OmicsNet Tutorial: Basic Network Exploration and Manipulation

Computer Requirement

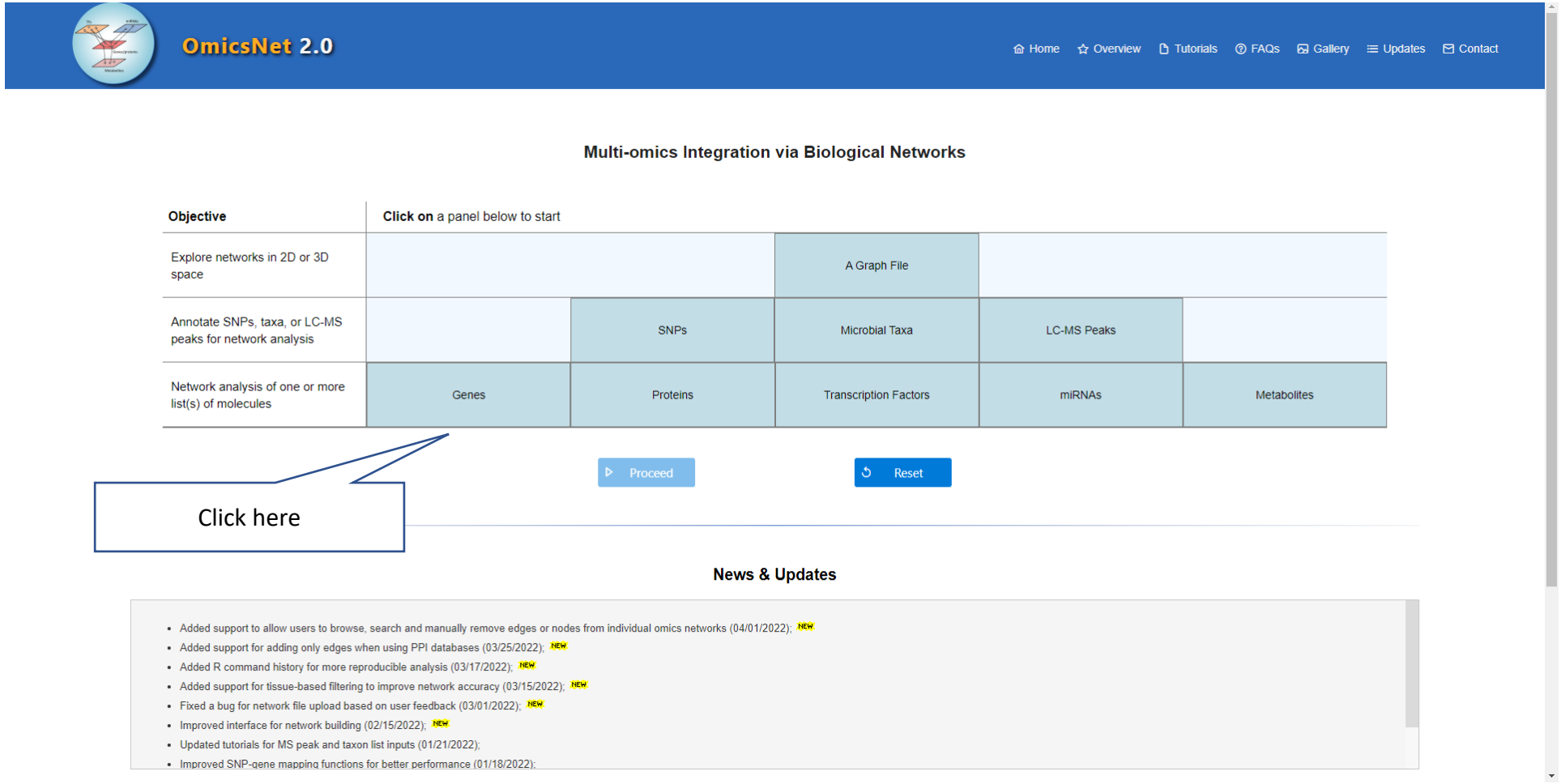
- Modern browser supporting **WebGL**
- Chrome 50+, Firefox 47+, Safari 10.2+ and Edge 12+
- Please make sure WebGL is enabled in your browser
  - Please consult this web page to verify: https://get.webgl.org/
- If not enabled, please consult our **FAQ** page for instructions
- For best performance and visualization, use:
- Latest version of **Google Chrome**
- A modern computer with at least 4GB of physical RAM
- A 15-inch screen or bigger (larger is better)
- Retina Display is supported

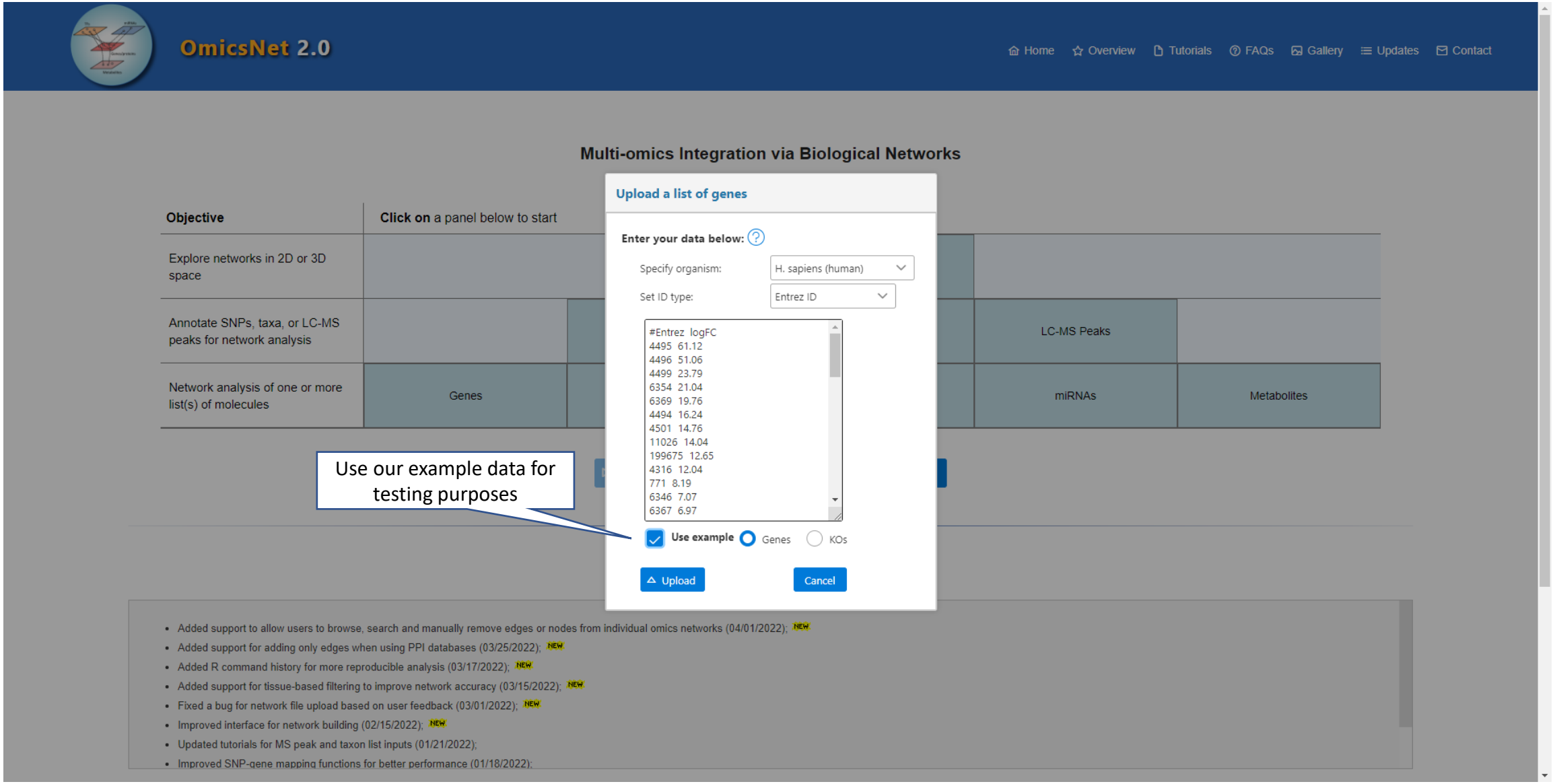
Motivation

- Demonstrate the basic steps for network creation:
  - From a list of molecules
  - From a network file

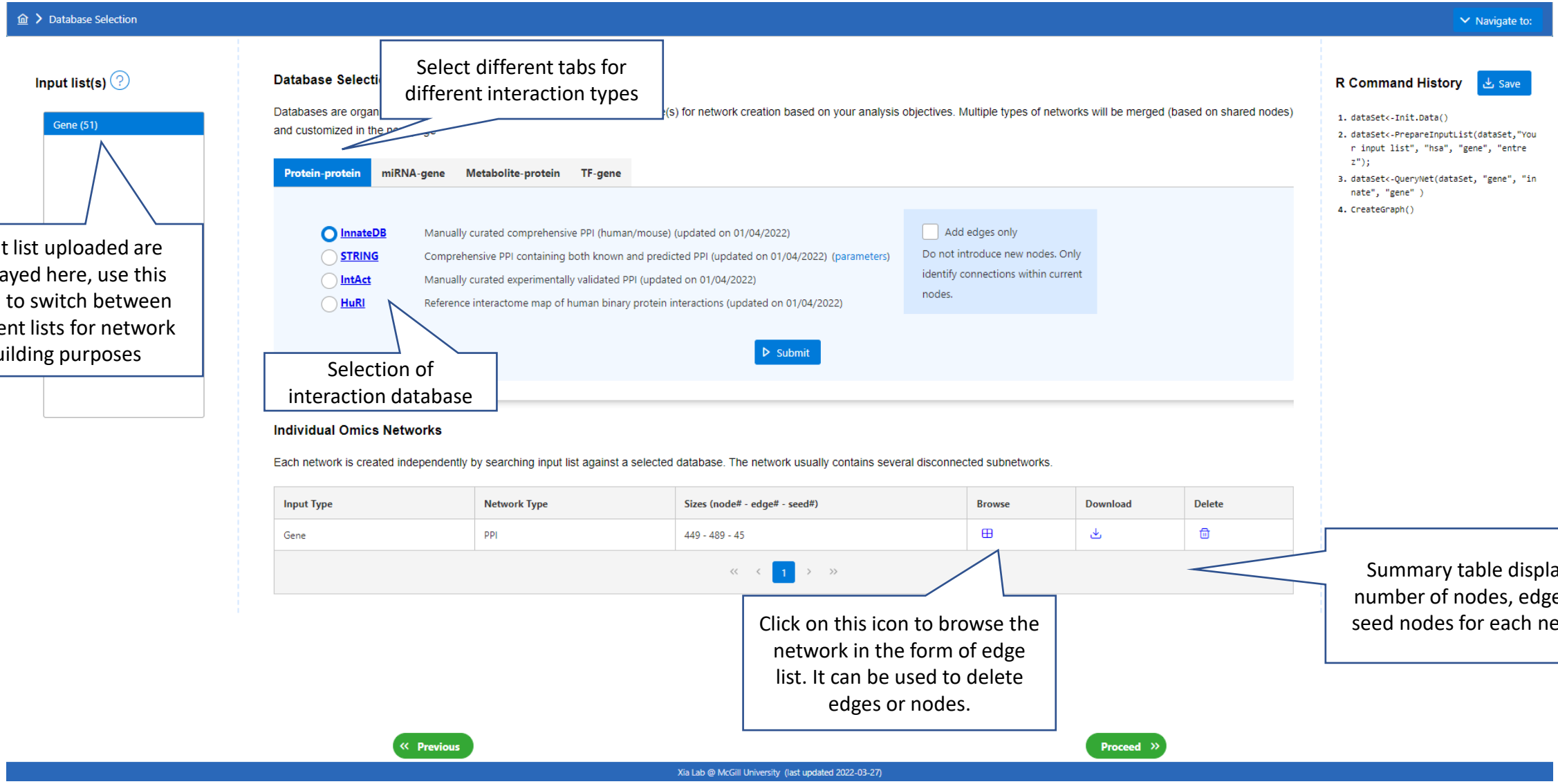
- Showcase the main functionalities of OmicsNet Network Viewer
  - Network exploration
  - Network customization
  - Functional analyses

