



OmicNet Tutorial: Basic Network Exploration and Manipulation

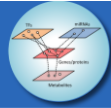
Computer Requirement

- 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

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Multi-omics Integration via Biological Networks

Objective	Click on a panel below to start				
Explore networks in 2D or 3D space			A Graph File		
Annotate SNPs, taxa, or LC-MS peaks for network analysis		SNPs	Microbial Taxa	LC-MS Peaks	
Network analysis of one or more list(s) of molecules	Genes	Proteins	Transcription Factors	miRNAs	Metabolites

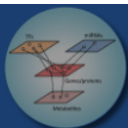
▶ Proceed

↺ Reset

Click here

News & Updates

- Added support to allow users to browse, search and manually remove edges or nodes from individual omics networks (04/01/2022); **NEW**
- Added support for adding only edges when using PPI databases (03/25/2022); **NEW**
- Added R command history for more reproducible analysis (03/17/2022); **NEW**
- Added support for tissue-based filtering to improve network accuracy (03/15/2022); **NEW**
- Fixed a bug for network file upload based on user feedback (03/01/2022); **NEW**
- Improved interface for network building (02/15/2022); **NEW**
- Updated tutorials for MS peak and taxon list inputs (01/21/2022);
- Improved SNP-gene mapping functions for better performance (01/18/2022);



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	<div style="display: flex; justify-content: space-around;"><div style="border: 1px solid gray; padding: 5px; width: 150px; text-align: center;">Genes</div><div style="border: 1px solid gray; padding: 5px; width: 150px; text-align: center;">LC-MS Peaks</div><div style="border: 1px solid gray; padding: 5px; width: 150px; text-align: center;">miRNAs</div><div style="border: 1px solid gray; padding: 5px; width: 150px; text-align: center;">Metabolites</div></div>

Use our example data for testing purposes

Upload a list of genes

Enter your data below: ?

Specify organism:

Set ID type:

#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

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- Improved SNP-gene mapping functions for better performance (01/18/2022);

Database selection

Database Selection

Input list(s) ?

Gene (51)

Select different tabs for different interaction types

Database Selection

Databases are organized into categories (Protein-protein, miRNA-gene, Metabolite-protein, TF-gene) for network creation based on your analysis objectives. Multiple types of networks will be merged (based on shared nodes) and customized in the network.

Protein-protein miRNA-gene Metabolite-protein TF-gene

InnateDB Manually curated comprehensive PPI (human/mouse) (updated on 01/04/2022)

STRING Comprehensive PPI containing both known and predicted PPI (updated on 01/04/2022) ([parameters](#))

IntAct Manually curated experimentally validated PPI (updated on 01/04/2022)

HuRI Reference interactome map of human binary protein interactions (updated on 01/04/2022)

Add edges only
Do not introduce new nodes. Only identify connections within current nodes.

Submit

Individual Omics Networks

Each network is created independently by searching input list against a selected database. The network usually contains several disconnected subnetworks.

Input Type	Network Type	Sizes (node# - edge# - seed#)	Browse	Download	Delete
Gene	PPI	449 - 489 - 45			

Summary table displaying number of nodes, edges and seed nodes for each network

Click on this icon to browse the network in the form of edge list. It can be used to delete edges or nodes.

Previous Proceed

Input list uploaded are displayed here, use this panel to switch between different lists for network building purposes

Selection of interaction database

Click on this icon to browse the network in the form of edge list. It can be used to delete edges or nodes.

Summary table displaying number of nodes, edges and seed nodes for each network

Browse View

Use this function to delete multiple edges at once using different filtering options on selected columns

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 >>

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

Home > Database Selection > Network Builder

Filtering functions to trim network size

Network Tools ?

- Degree Filter
- Betweenness Filter
- Minimum Network
- Steiner Forest (PCSF)
- Tissue Filter
- P-value Filter
- Zero-order Network
- Reset to First-order

Multi-omics Network Building

If more than one network was generated in the previous page, they will be merged together to form multi-omics network through shared nodes. The network is then decomposed into connected subnetworks available for visual analysis in the next page. If the resulting subnetwork1 is too large, you can trim the network to be suitable for visual analytics (< 2000 nodes) using the **Network Tools** on the left.

