Getting started

MetExplore

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A use case of MetExplore

It is better to use Chrome web browser.

MetExplore (Cottret et al., 2010) is a web server dedicated to the analysis of genome scale metabolic networks. A special care was taken to allow analyzing metabolomics data in the context of this network.

►Go on the MetExplore homepage and click on the "Click here" button

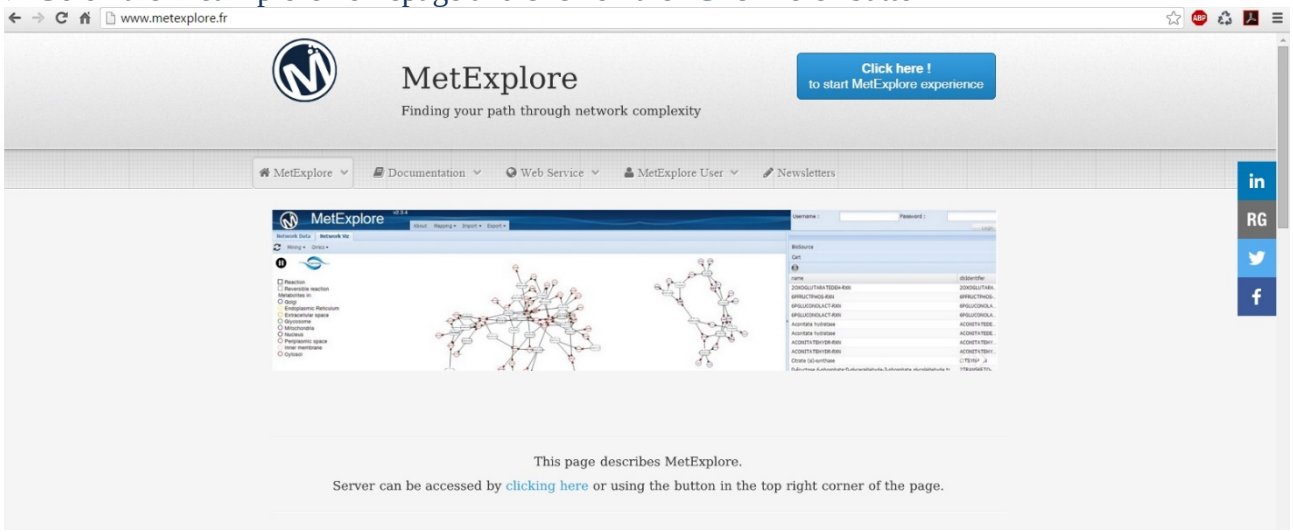


Figure 1: MetExplore homepage

MetExplore is providing access to BioCyc networks, KEGG networks and networks imported from SBML files (Hucka et al., 2003). All these files are present in the "public BioSource" repository. Note that you can also register and upload your own SBML files. You will then be the only one to be able to access these networks and will have the opportunity to share them with others.

►In the list of biosources click on: "Saccharomyces cerevisiae"
►Right click on the line of KEGG version of the network then click on "select Biosource" (you can also double click on it