Create a network from a list of genes

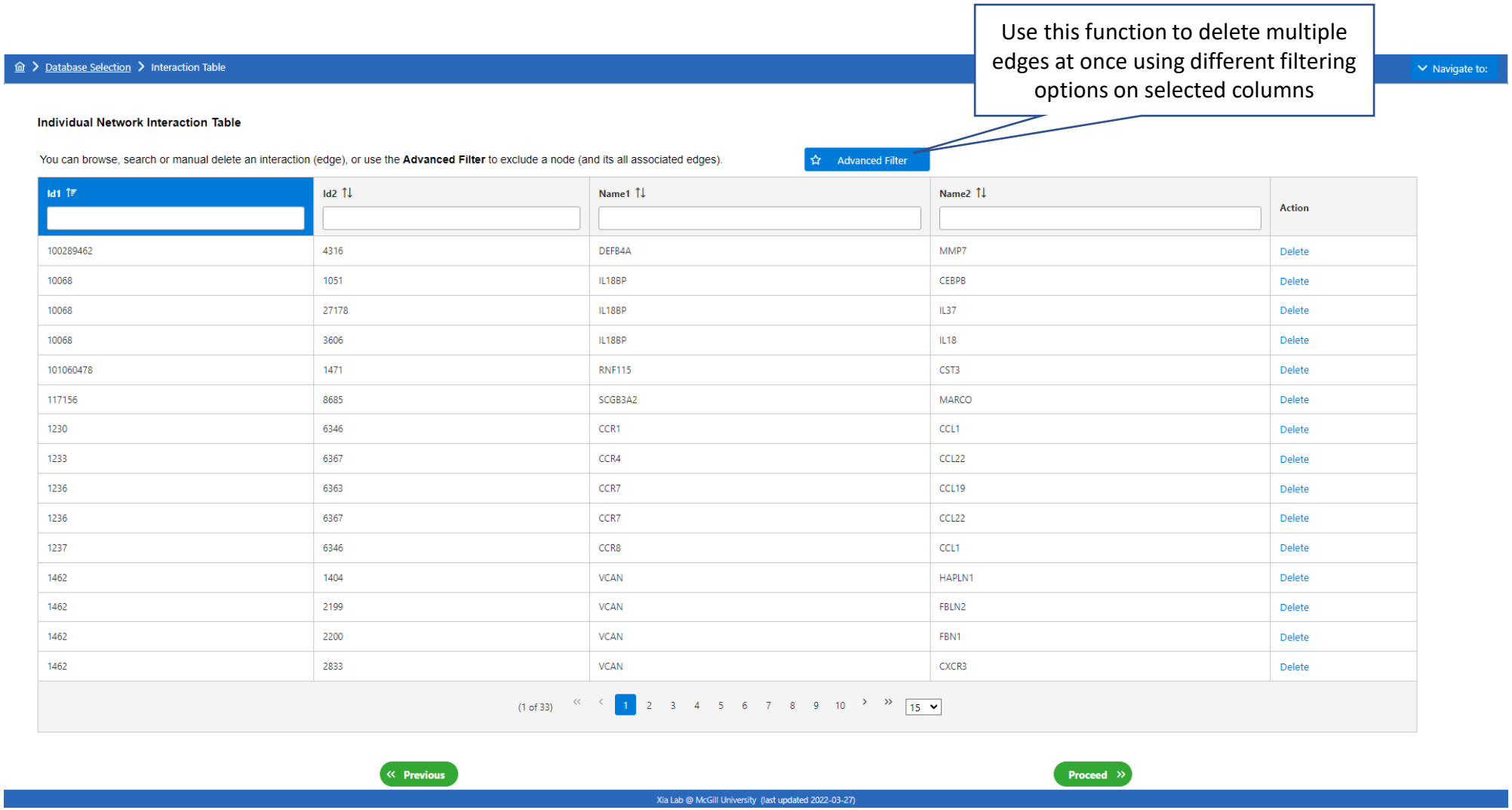



OmicsNet 2.0
Home
Overview
Tutorials
FAQs
Gallery
Updates
Contact
Multi-omics Integration via Biological Networks
Objective
Click on a panel below to start
Explore networks in 2D or 3D space
Annotate SNPs, taxa, or LC-MS peaks for network analysis
Network analysis of one or more list(s) of molecules
Genes
LC-MS Peaks
miRNAs
Metabolites
Upload a list of genes
Enter your data below:
Specify organism:
H. sapiens (human)
Set ID type:
Entrez ID
#Entrez logFC
4495 61.12
4496 51.06
4499 23.79
6354 21.04
6369 19.76
4494 16.24
4501 14.76
11026 14.04
199675 12.65
4316 12.04
771 8.19
6346 7.07
6367 6.97
Use example
Genes
KOs
Upload
Cancel
Use our example data for testing purposes
Added support to allow users to browse, search and manually remove edges or nodes from individual omics networks (04/01/2022);
Added support for adding only edges when using PPI databases (03/25/2022);
Added R command history for more reproducible analysis (03/17/2022);
Added support for tissue-based filtering to improve network accuracy (03/15/2022);
Fixed a bug for network file upload based on user feedback (03/01/2022);
Improved interface for network building (02/15/2022);
Updated tutorials for MS peak and taxon list inputs (01/21/2022);
Improved SNP-gene mapping functions for better performance (01/18/2022);