Subnetworks	Sizes (node# - edge# - seed#)	Topology	Download
subnetwork1	415 - 462 - 37	View	Download
subnetwork2	17 - 16 - 2	View	Download
subnetwork3	5 - 4 - 1	View	Download
subnetwork4	3 - 2 - 1	View	Download
subnetwork5	3 - 2 - 1	View	Download
subnetwork6	2 - 1 - 1	View	Download
subnetwork7	2 - 1 - 1	View	Download
subnetwork8	2 - 1 - 1	View	Download

Navigation: << < 1 > >>

R Command History [Save](#)

```
1. dataSet<-Init.Data()
2. dataSet<-PrepareInputList(dataSet,"Your input list", "hsa", "gene", "entrez");
3. dataSet<-QueryNet(dataSet, "gene", "in nate", "gene")
4. CreateGraph()
5. CreateGraph()
```

Navigation: << Previous Proceed >>

Xia Lab @ McGill University (last updated 2022-03-27)

This function is to clear filters applied and reset the subnetworks as initially displayed

Click here to proceed to visualization

Network Builder

Database Selection Navigate to:

Input list(s) ?

Gene (51)

Input list uploaded are displayed here, use this panel to switch between different lists for network building purposes

Database Selection

Select different tabs for different interaction types

Databases are organized into categories (s) for network creation based on your analysis objectives. Multiple types of networks will be merged (based on shared nodes) and customized in the network.

Protein-proteinmiRNA-geneMetabolite-proteinTF-gene

- InnateDB** Manually curated comprehensive PPI (human/mouse) (updated on 01/04/2022)
- STRING** Comprehensive PPI containing both known and predicted PPI (updated on 01/04/2022) ([parameters](#))
- IntAct** Manually curated experimentally validated PPI (updated on 01/04/2022)
- HuRI** Reference interactome map of human binary protein interactions (updated on 01/04/2022)

Add edges only
Do not introduce new nodes. Only identify connections within current nodes.

▶ Submit

R Command History Save

1. dataSet<-Init.Data()
2. dataSet<-PrepareInputList(dataSet,"Your input list", "hsa", "gene", "entrez");
3. dataSet<-QueryNet(dataSet, "gene", "innate", "gene")
4. CreateGraph()

Individual Omics Networks

Each network is created independently by searching input list against a selected database. The network usually contains several disconnected subnetworks.

Input Type	Network Type	Sizes (node# - edge# - seed#)	Browse	Download	Delete
Gene	PPI	449 - 489 - 45			

<< < 1 > >>

Summary table displaying number of nodes, edges and seed nodes for each network

Click on this icon to browse the network in the form of edge list. It can be used to delete edges or nodes.

<< PreviousProceed >>

Network Viewer

Change node color and size based on molecule type

Click on this icon for panning mode and one above for rotation (default)

By default, seed nodes are highlighted in blue halo, click on this icon to unhighlight them

The screenshot displays the Network Viewer interface. At the top, there are navigation and styling options: Network: subnetwork, Background: Black, Layout: Standard, Styling: - Specify -, Drag scope: -- Specify --, Download: -- Specify --, Advanced Options, and Modify. The main area shows a network graph with nodes of varying sizes and colors (red and blue) connected by edges. Two nodes are labeled: SERPINA1 and HIST2H2AC. On the left, the 'Global Node Styles' panel allows adjusting node size and color. Below it is the 'Node Table' with columns for ID, Name, Degree, and Expr. The 'Current Selections' panel lists input nodes: VCAN, PLD3, CA12, MT1X, and CPVL. On the right, the 'Function Explorer' and 'Module Explorer' panels provide additional analysis tools. A toolbar on the left contains icons for navigation and styling.

ID	Name	Degree	Expr.	
<input type="checkbox"/>	8338	HIST2H2AC	108	3.61
<input type="checkbox"/>	9260	PDLIM7	34	3.1
<input type="checkbox"/>	5265	SERPINA1	32	5.65
<input type="checkbox"/>	5473	PPBP	24	6.76
<input type="checkbox"/>	7316	UBC	22	
<input type="checkbox"/>	8337	HIST2H2AA3	22	3.4
<input type="checkbox"/>	2203	FBP1	20	1.18
<input type="checkbox"/>	1462	VCAN		5.27
<input type="checkbox"/>	6363	CCL12		4.08
<input type="checkbox"/>	2637			-9.89
<input type="checkbox"/>				21.04
<input type="checkbox"/>				4.05
<input type="checkbox"/>				-3.94
<input type="checkbox"/>				-3.11
<input type="checkbox"/>				8.19
<input type="checkbox"/>	4316	MMP7	12	12.04
<input type="checkbox"/>	4501	MT1X	11	14.76
<input type="checkbox"/>	6367	CCL22	11	6.97
<input type="checkbox"/>	1471	CST3	7	-4.17
<input type="checkbox"/>	84504	CPVL	6	2.65

- 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.

