MetExplore: Omics data analysis in the context of metabolic networks

Maxime Chazalviel, Adrien Rohan, Nathalie Poupin, Florence Vinson, Clément Frainay, Ludovic Cottret, Fabien Jourdan

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Omics data analysis in the context of metabolic networks

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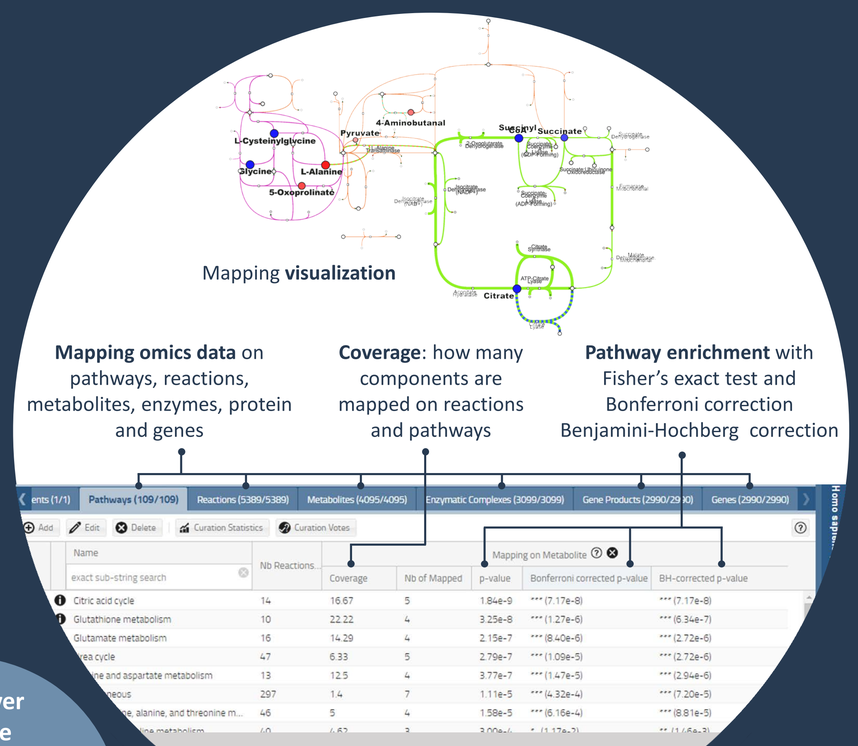
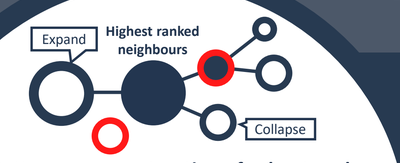
MetExplore
is a **well-established sustainable web server** dedicated to the **analysis of genome scale metabolic networks**

- 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**

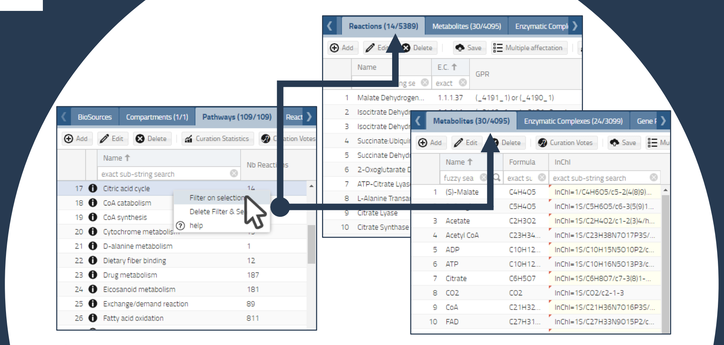


Multi omics mapping



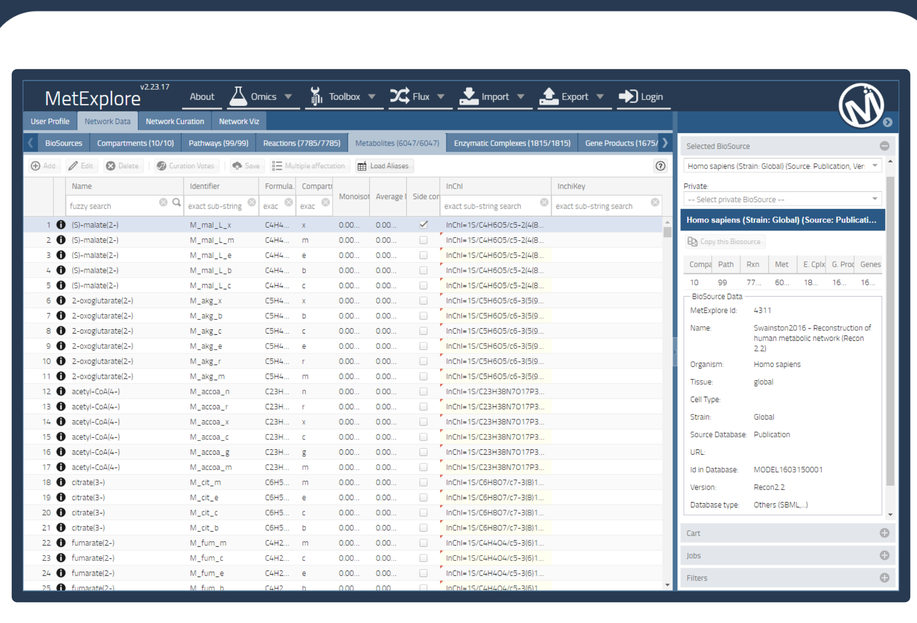
- Bottom up **reconstruction of subnetwork**
- Iterative expansion guided by our **recommender system** [MetaboRank]
- Based on the ***Degree Of Interest*** [DOI] method for large network exploration