Database selection

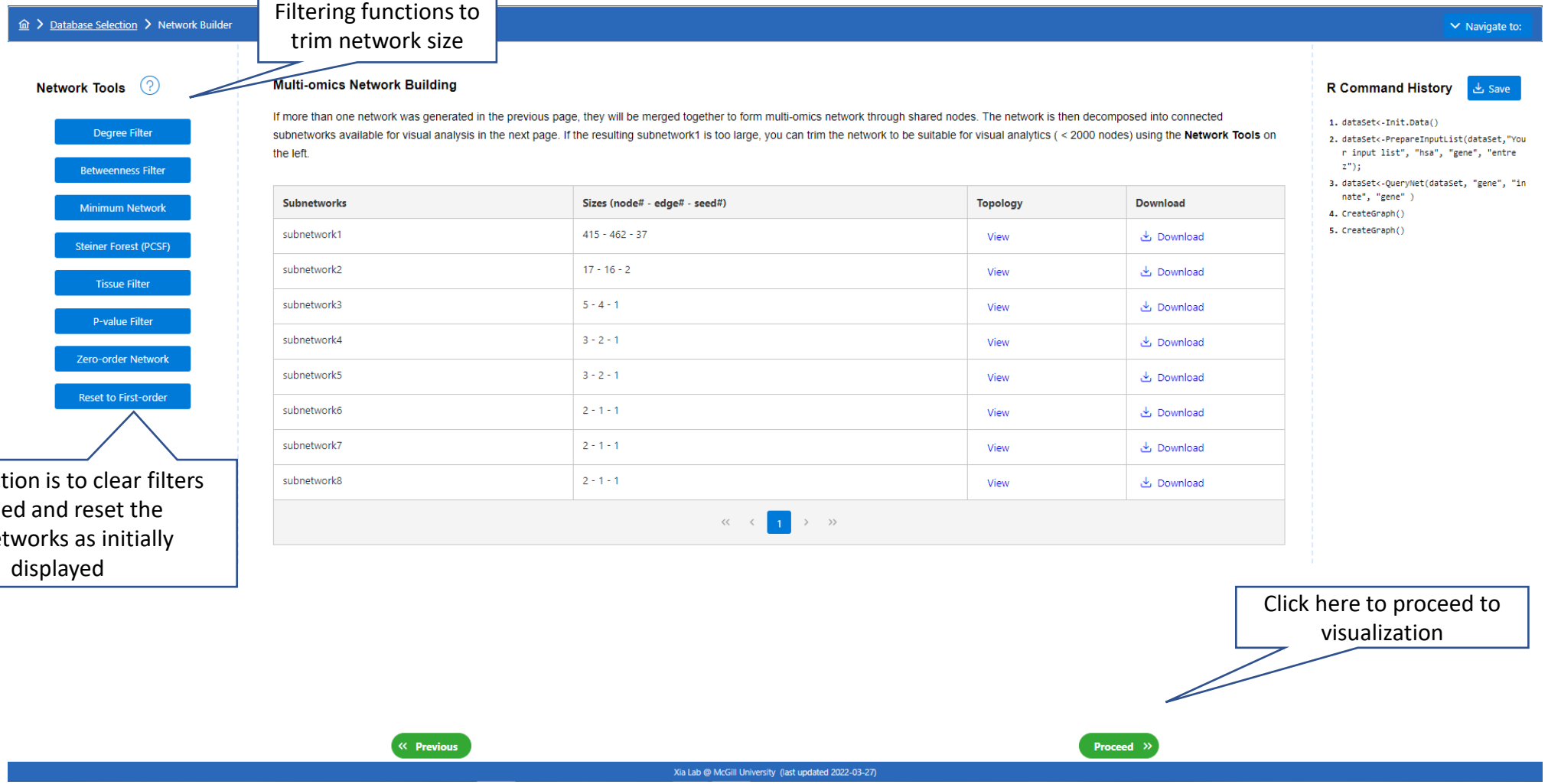


Browse View

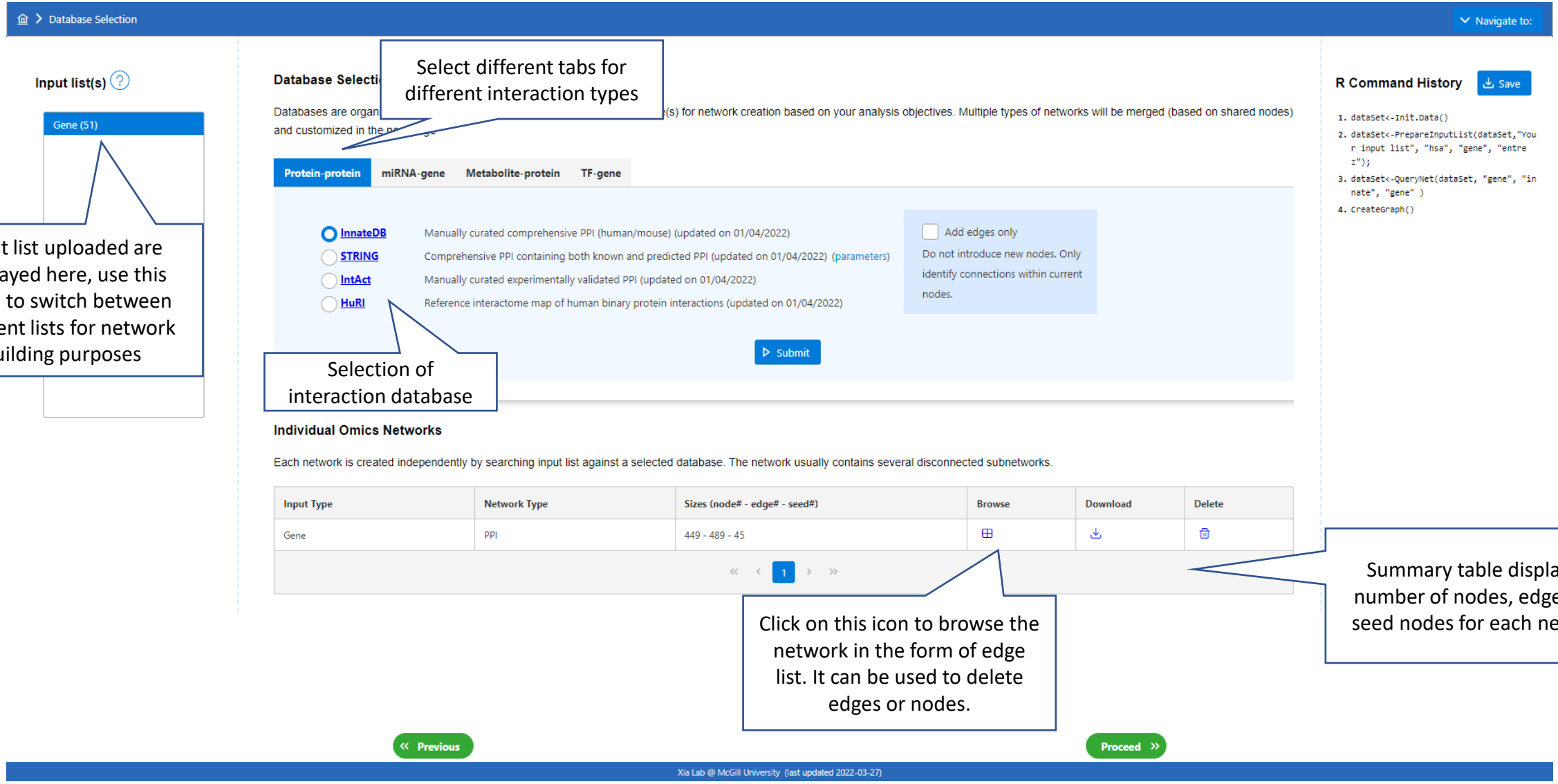

Use this function to delete multiple edges at once using different filtering options on selected columns
Database Selection
Interaction Table
Navigate to:
Individual Network Interaction Table
You can browse, search or manual delete an interaction (edge), or use the Advanced Filter to exclude a node (and its all associated edges).
Advanced Filter
Id1
Id2
Name1
Name2
Action
100289462 4316 DEFB4A MMP7 Delete
10068 1051 IL18BP CEBPB Delete
10068 27178 IL18BP IL37 Delete
10068 3606 IL18BP IL18 Delete
101060478 1471 RNF115 CST3 Delete
117156 8685 SCGB3A2 MARCO Delete
1230 6346 CCR1 CCL1 Delete
1233 6367 CCR4 CCL22 Delete
1236 6363 CCR7 CCL19 Delete
1236 6367 CCR7 CCL22 Delete
1237 6346 CCR8 CCL1 Delete
1462 1404 VCAN HAPLN1 Delete
1462 2199 VCAN FBLN2 Delete
1462 2200 VCAN FBN1 Delete
1462 2833 VCAN CXCR3 Delete
(1 of 33)
1 2 3 4 5 6 7 8 9 10
15
Previous
Proceed
Xia Lab @ McGill University (last updated 2022-03-27)

Network Builder

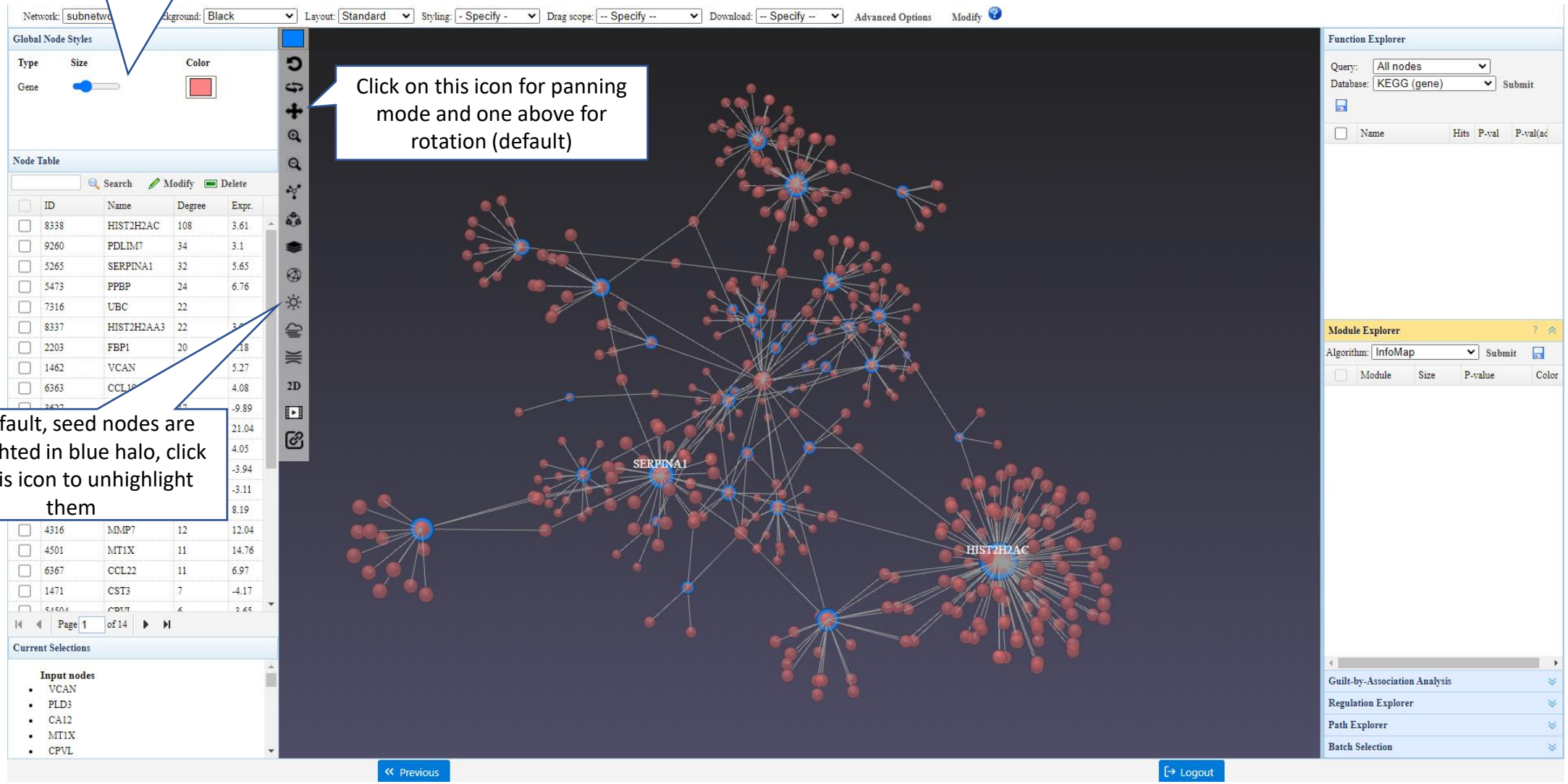
In this page, network created from last page is decomposed into connected subnetworks which will be used for visual analysis on the next page