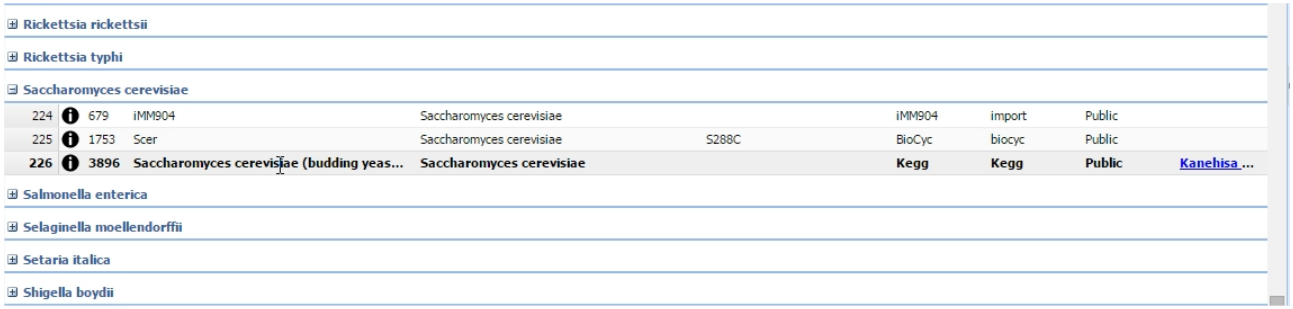
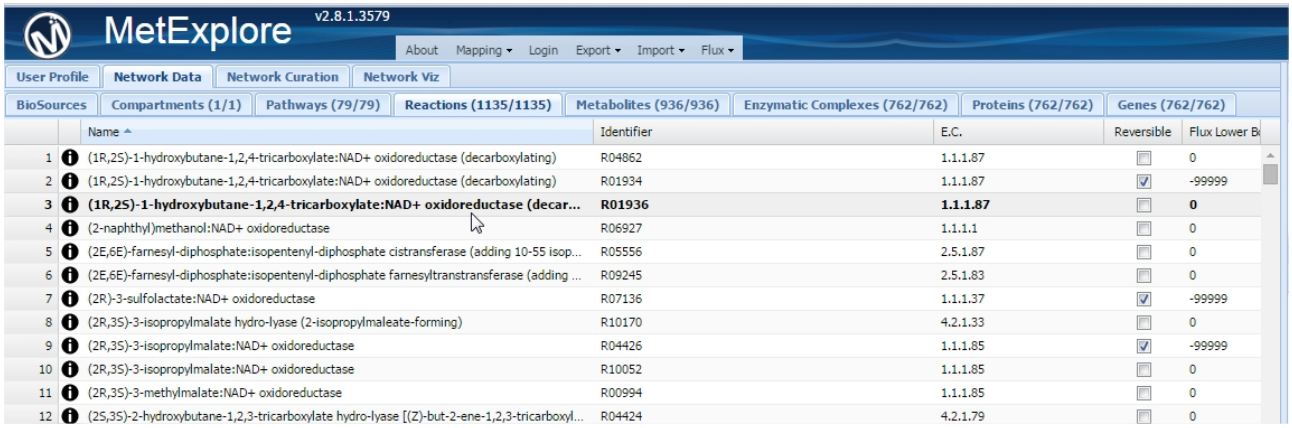


Figure 2: BioSource selection interface in MetExplore

The content of the metabolic network will be displayed in a tabular format.
Information on Compartments, Pathways, Reactions, Metabolites, Enzymes, Proteins and Genes are available.



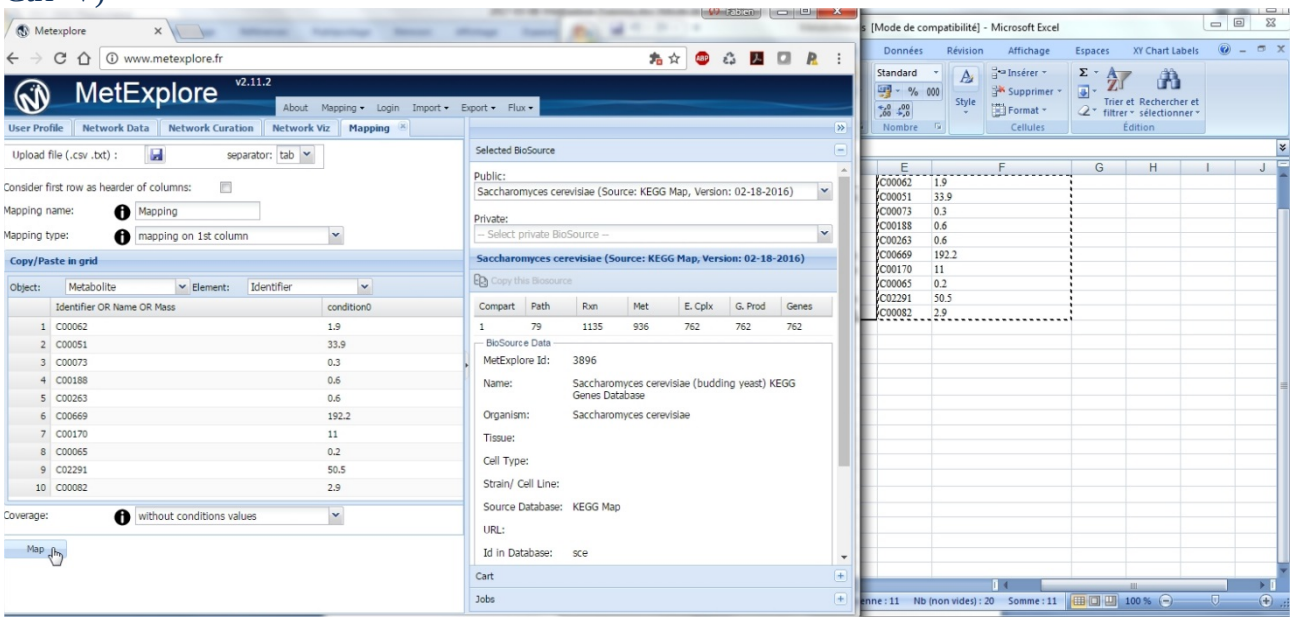
	Name	Identifier	E.C.	Reversible	Flux Lower B
1	(1R,2S)-1-hydroxybutane-1,2,4-tricarboxylate:NAD+ oxidoreductase (decarboxylating)	R04862	1.1.1.87		0
2	(1R,2S)-1-hydroxybutane-1,2,4-tricarboxylate:NAD+ oxidoreductase (decarboxylating)	R01934	1.1.1.87	✓	-99999
3	**(1R,2S)-1-hydroxybutane-1,2,4-tricarboxylate:NAD+ oxidoreductase (decar...**	**R01936**	**1.1.1.87**		**0**
4	(2-naphthyl)methanol:NAD+ oxidoreductase	R06927	1.1.1.1		0
5	(2E,6E)-farnesyl-diphosphate:isopentenyl-diphosphate cistransferase (adding 10-55 isop...	R05556	2.5.1.87		0
6	(2E,6E)-farnesyl-diphosphate:isopentenyl-diphosphate farnesyltranstransferase (adding ...	R09245	2.5.1.83		0
7	(2R)-3-sulfolactate:NAD+ oxidoreductase	R07136	1.1.1.37	✓	-99999
8	(2R,3S)-3-isopropylmalate hydro-lyase (2-isopropylmaleate-forming)	R10170	4.2.1.33		0
9	(2R,3S)-3-isopropylmalate:NAD+ oxidoreductase	R04426	1.1.1.85	✓	-99999
10	(2R,3S)-3-isopropylmalate:NAD+ oxidoreductase	R10052	1.1.1.85		0
11	(2R,3S)-3-methylmalate:NAD+ oxidoreductase	R00994	1.1.1.85		0
12	(2S,3S)-2-hydroxybutane-1,2,3-tricarboxylate hydro-lyase [(Z)-but-2-ene-1,2,3-tricarboxyl...	R04424	4.2.1.79		0