Computer assisted exploration



- 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

39 trainings
682 trainees
846 Registered users

Other features

Flux computation

MetaboRank computation on human network

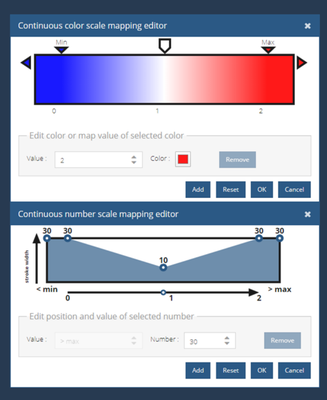
Metabolic network **annotation**
- **Import/export**
- **Curation**
- **Collaboration**

www.metexplore.fr

MetExploreViz v3 2020

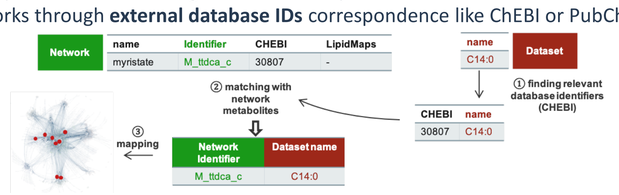
New GUI for style configuration and visual mapping of data
- Per type metabolite / reaction and edges
- Per style default / mapping / bypass
- New scale editor for continuous values
- Update all styles for nodes or edges

New GUI for interaction

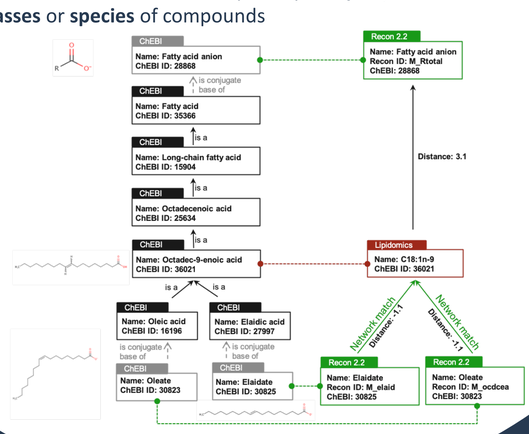


Advanced metabolites and lipids matching

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

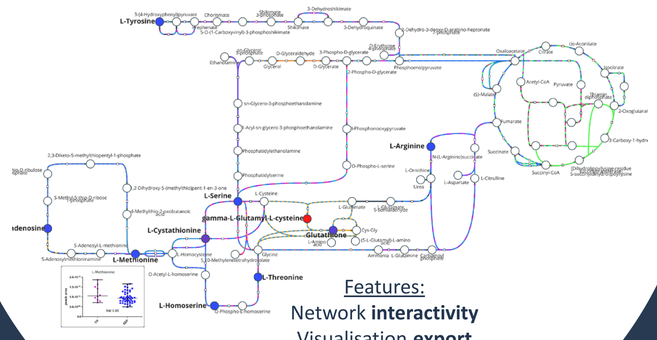


- In order to have more matches and especially on **lipids**, it uses **ChEBI onthology** to connect **classes** or **species** of compounds

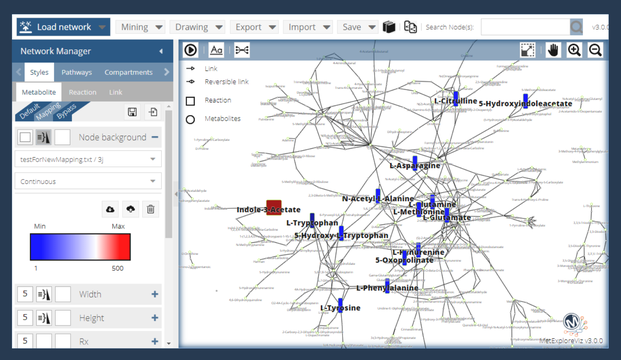


[MetExploreViz] Basic features

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**



[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) Nucelic 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