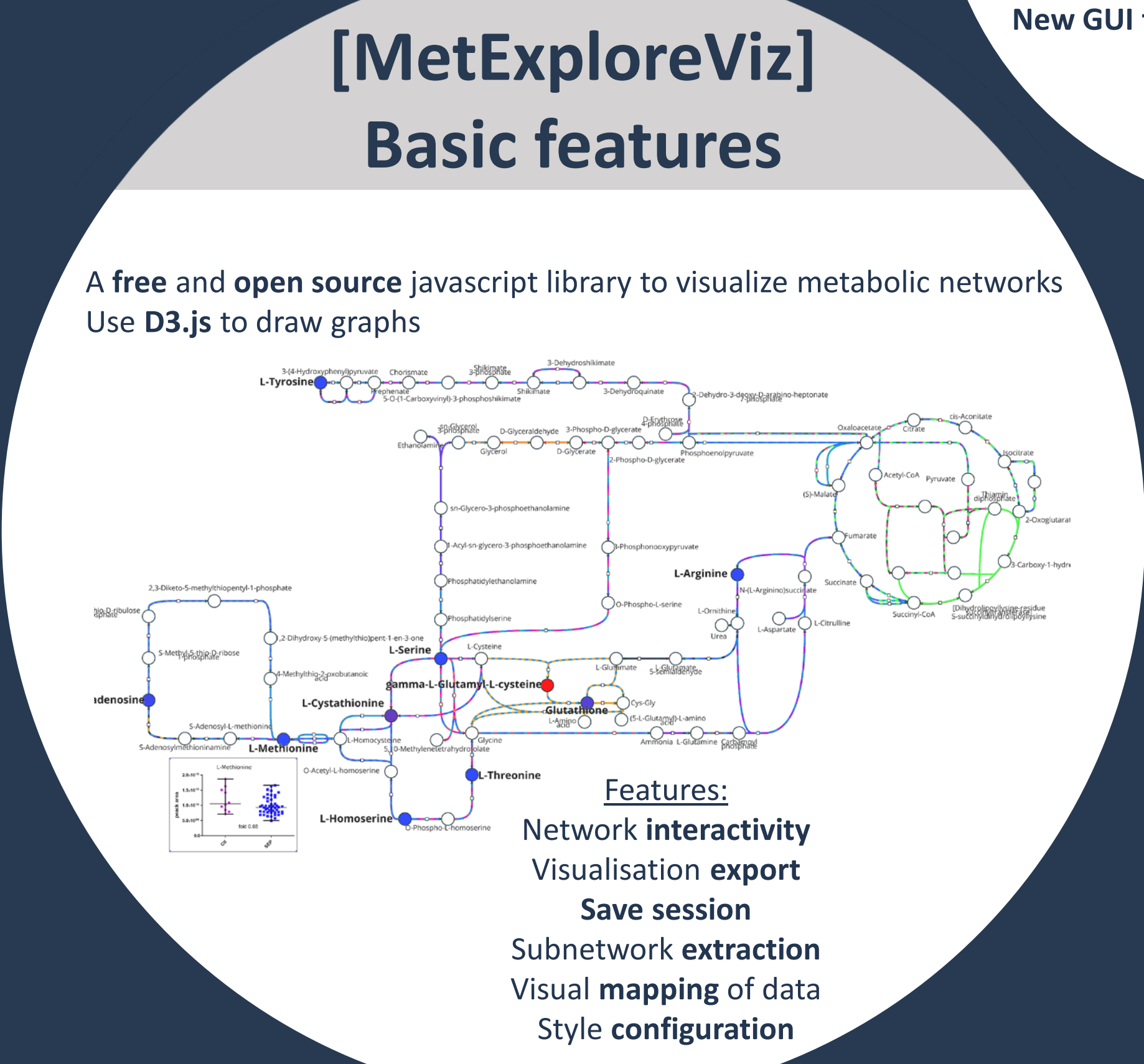
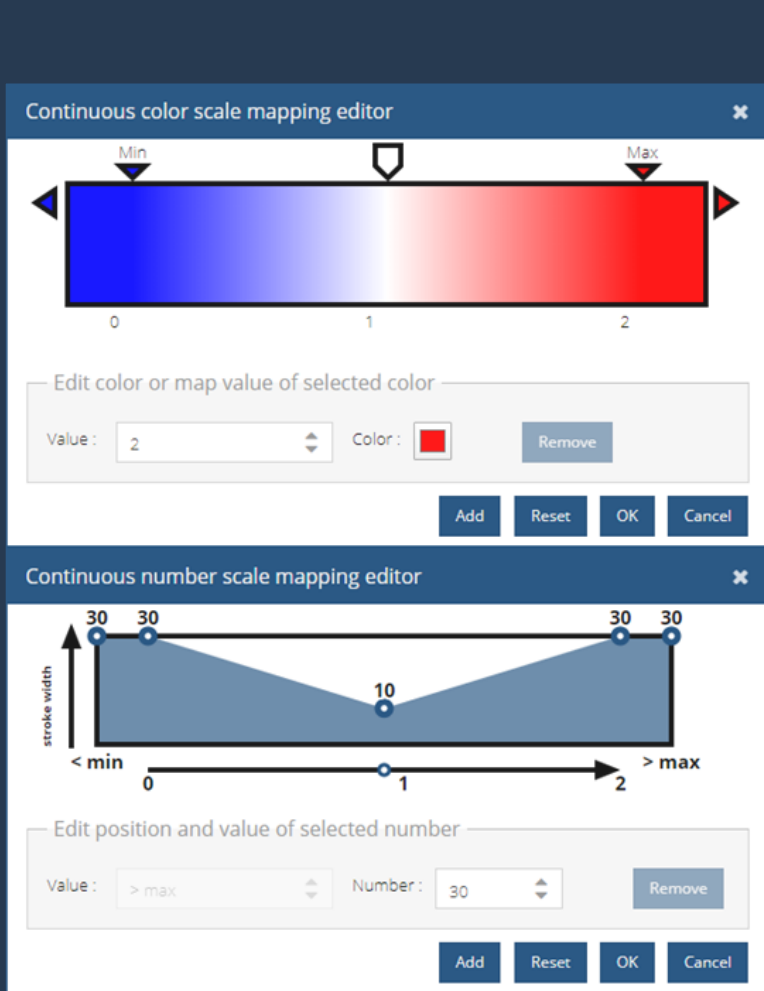