Network Builder



Network Viewer



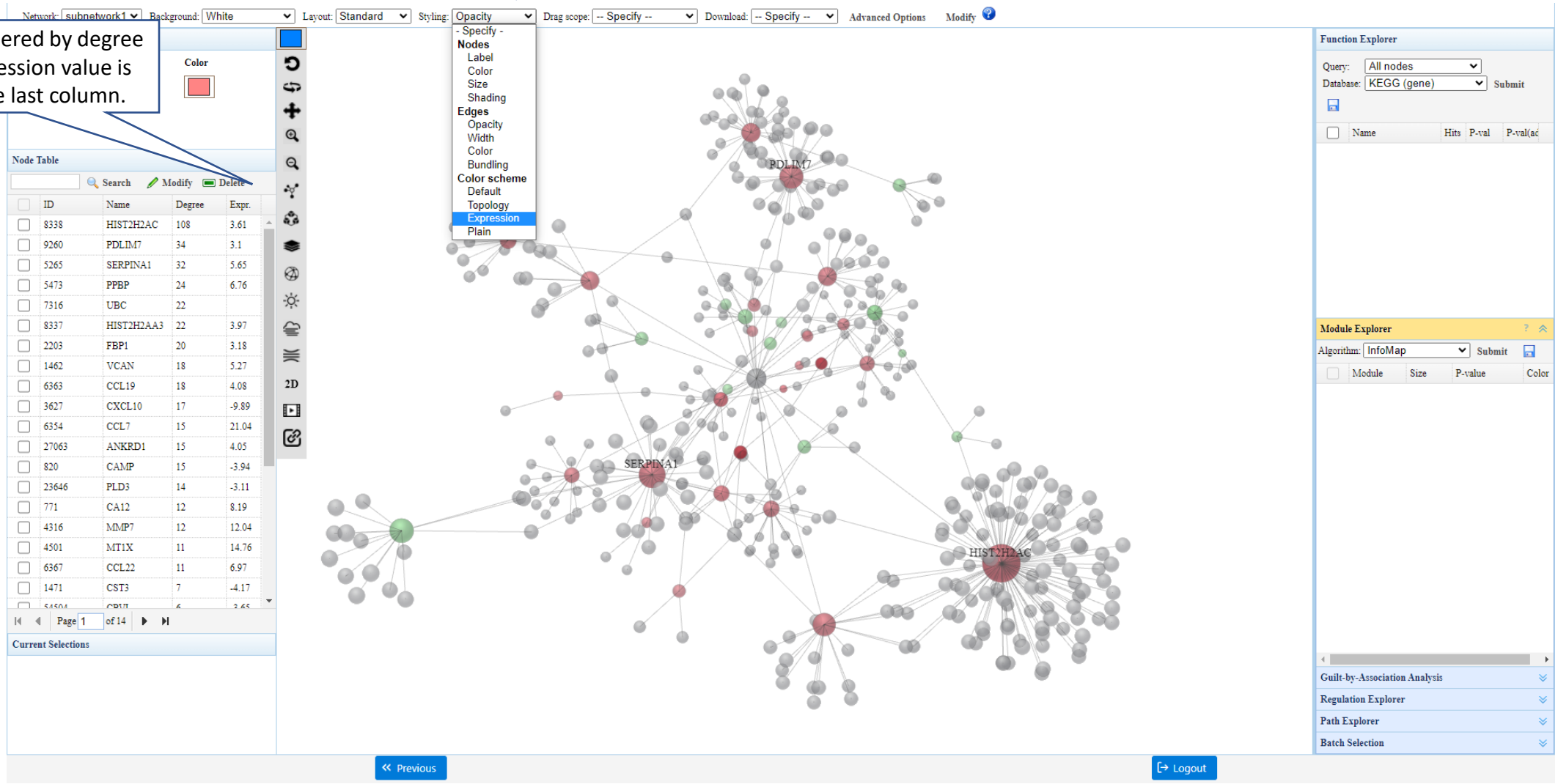
- Navigation: Camera rotation, panning, zooming, drag-n-drop

Color nodes based on expression values

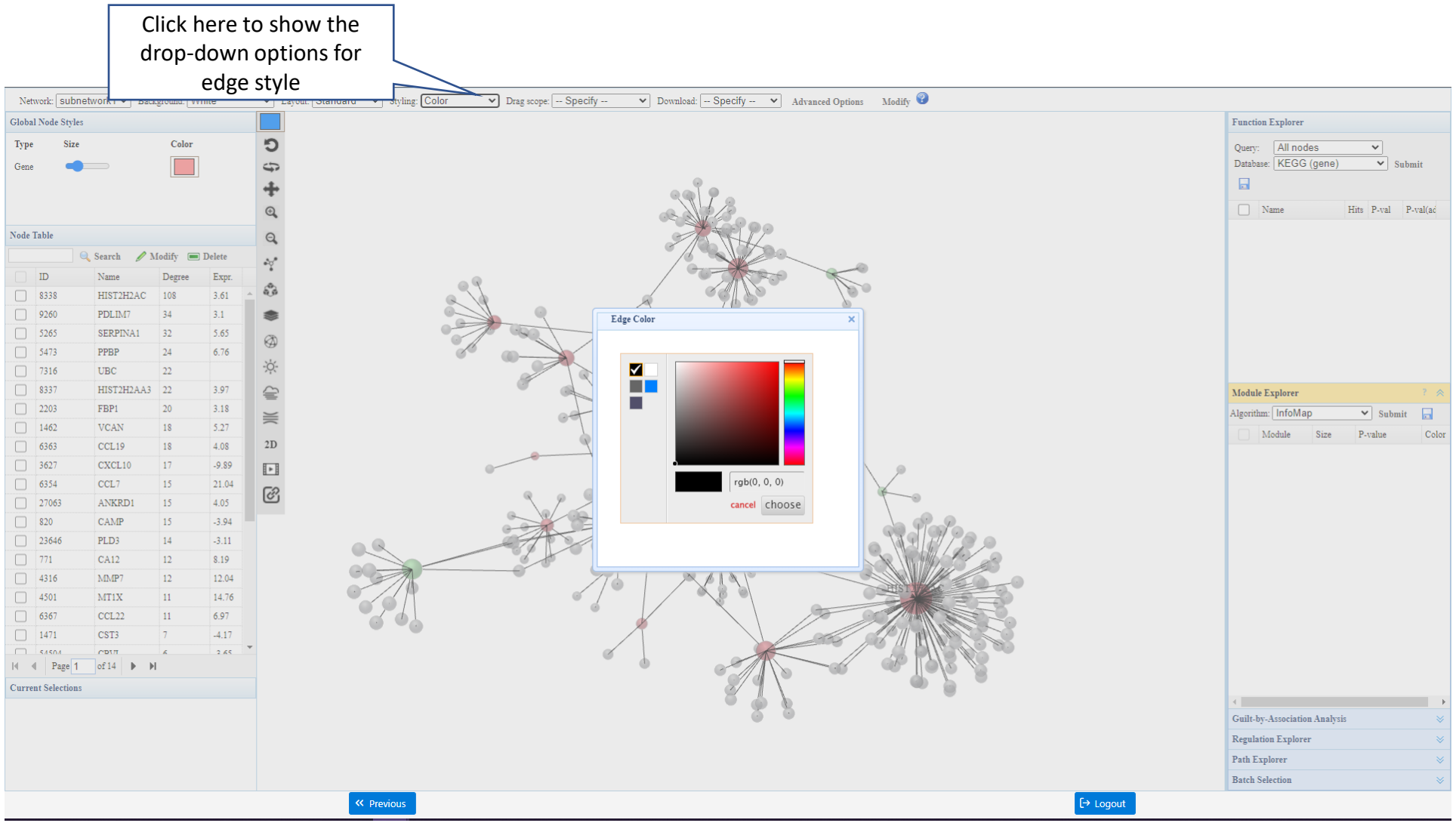
Open this drop-down menu to change background color

This dropdown menu has many features for customizing nodes/edges

Node table ordered by degree number. Expression value is shown on the last column.