Figure 3: MetExplore representation of metabolic network content.

We are going to perform this mapping on yeast and using the metabolite identifiers found in the KEGG database

► Select "Mapping" in the menu at the top of the page.

► Copy (ctrl+C on the excel table) and paste (click on the first line of the MetExplore table and Ctrl+V)

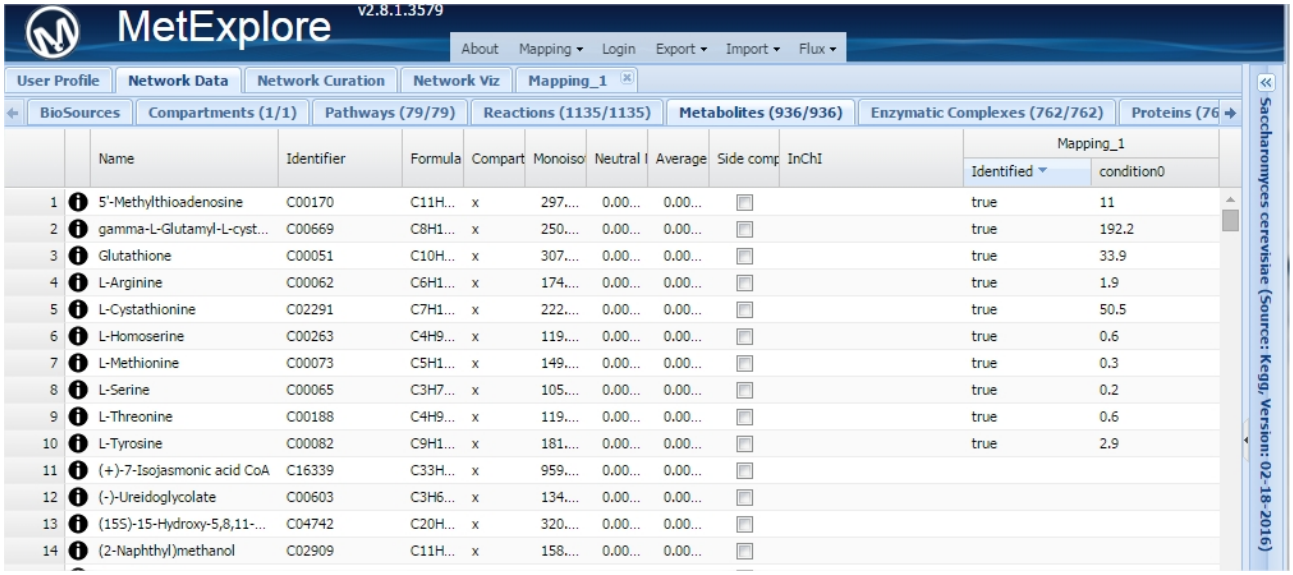


	Identifier OR Name OR Mass	condition0
1	C00062	1.9
2	C00051	33.9
3	C00073	0.3
4	C00188	0.6
5	C00263	0.6
6	C00669	192.2
7	C00170	11
8	C00065	0.2
9	C02291	50.5
10	C00082	2.9

Figure 4: import metabolites in MetExplore

► Click on the "Map" button

Coming back to the tabular view, you will see which metabolites were mapped. (in the metabolite panel)



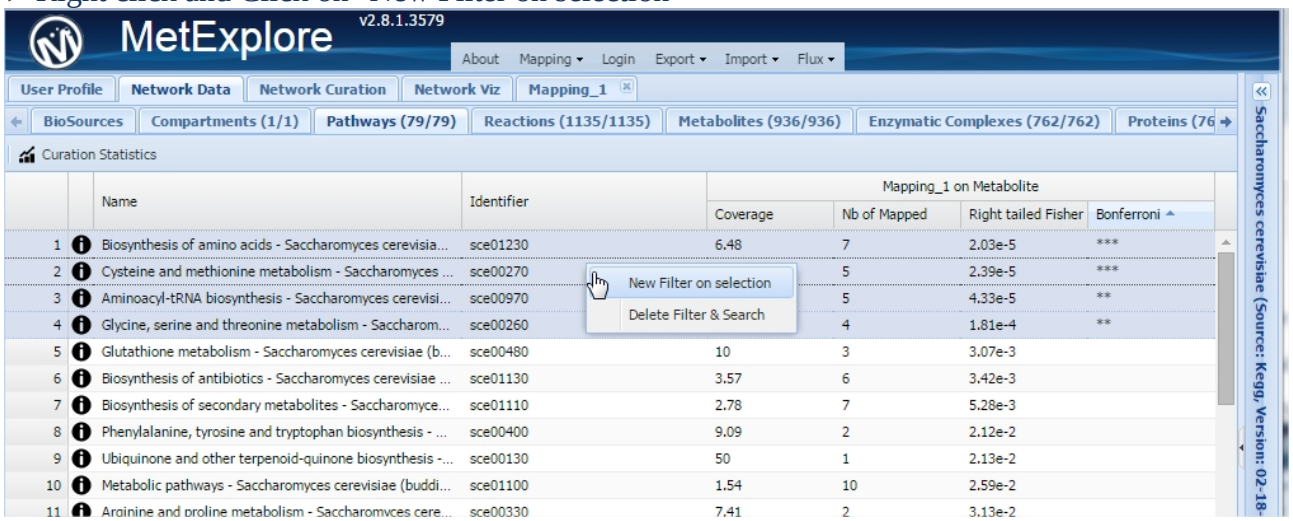
	Name	Identifier	Formula	Compart	Monoiso	Neutral	Average	Side comp	InChI	Mapping_1 Identified	Mapping_1 condition0
1	5'-Methylthioadenosine	C00170	C11H...	x	297....	0.00...	0.00...			true	11
2	gamma-L-Glutamyl-L-cyst...	C00669	C8H1...	x	250....	0.00...	0.00...			true	192.2
3	Glutathione	C00051	C10H...	x	307....	0.00...	0.00...			true	33.9
4	L-Arginine	C00062	C6H1...	x	174....	0.00...	0.00...			true	1.9
5	L-Cystathionine	C02291	C7H1...	x	222....	0.00...	0.00...			true	50.5
6	L-Homoserine	C00263	C4H9...	x	119....	0.00...	0.00...			true	0.6
7	L-Methionine	C00073	C5H1...	x	149....	0.00...	0.00...			true	0.3
8	L-Serine	C00065	C3H7...	x	105....	0.00...	0.00...			true	0.2
9	L-Threonine	C00188	C4H9...	x	119....	0.00...	0.00...			true	0.6
10	L-Tyrosine	C00082	C9H1...	x	181....	0.00...	0.00...			true	2.9
11	(+)-7-Isojasmonic acid CoA	C16339	C33H...	x	959....	0.00...	0.00...				
12	(-)-Ureidoglycolate	C00603	C3H6...	x	134....	0.00...	0.00...				
13	(15S)-15-Hydroxy-5,8,11-...	C04742	C20H...	x	320....	0.00...	0.00...				
14	(2-Naphthyl)methanol	C02909	C11H...	x	158....	0.00...	0.00...				