The screenshot displays a network visualization software interface. At the top, there are several dropdown menus for configuration: Network (subnetwork1), Background (White), Layout (Standard), Styling (Opacity), Drag scope (-- Specify --), and Download (-- Specify --). A toolbar on the left contains various icons for navigation and manipulation. A central network graph shows nodes of varying sizes and colors (red, green, grey) connected by edges. A 'Node Table' on the left lists nodes with columns for ID, Name, Degree, and Expr. A 'Function Explorer' and 'Module Explorer' are on the right. A 'Color' palette is visible above the node table. A 'Styling' dropdown menu is open, showing options for Nodes (Label, Color, Size, Shading) and Edges (Opacity, Width, Color, Bundling, Color scheme, Topology).

ID	Name	Degree	Expr.
8338	HIST2H2AC	108	3.61
9260	PDLIM7	34	3.1
5265	SERPINA1	32	5.65
5473	PPBP	24	6.76
7316	UBC	22	
8337	HIST2H2AA3	22	3.97
2203	FBP1	20	3.18
1462	VCAN	18	5.27
6363	CCL19	18	4.08
3627	CXCL10	17	-9.89
6354	CCL7	15	21.04
27063	ANKRD1	15	4.05
820	CAMP	15	-3.94
23646	PLD3	14	-3.11
771	CA12	12	8.19
4316	MMP7	12	12.04
4501	MT1X	11	14.76
6367	CCL22	11	6.97
1471	CST3	7	-4.17

Change edge coloring and opacity

Click here to show the drop-down options for edge style

The screenshot displays a network visualization software interface. The main window shows a network graph with nodes and edges. A dialog box titled "Edge Color" is open, showing a color selection interface with a color wheel and a color bar. The current color is black, with the RGB value "rgb(0, 0, 0)" displayed. The dialog box has "cancel" and "choose" buttons. The interface includes a "Global Node Styles" panel on the left, a "Node Table" with a list of nodes, and a "Function Explorer" and "Module Explorer" on the right. The "Node Table" contains the following data:

ID	Name	Degree	Expr.	
<input type="checkbox"/>	8338	HIST2H2AC	108	3.61
<input type="checkbox"/>	9260	PDLM7	34	3.1
<input type="checkbox"/>	5265	SERPINA1	32	5.65
<input type="checkbox"/>	5473	PPBP	24	6.76
<input type="checkbox"/>	7316	UBC	22	
<input type="checkbox"/>	8337	HIST2H2AA3	22	3.97
<input type="checkbox"/>	2203	FBP1	20	3.18
<input type="checkbox"/>	1462	VCAN	18	5.27
<input type="checkbox"/>	6363	CCL19	18	4.08
<input type="checkbox"/>	3627	CXCL10	17	-9.89
<input type="checkbox"/>	6354	CCL7	15	21.04
<input type="checkbox"/>	27063	ANKRD1	15	4.05
<input type="checkbox"/>	820	CAMP	15	-3.94
<input type="checkbox"/>	23646	PLD3	14	-3.11
<input type="checkbox"/>	771	CA12	12	8.19
<input type="checkbox"/>	4316	MMP7	12	12.04
<input type="checkbox"/>	4501	MTIX	11	14.76
<input type="checkbox"/>	6367	CCL22	11	6.97
<input type="checkbox"/>	1471	CST3	7	-4.17
<input type="checkbox"/>	84504	CD137	6	2.65

- Reducing edge opacity improves visualization of dense networks

Enrichment analysis identifies involved pathways

The screenshot displays a network visualization software interface. The central part of the screen shows a complex network graph with nodes of various sizes and colors (red, blue, green, grey) connected by edges. The interface includes several panels:

- Global Node Styles:** Controls for Type, Size, and Color.
- Node Table:** A table listing nodes with columns for ID, Name, Degree, and Expr. The table is currently on Page 1 of 14.
- Function Explorer:** A panel for performing enrichment analysis. It shows a query for 'All nodes' in the 'KEGG (gene)' database. The results table is as follows:

Name	Hits	P-val	P-val(ad)	Color
Renal cell carcinoma	39	1.5e-19	5.05e-17	
Phosphatidylinositol sig	28	9.26e-15	1.56e-16	
Hypertrophic cardiomyo	31	4.03e-18	3.89e-16	
Colorectal cancer	36	4.63e-18	3.89e-16	
Shigellosis	33	1.36e-15	9.15e-14	
Sphingolipid signaling p	30	8.33e-13	4.67e-11	
Fc epsilon RI signaling	21	3.09e-12	1.48e-10	
Hematopoietic cell linea	26	3.01e-10	1.26e-8	
FoxO signaling pathwa	33	8.69e-10	3.24e-8	
- Module Explorer:** A panel for exploring modules, currently showing the 'Phosphatidylinositol signaling system' module.