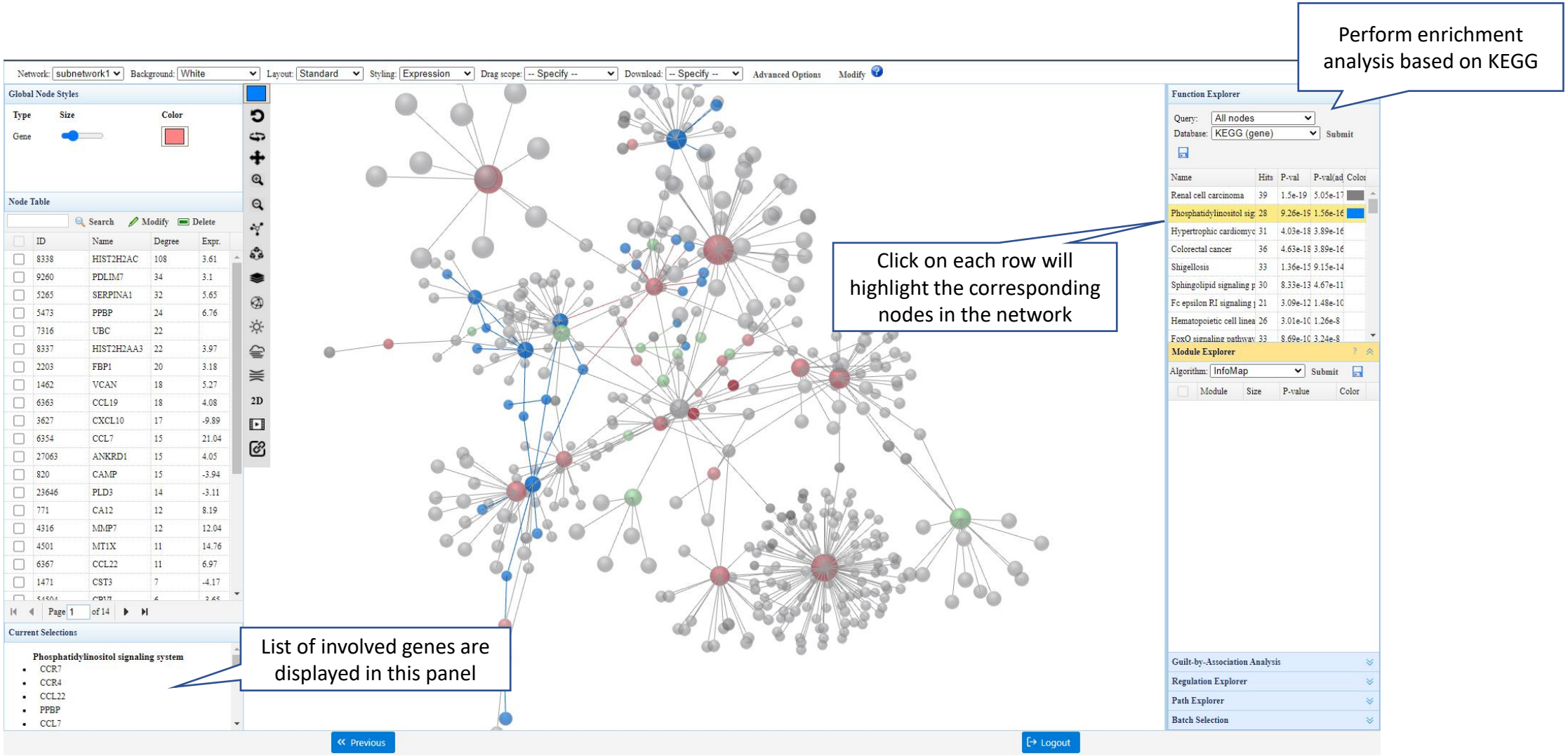


Change edge coloring and opacity

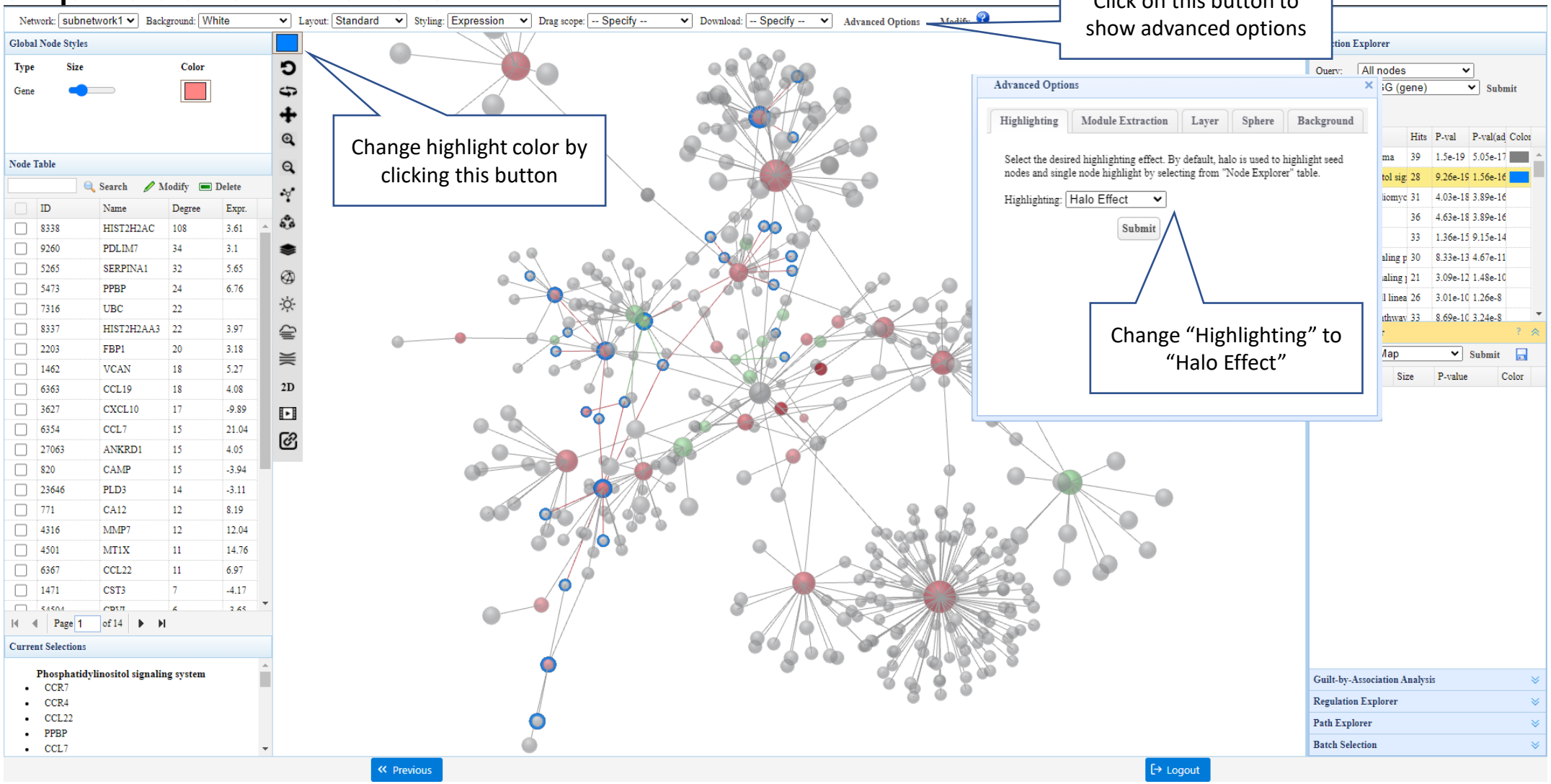


- Reducing edge opacity improves visualization of dense networks

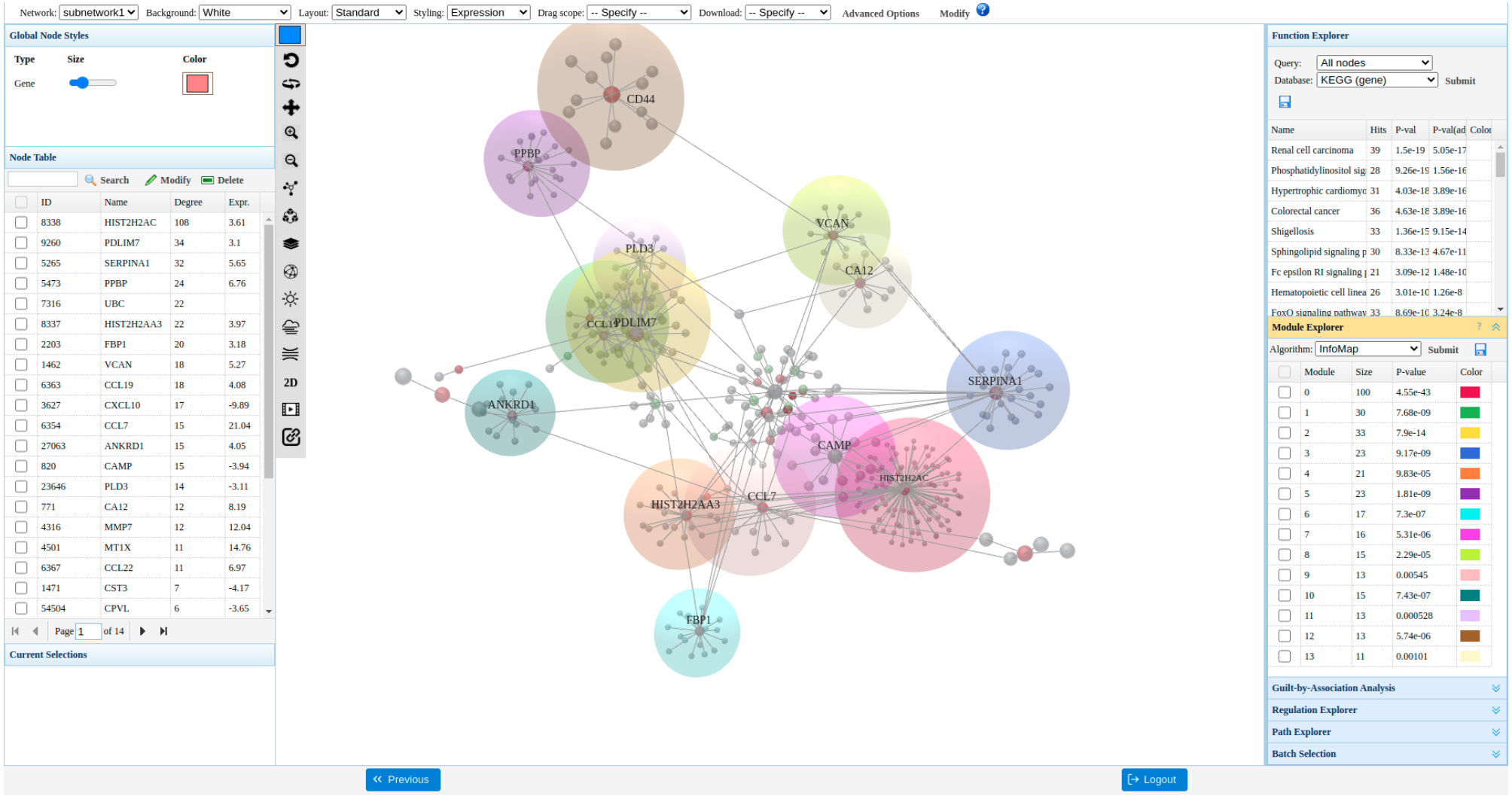
Enrichment analysis identifies involved pathways



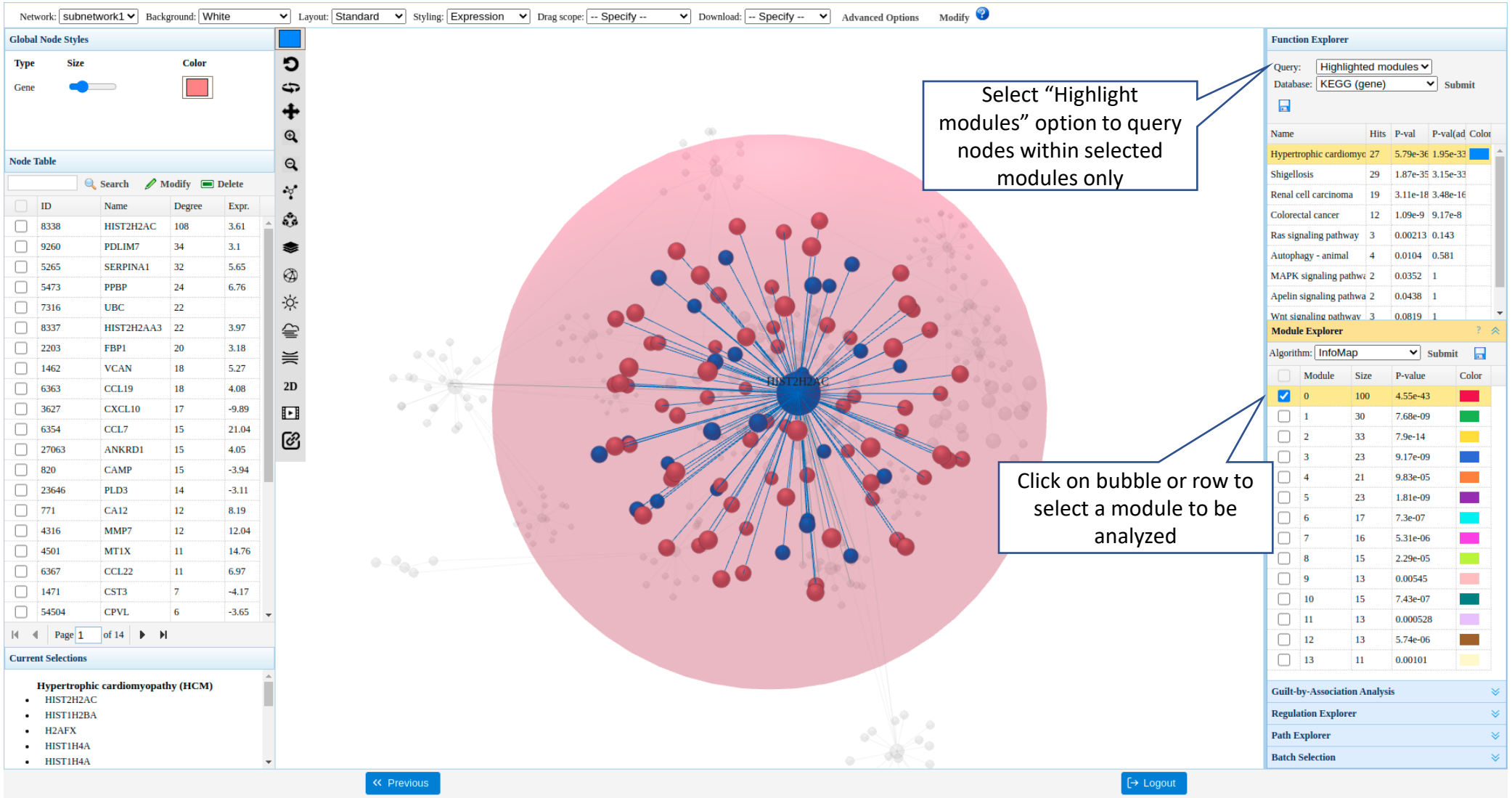
Highlighting using halo effect does not mask coloring by expression value