Figure 5: MetExplore output of a mapping.

By selecting lines in a table it is possible (when right clicking on it) to filter all the other tables based on this selection.

►Go to the pathways panel and select the 4 first pathways (they are ordered according to the pathway enrichment result)

►Right click and Click on "New Filter on selection"



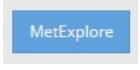
	Name	Identifier	Mapping_1 on Metabolite Coverage	Nb of Mapped	Right tailed Fisher	Bonferroni
1	Biosynthesis of amino acids - Saccharomyces cerevisia...	sce01230	6.48	7	2.03e-5	***
2	Cysteine and methionine metabolism - Saccharomyces ...	sce00270		5	2.39e-5	***
3	Aminoacyl-tRNA biosynthesis - Saccharomyces cerevisi...	sce00970		5	4.33e-5	**
4	Glycine, serine and threonine metabolism - Saccharom...	sce00260		4	1.81e-4	**
5	Glutathione metabolism - Saccharomyces cerevisiae (b...	sce00480	10	3	3.07e-3	
6	Biosynthesis of antibiotics - Saccharomyces cerevisiae ...	sce01130	3.57	6	3.42e-3	
7	Biosynthesis of secondary metabolites - Saccharomyce...	sce01110	2.78	7	5.28e-3	
8	Phenylalanine, tyrosine and tryptophan biosynthesis - ...	sce00400	9.09	2	2.12e-2	
9	Ubiquinone and other terpenoid-quinone biosynthesis -...	sce00130	50	1	2.13e-2	
10	Metabolic pathways - Saccharomyces cerevisiae (buddi...	sce01100	1.54	10	2.59e-2	
11	Arginine and proline metabolism - Saccharomyces cere...	sce00330	7.41	2	3.13e-2	

Figure 6: MetExplore filtering on pathways

Now, all the other panels will contain elements (reactions, metabolites...) corresponding to this pathway.

►Go to the reaction panel. Right click on the table and click on "Copy all to cart"

Now all selected reactions are in the car and can be used for visualization

►Select the "Network Viz" panel and cilck on 

button to create the view.

Figure 7: Network visualisation in MetExplore

►Click on the "Omics" menu and then on "Import mapping"
Metabolites mapped our now colored in blue.

