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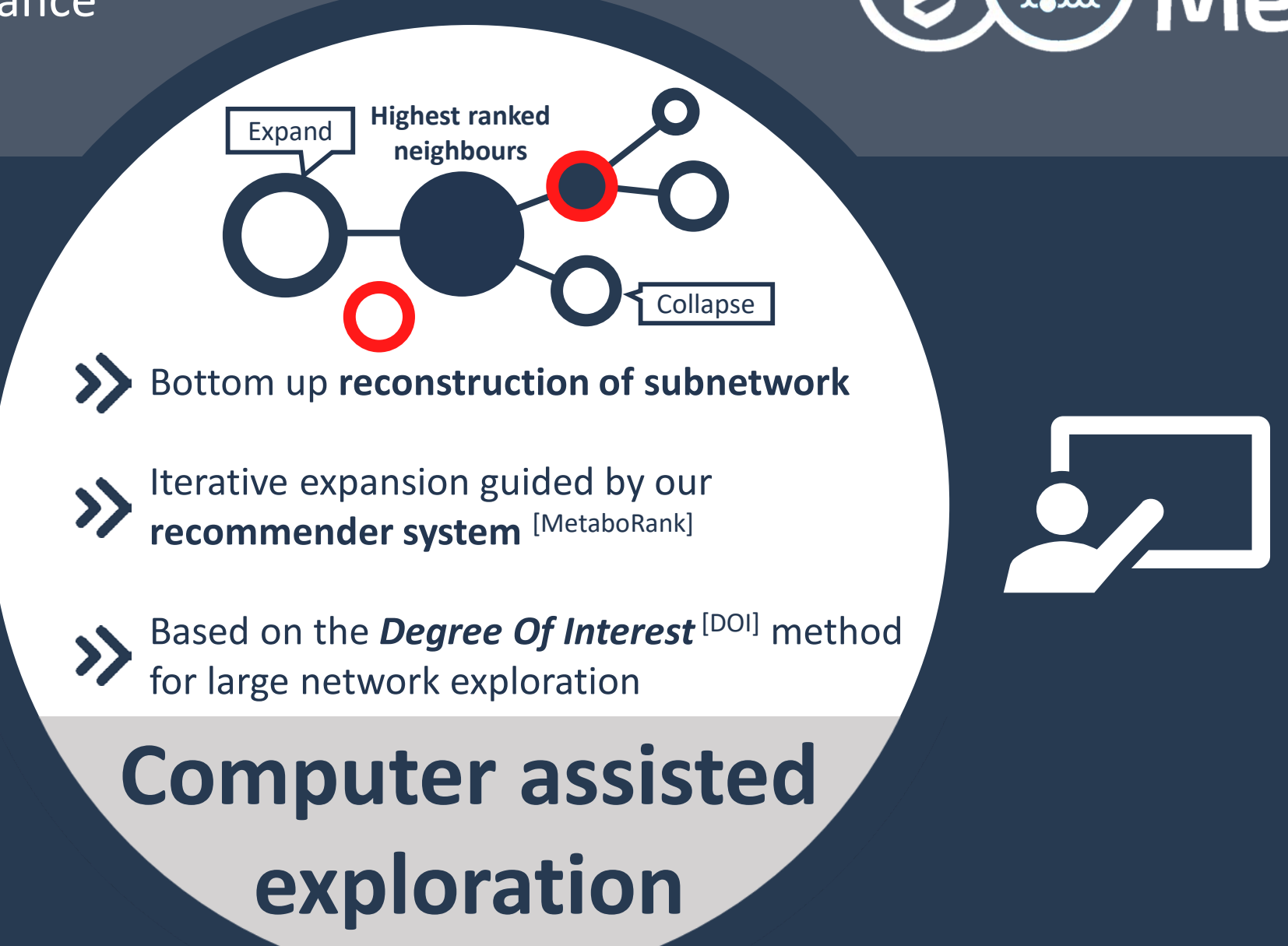