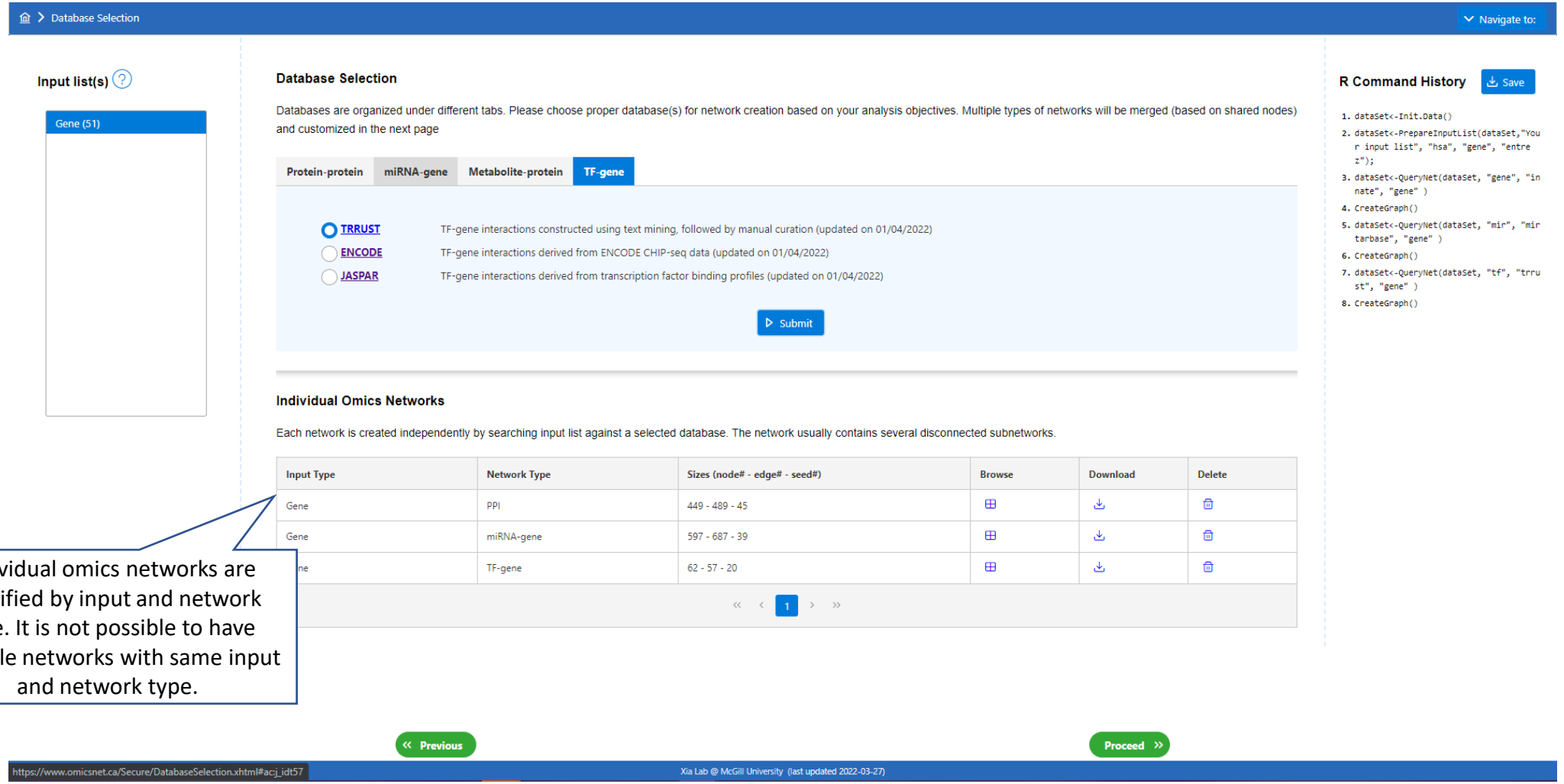
Module-based layout reveals graph communities within the network