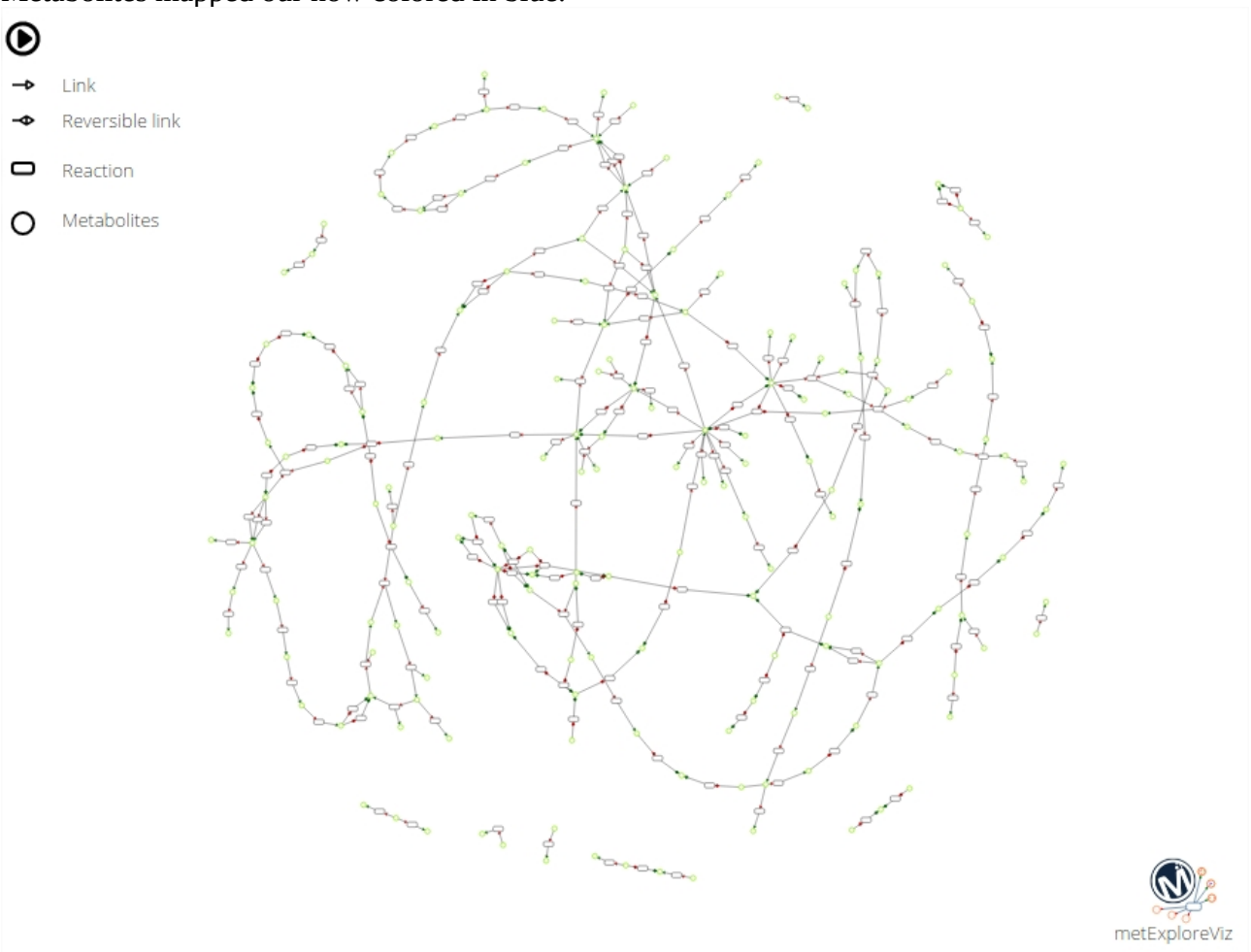
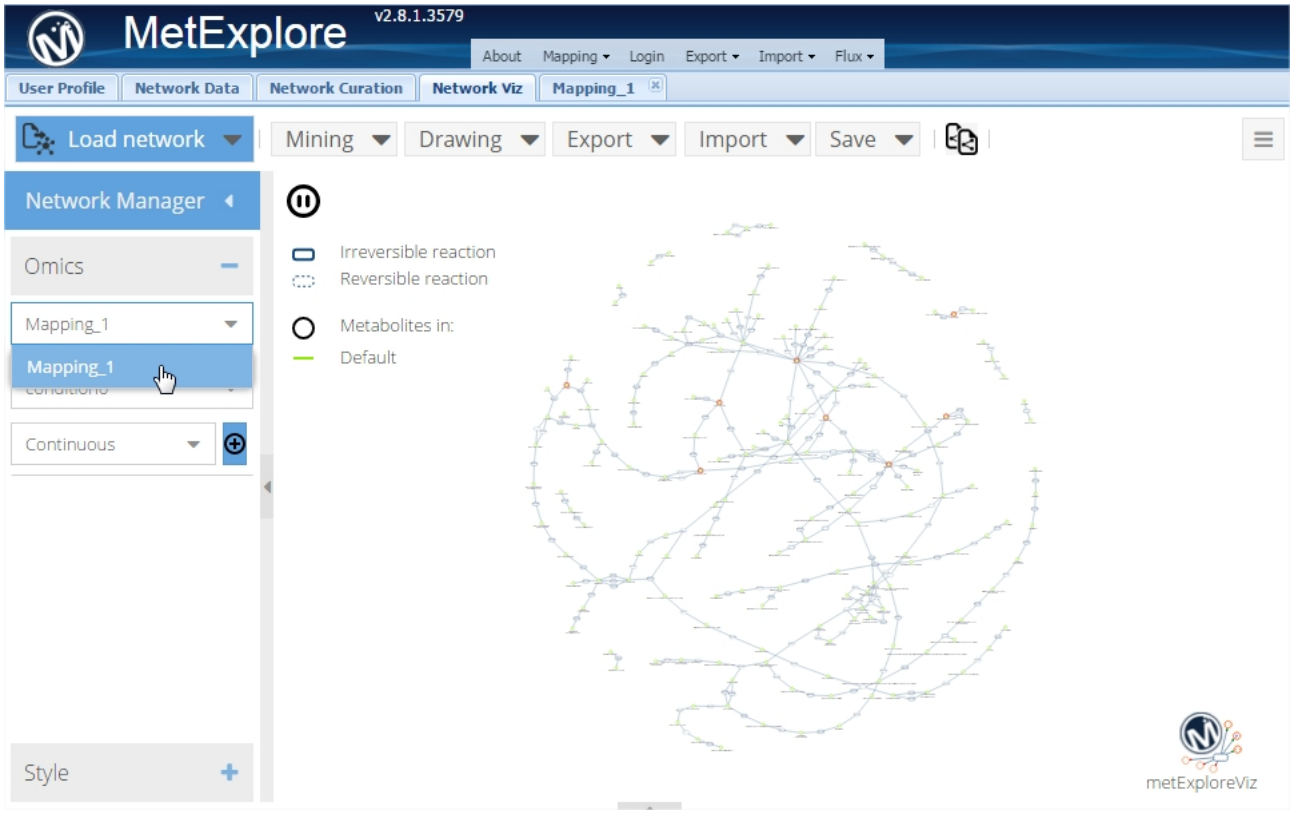