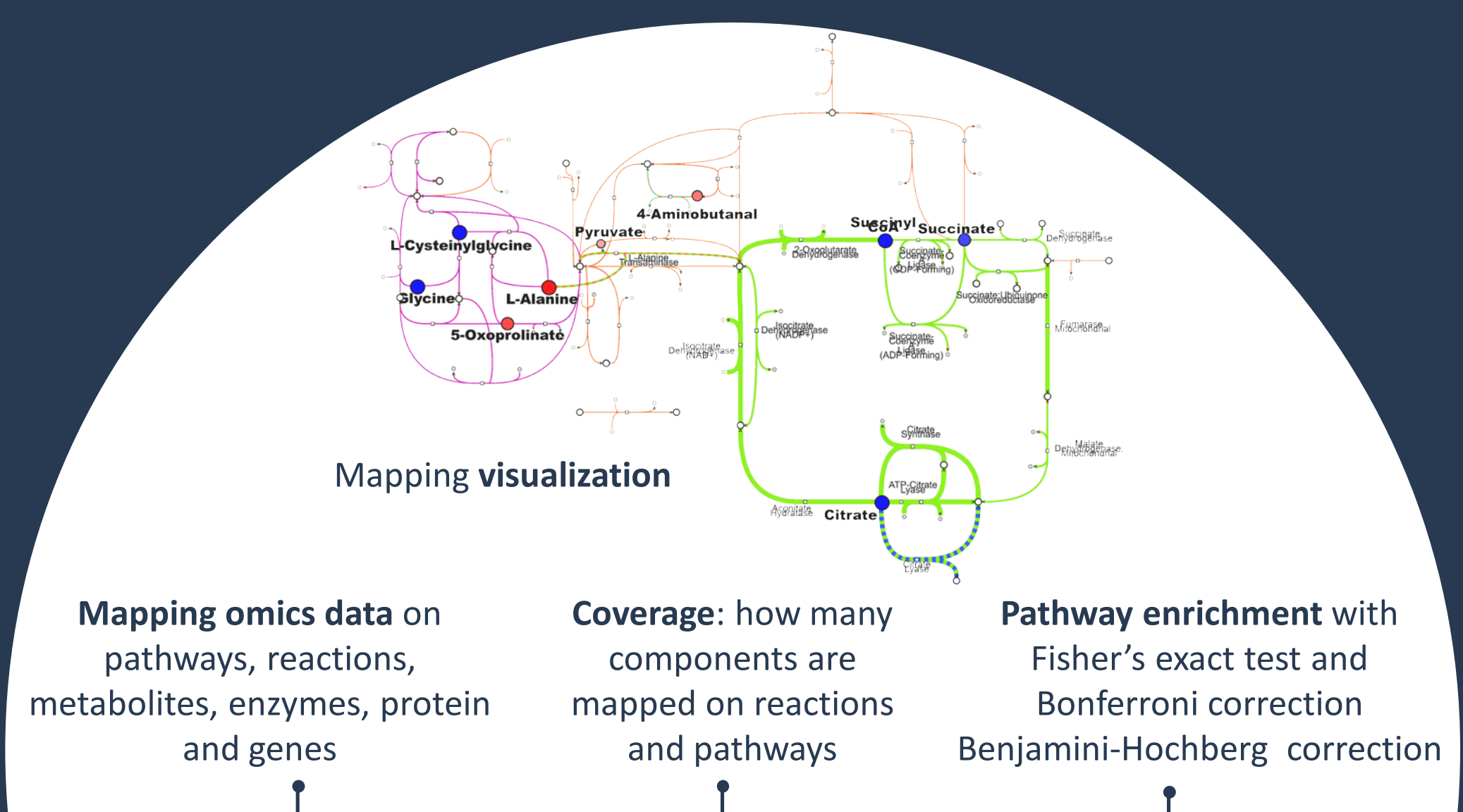
Omics data analysis in the context of metabolic networks