Annotations on the image provide additional context:

- A callout box at the top right states: "Perform enrichment analysis based on KEGG".
- A callout box pointing to the Function Explorer table states: "Click on each row will highlight the corresponding nodes in the network".
- A callout box pointing to the Current Selections panel states: "List of involved genes are displayed in this panel".

Navigation buttons for "Previous" and "Logout" are visible at the bottom of the interface.

Highlighting using halo effect does not mask coloring by expression value

Click on this button to show advanced options

Change highlight color by clicking this button

Change "Highlighting" to "Halo Effect"

Network: subnetwork1 Background: White Layout: Standard Styling: Expression Drag scope: -- Specify -- Download: -- Specify -- Advanced Options

Global Node Styles

Type	Size	Color
Gene	<input type="range"/>	<input type="color"/>

Node Table

ID	Name	Degree	Expr.
<input type="checkbox"/>	8338 HIST2H2AC	108	3.61
<input type="checkbox"/>	9260 PDLIM7	34	3.1
<input type="checkbox"/>	5265 SERPINA1	32	5.65
<input type="checkbox"/>	5473 PPBP	24	6.76
<input type="checkbox"/>	7316 UBC	22	
<input type="checkbox"/>	8337 HIST2H2AA3	22	3.97
<input type="checkbox"/>	2203 FBP1	20	3.18
<input type="checkbox"/>	1462 VCAN	18	5.27
<input type="checkbox"/>	6363 CCL19	18	4.08
<input type="checkbox"/>	3627 CXCL10	17	-9.89
<input type="checkbox"/>	6354 CCL7	15	21.04
<input type="checkbox"/>	27063 ANKRD1	15	4.05
<input type="checkbox"/>	820 CAMP	15	-3.94
<input type="checkbox"/>	23646 PLD3	14	-3.11
<input type="checkbox"/>	771 CA12	12	8.19
<input type="checkbox"/>	4316 MMP7	12	12.04
<input type="checkbox"/>	4501 MT1X	11	14.76
<input type="checkbox"/>	6367 CCL22	11	6.97
<input type="checkbox"/>	1471 CST3	7	-4.17