MetExploreViz v3 2020

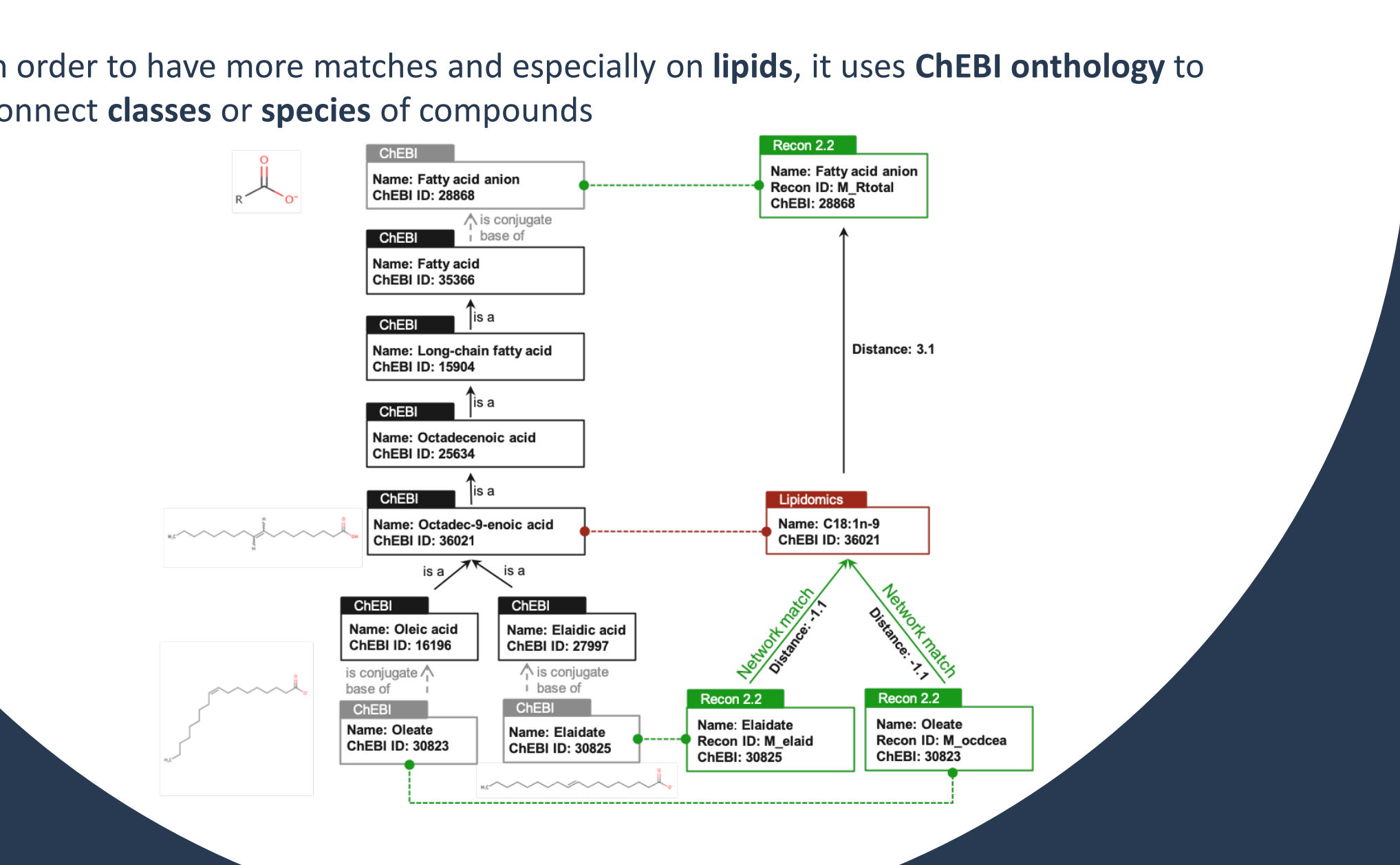
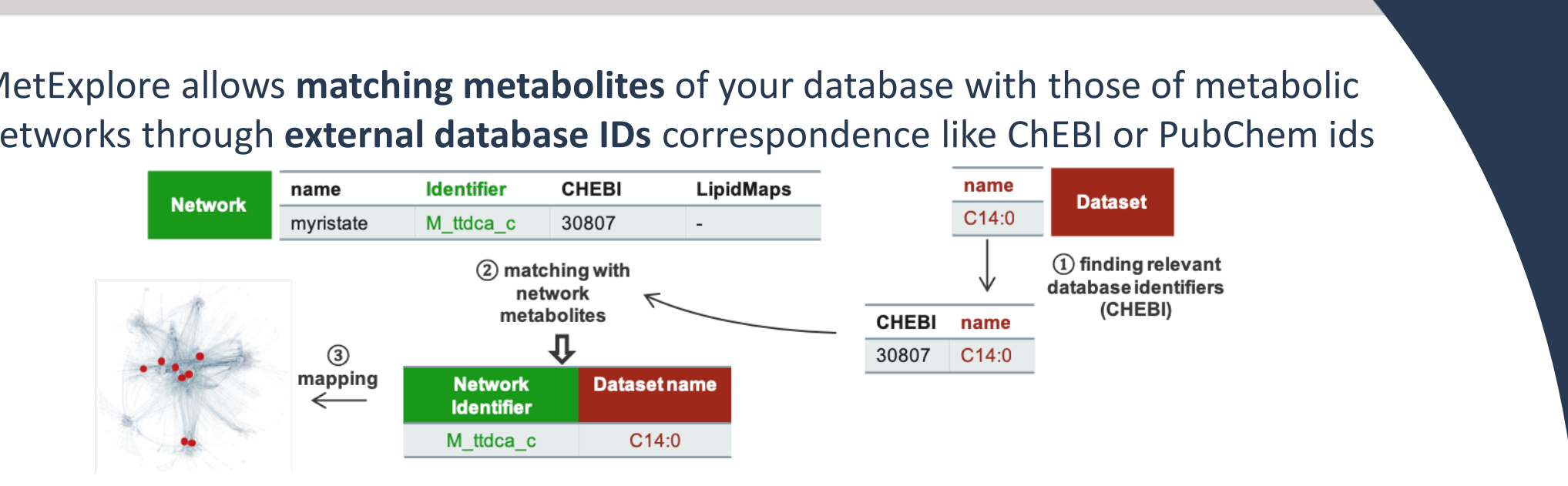
New GUI for style configuration and visual mapping of data

- » Per type metabolite / reaction and edges
- » Per style default / mapping / bypass
- » New scale editor for continuous values
- » Update all styles for nodes or edges

New GUI for interaction



Advanced metabolites and lipids matching



[MetExploreViz] Maxime Chazalviel, Clément Frainay, Nathalie Poupin, Florence Vinson, Benjamin Merlet, Yoann Gloaguen, Ludovic Cottret and Fabien Jourdan. MetExploreViz: web component for interactive metabolic network visualization. (2017) Bioinformatics. [MetaboRank] Frainay, C., Aros, S., Chazalviel, M., Garcia, T., Vinson, F., Weiss, N., ... Jourdan, F. (2018). MetaboRank: network-based recommendation system to interpret and enrich metabolomics results. Bioinformatics (Oxford, England), 35(2), 274–283. doi:10.1093/bioinformatics/bty577 [MetExplore V2] Ludovic Cottret, Clément Frainay, Maxime Chazalviel, Floréal Cabanettes, Yoann Gloaguen, Etienne Camenen, Benjamin Merlet, Jean-Charles Portais, Stéphanie Heux, Nathalie Poupin, Florence Vinson and Fabien Jourdan. MetExplore: Manage and Explore metabolic networks. (2018) Nucleic Acids Research. [DOI] F. van Ham and A. Perer. "Search, Show Context, Expand on Demand": Supporting Large Graph Exploration with Degree-of-Interest," in IEEE Transactions on Visualization and Computer Graphics, vol. 15, no. 6, pp. 953-960, Nov.-Dec. 2009. doi: 10.1109/TVCG.2009.108