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Multi omics mapping

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)	*** (7.17e-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)

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

MetExplore highly facilitates metabolic network exploration thanks to interactive tables and smart filters

- Exact search on each attributes
- Fuzzy search on metabolite names

Interactive browsing of metabolic network content

297 Private networks

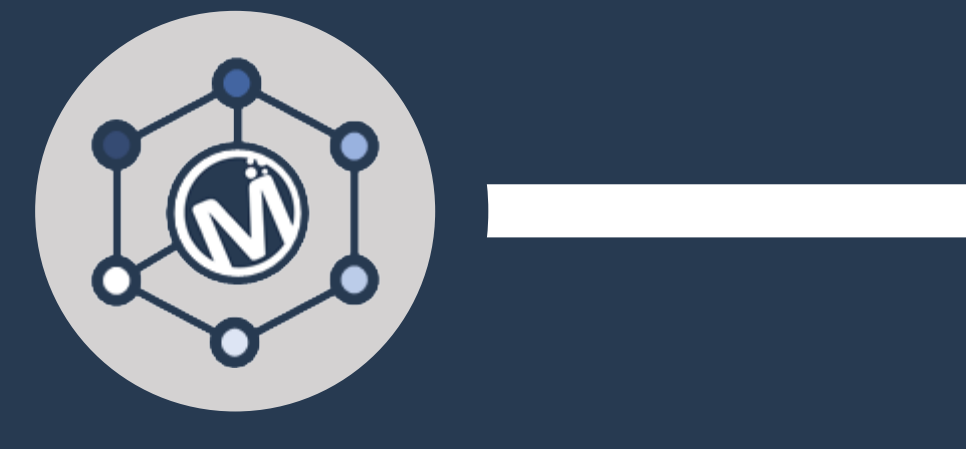
404 organisms

1196 Public networks

Other features

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

www.metexplore.fr

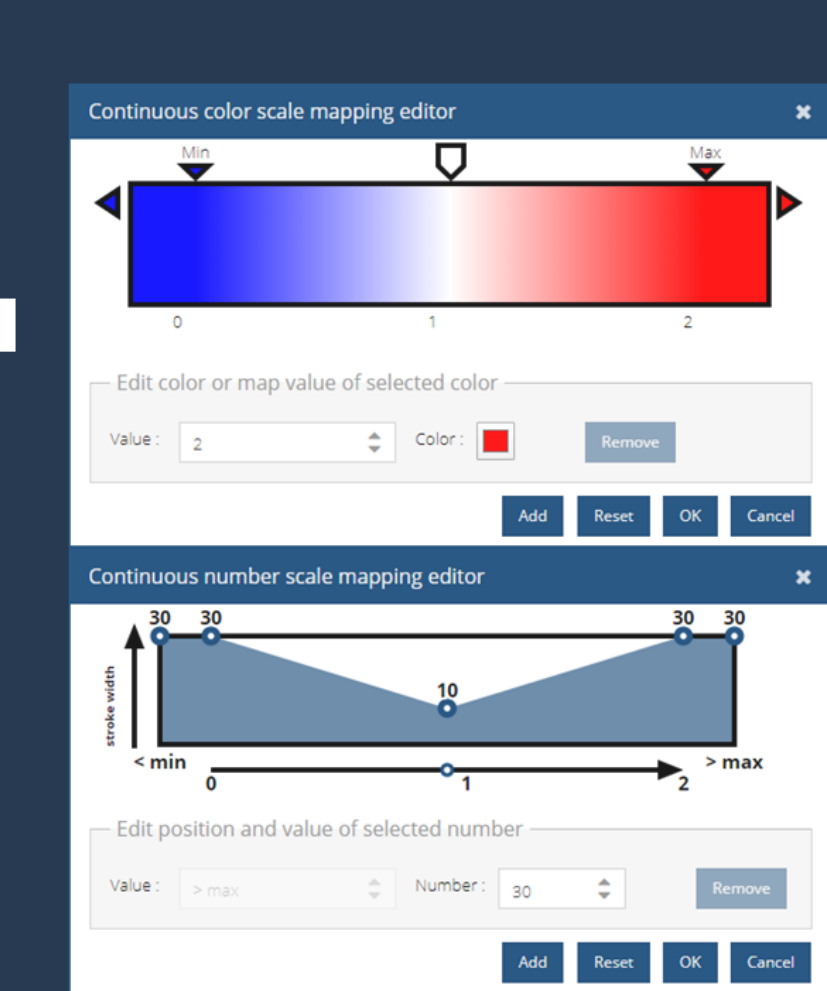


MetExploreViz v3 2020

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



[MetExploreViz] Basic features

A free and open source javascript library to visualize metabolic networks Use D3.js to draw graphs

Features:

- Network interactivity
- Visualisation export
- Save session
- Subnetwork extraction
- Visual mapping of data
- Style configuration

Advanced metabolites and lipids matching

MetExplore allows matching metabolites of your database with those of metabolic networks through external database IDs correspondence like ChEBI or PubChem ids

In order to have more matches and especially on lipids, it uses ChEBI ontology to connect classes or species of compounds

[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