Figure 8: Network based on enriched pathways in MetExplore

►On the left of the panel in the "Omics" box select "Mapping_1". It will highlight in red metabolites mapped.



►Click on "Mining->Highlight subnetwork" to emphasize the union of all lightest paths between each pair on identified metabolites

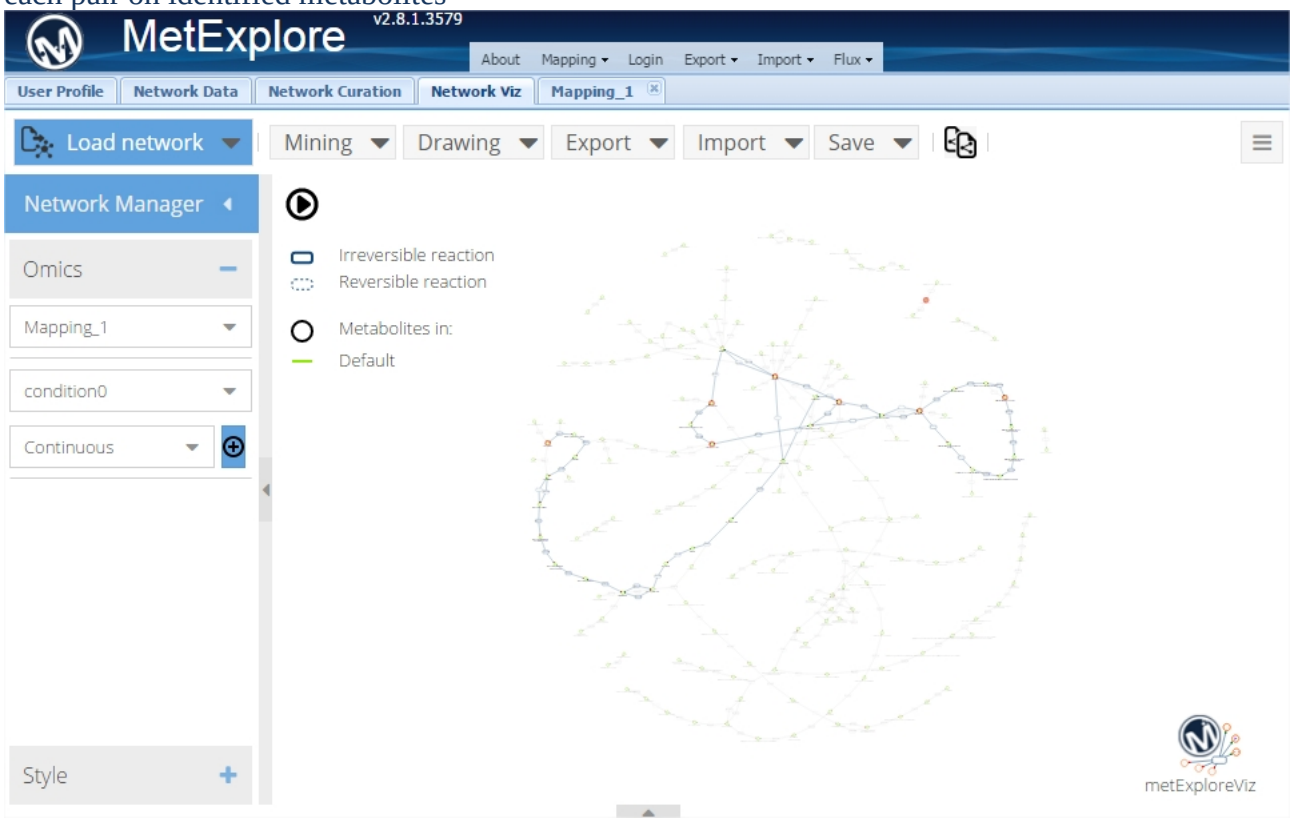
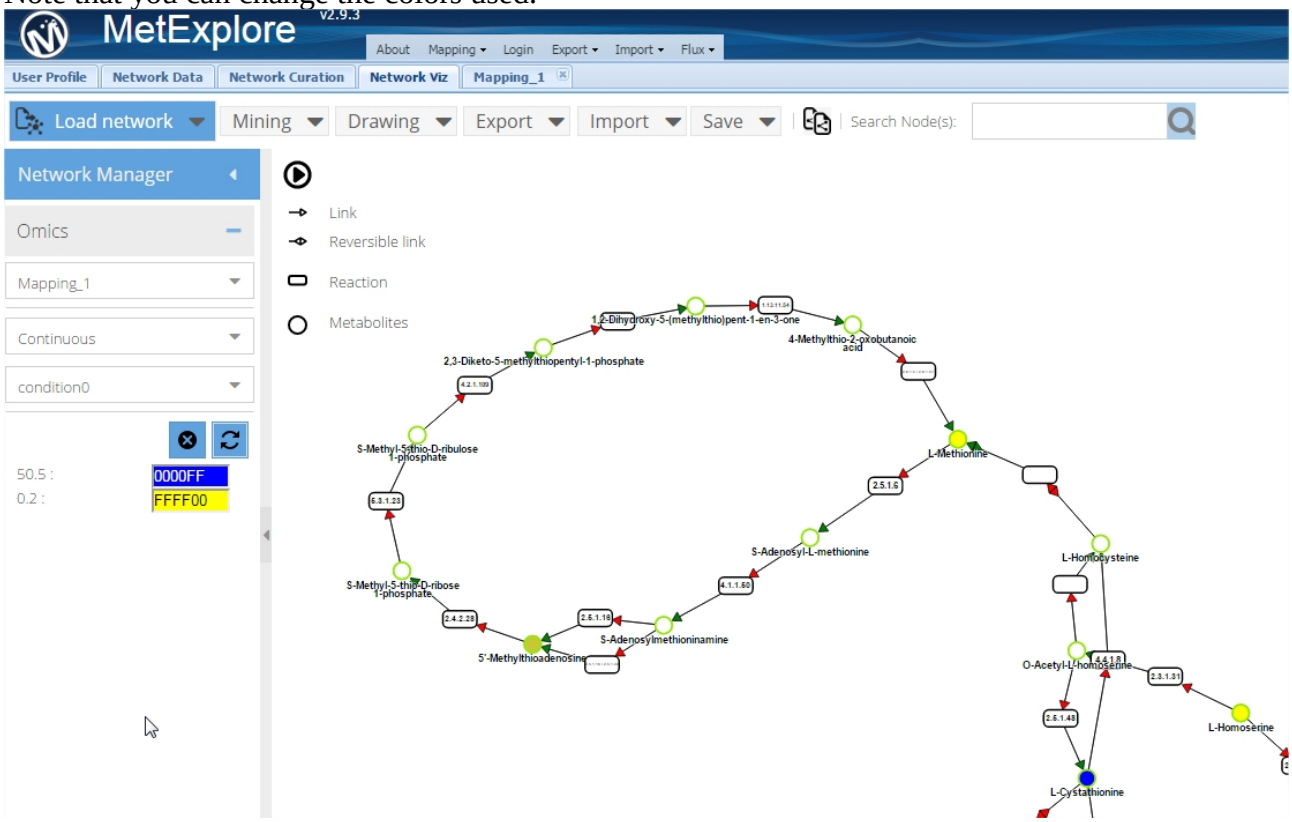


Figure 9: sub-network connecting identified metabolites

►Click on "Mining->Extract subnetwork" to keep only the subnetwork.

►Click on the "+" button to perform a continuous mapping of data on nodes.
Note that you can change the colors used.



This computation is performed on a selection of reactions. It is also possible to do it on the entire network. It will allow connecting other metabolites.

In MetExplore, mapping can be saved in the database (function accessible through web services). Then it is possible to access the mapping through a single URL (here it is the mapping of Metabolights dataset MTBLS174 on Recon2 human metabolic network):
http://metexplore.toulouse.inra.fr/metexplore2/?idMapping=38285