Module-wise analysis

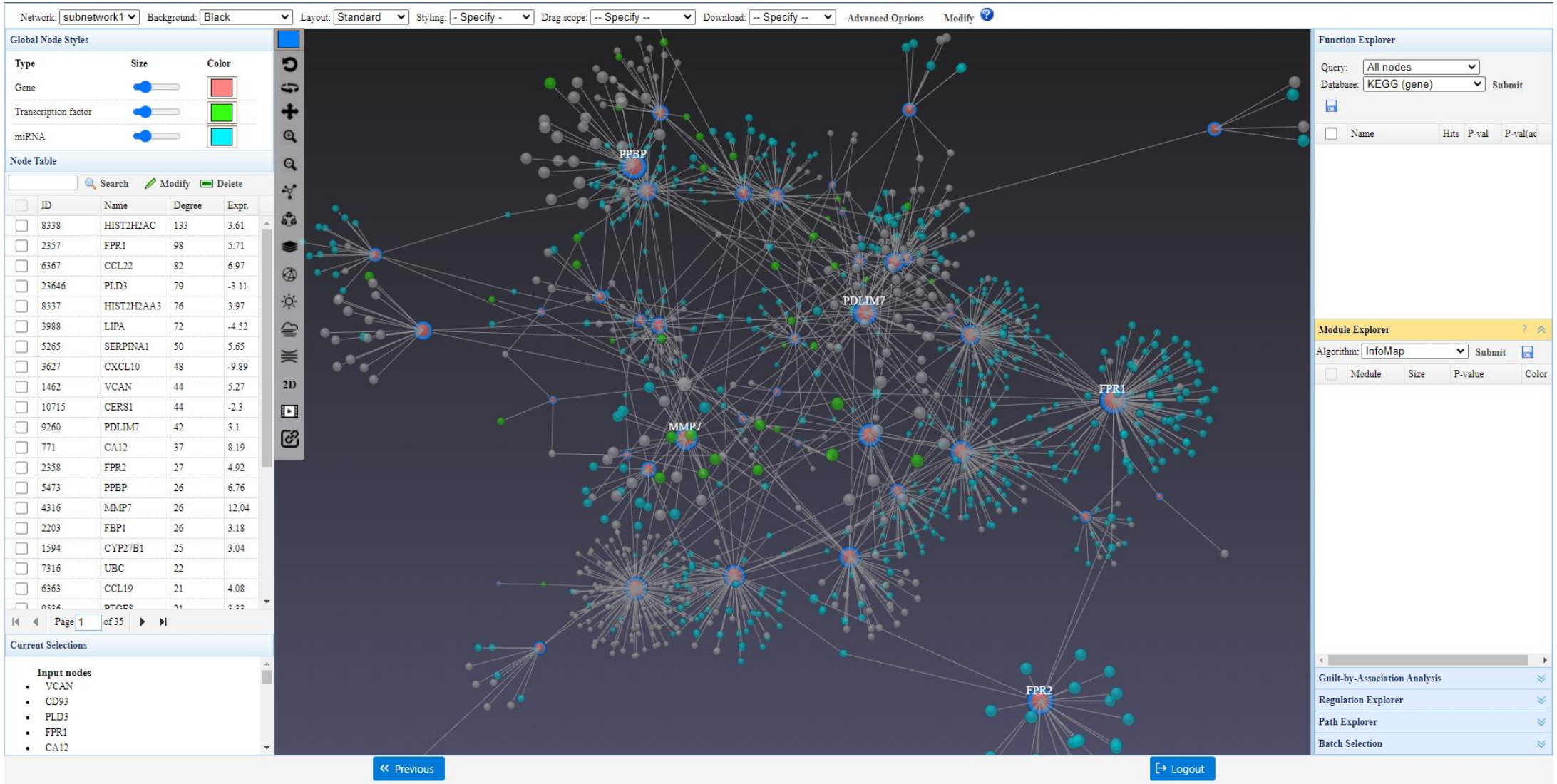


Explore gene regulation

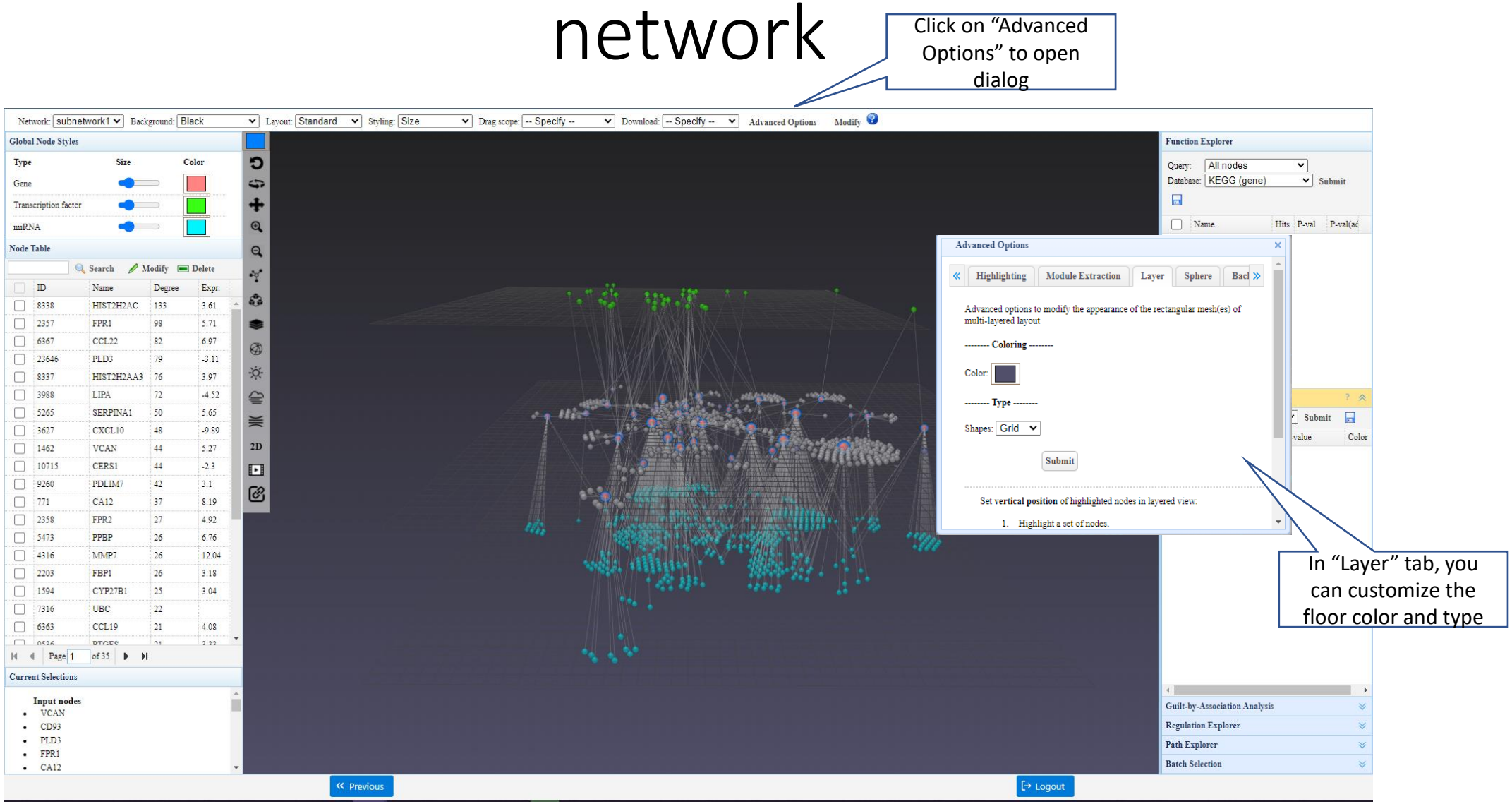


- Go back on **Database Selection** page and add miRNA-gene and TF-gene. Use different tabs for

Composite network

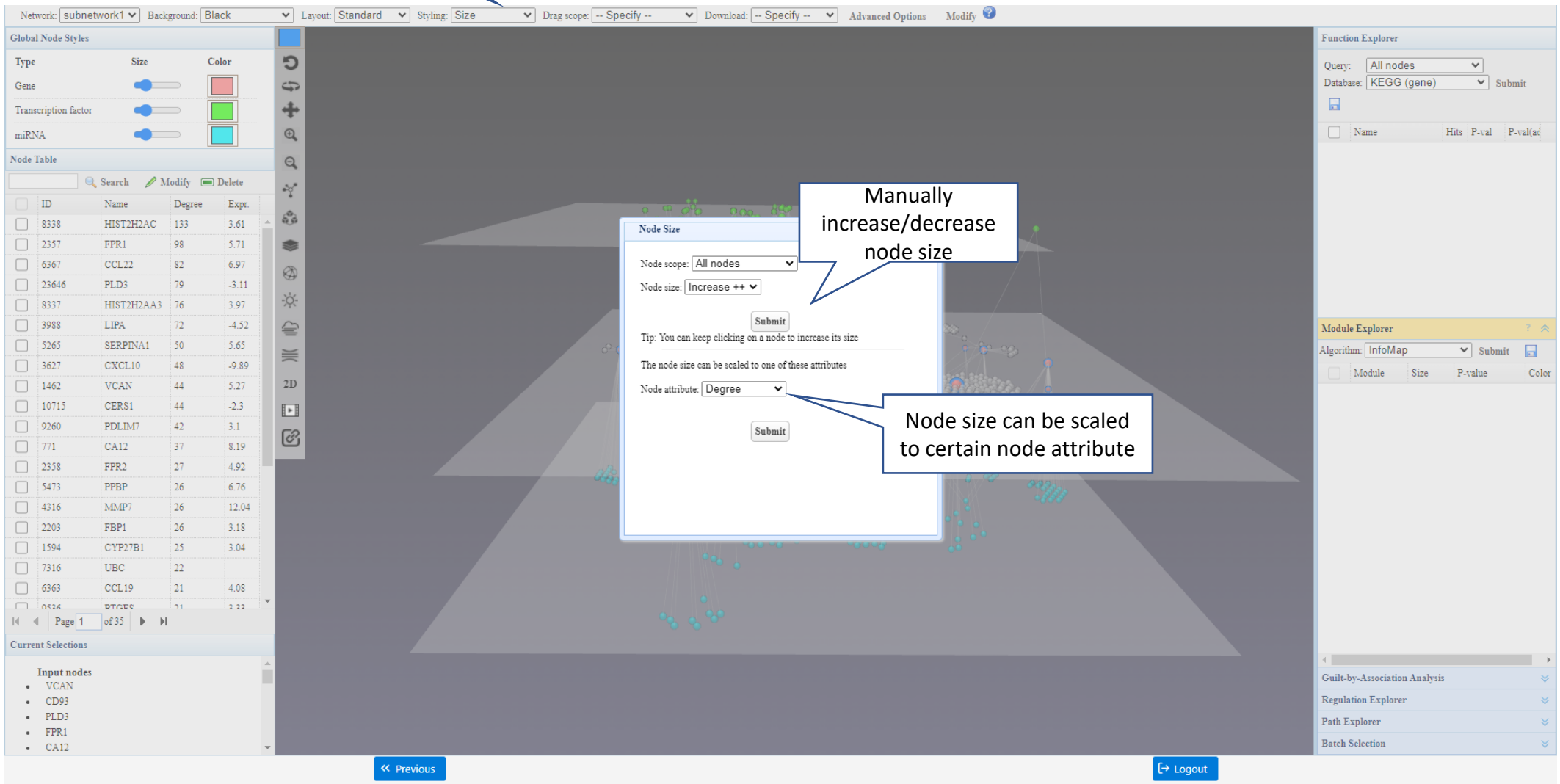


2D perspective layered layout for composite network

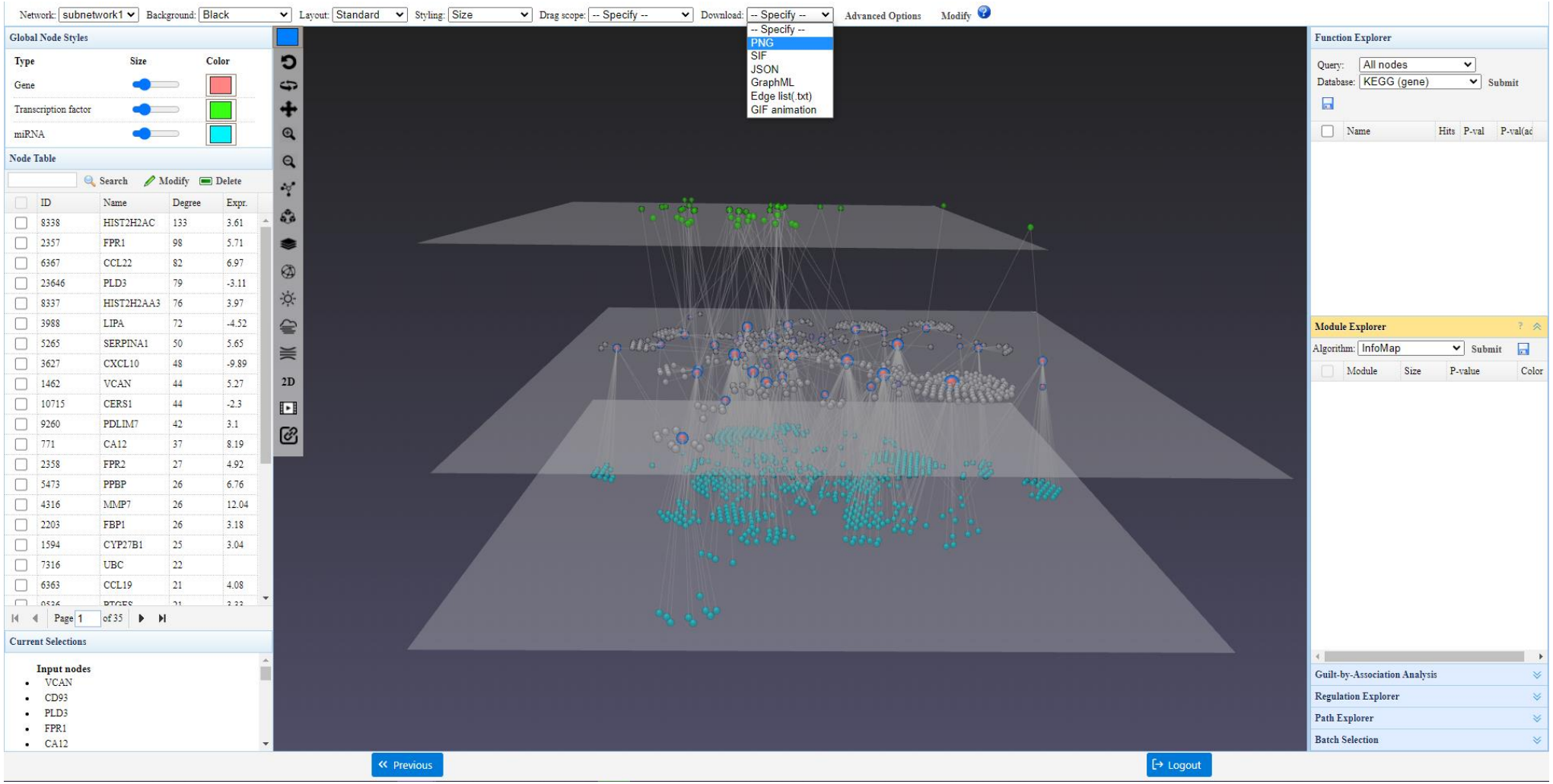


Change node size

Select Node size option to open dialog

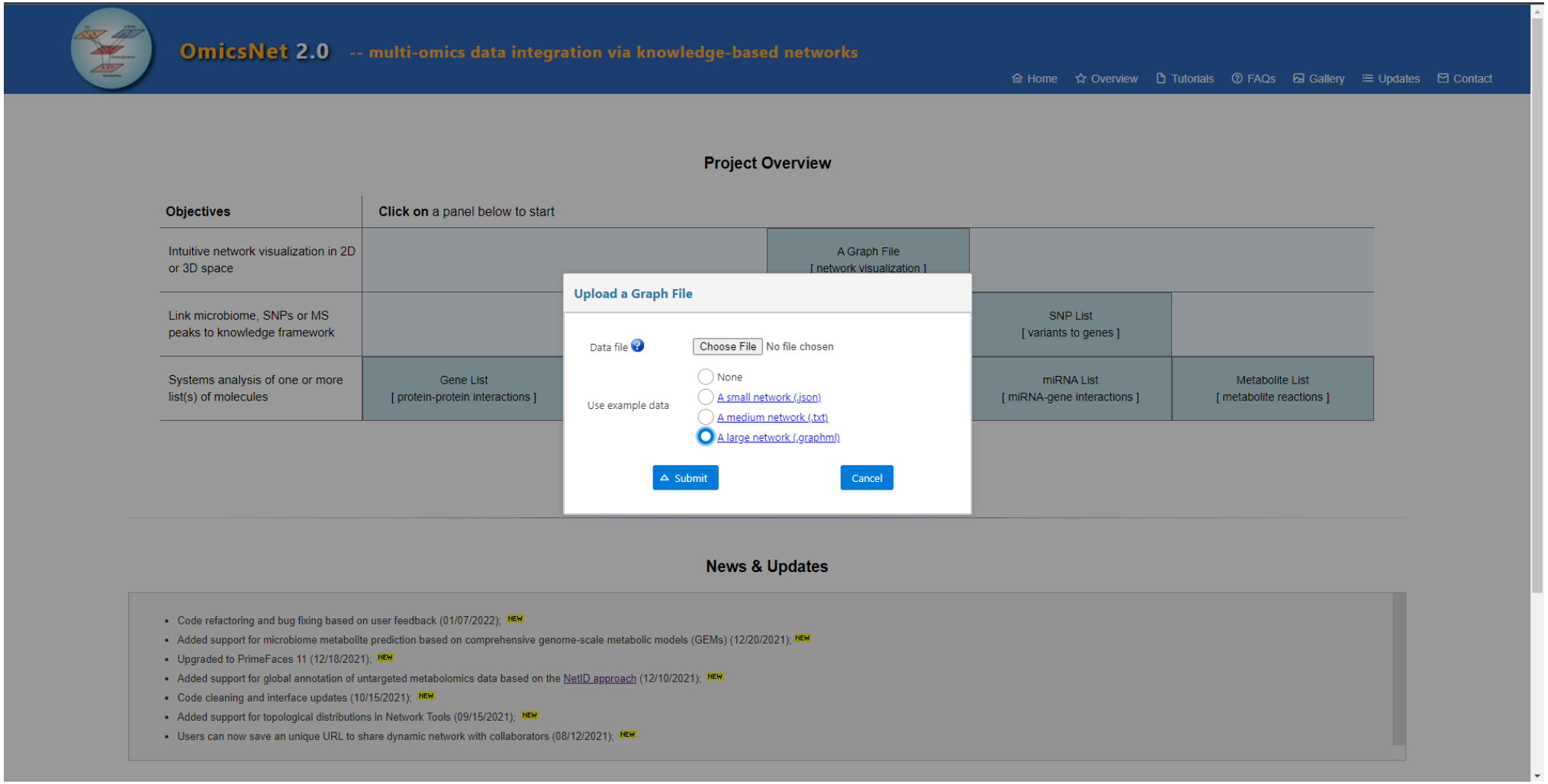


Export current network

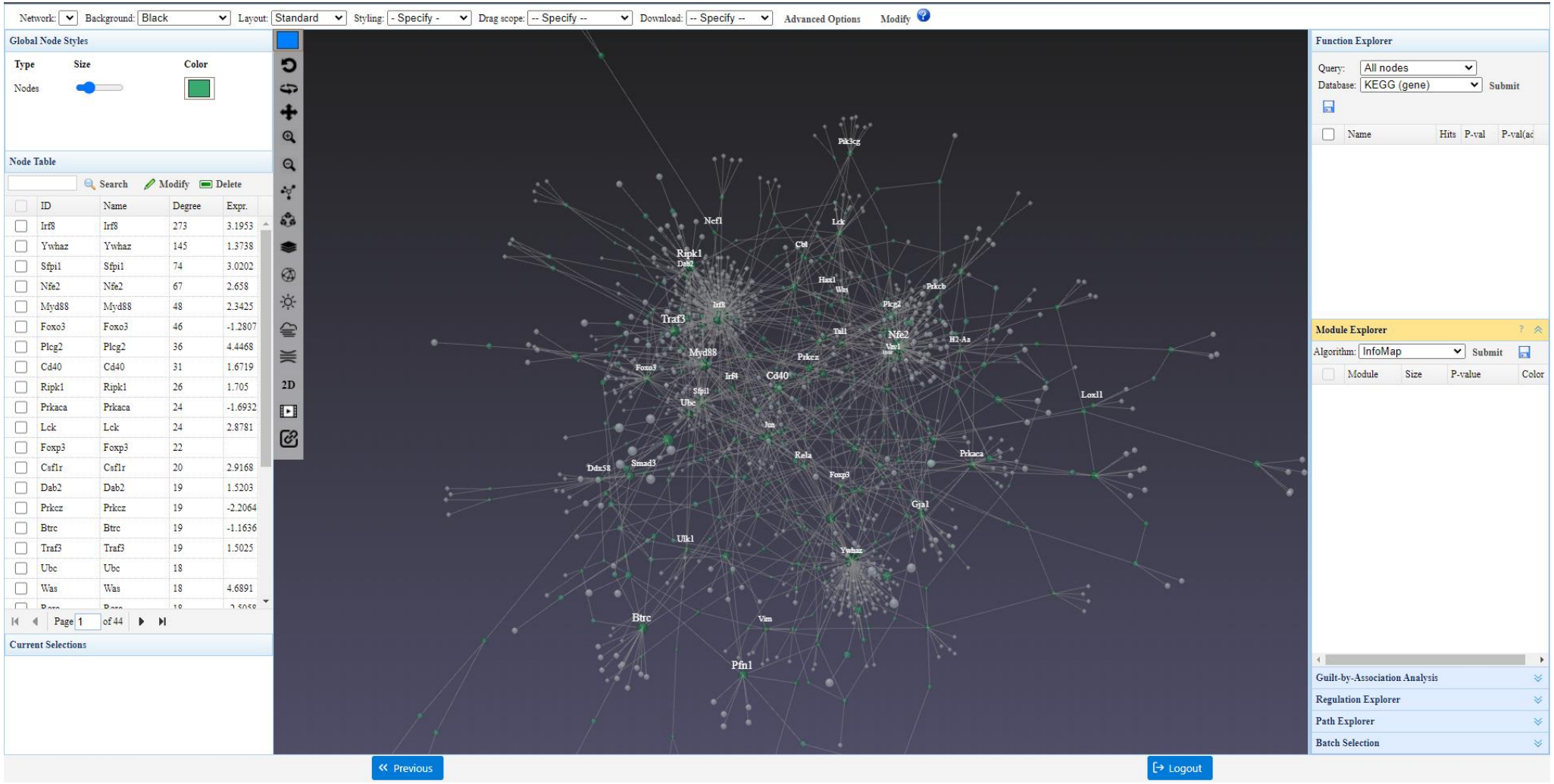


- You can choose to export an image (PNG) or network file (.SIF format, edge list in (.txt) and .graphml)

Load network using network file

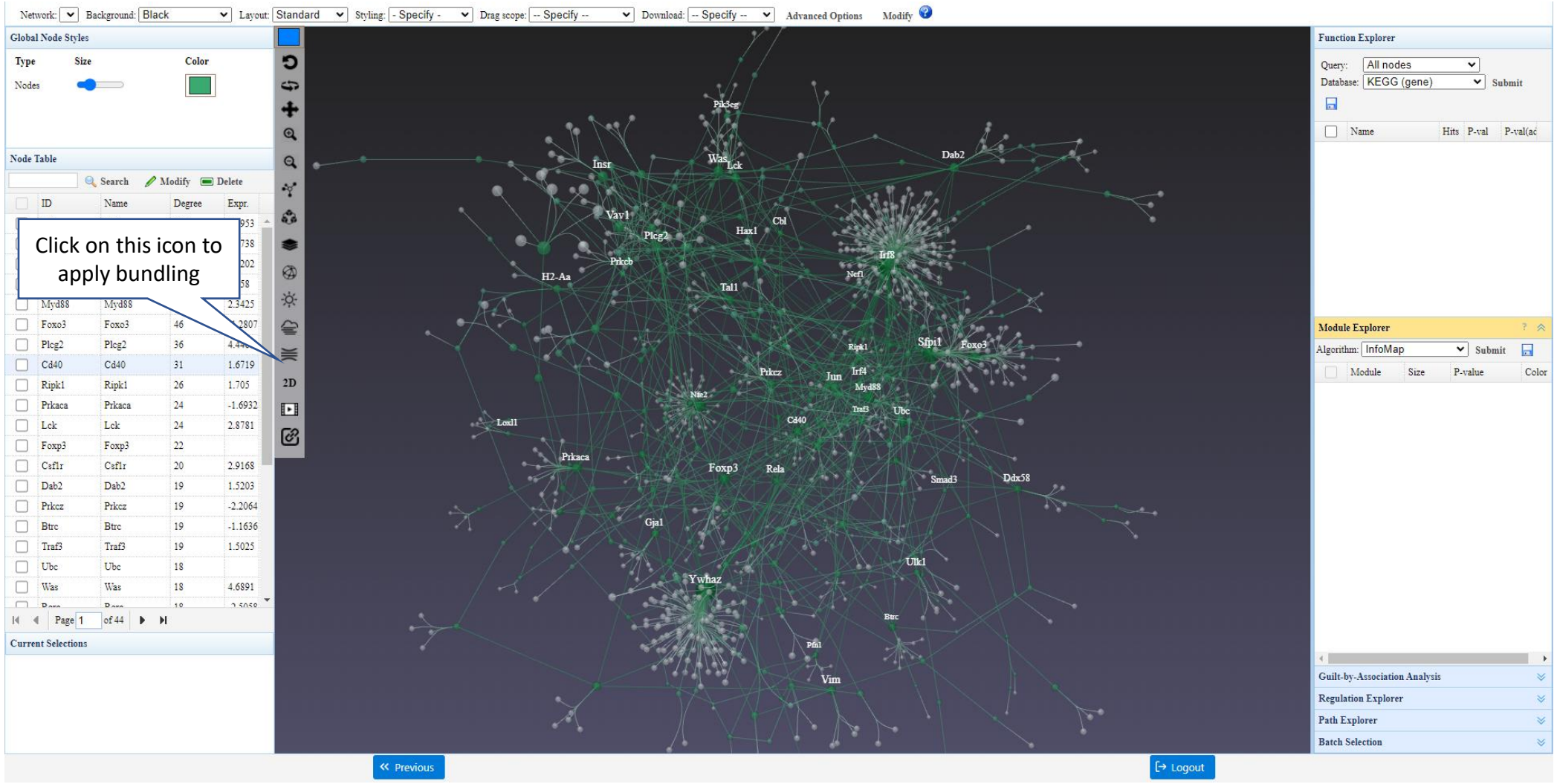


Network from graph file



- The coloring of nodes is based on node degrees
- The functional explorer and module explorer are deactivated

Edge bundling helps reducing visual occlusion



The End