Advanced Options

Highlighting: Halo Effect

Submit

Node Explorer

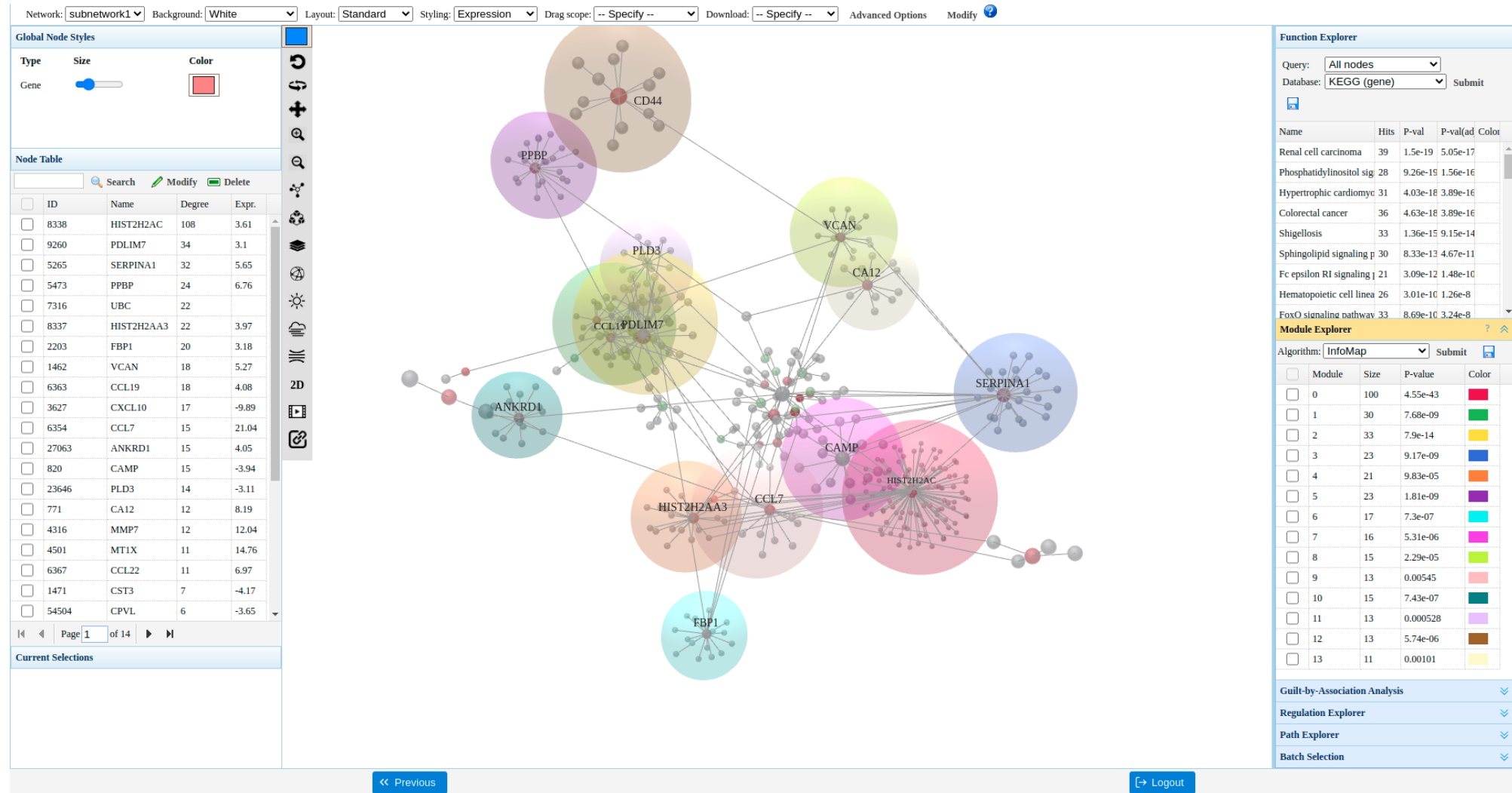
	Hits	P-val	P-val(ad)	Color
ma	39	1.5e-19	5.05e-17	
tol sig	28	9.26e-15	1.56e-16	
biomyc	31	4.03e-18	3.89e-16	
	36	4.63e-18	3.89e-16	
	33	1.36e-15	9.15e-14	
aling p	30	8.33e-13	4.67e-11	
aling p	21	3.09e-12	1.48e-10	
l linea	26	3.01e-10	1.26e-8	
thrvav	33	8.69e-10	3.24e-8	

Current Selections

- Phosphatidylinositol signaling system
 - CCR7
 - CCR4
 - CCL22
 - PPBP
 - CCL7

Navigation: << Previous Logout >>

Module-based layout reveals graph communities within the network



Module-wise analysis

The screenshot displays a network analysis software interface. At the top, there are settings for Network (subnetwork1), Background (White), Layout (Standard), Styling (Expression), Drag scope (-- Specify --), and Download (-- Specify --). The main area shows a network graph with a central node labeled HIST2H2AC, surrounded by other nodes connected by edges. A large pink bubble highlights a significant cluster of nodes.

On the left, the **Global Node Styles** panel allows adjusting the size and color of nodes. Below it is the **Node Table** with columns for ID, Name, Degree, and Expr. The table lists various genes and their properties.

On the right, the **Function Explorer** panel shows a query for highlighted modules in the KEGG (gene) database. Below it is the **Module Explorer** panel, which displays a table of modules with columns for Module, Size, P-value, and Color. Module 0 is selected.

At the bottom left, the **Current Selections** panel shows the selected module: **Hypertrophic cardiomyopathy (HCM)**, listing associated genes: HIST2H2AC, HIST1H2BA, H2AFX, HIST1H4A, and HIST1H4A.

Two callout boxes provide instructions: "Select 'Highlight modules' option to query nodes within selected modules only" and "Click on bubble or row to select a module to be analyzed".

Name	Hits	P-val	P-val(ad)	Color
Hypertrophic cardiomyoc	27	5.79e-36	1.95e-33	Blue
Shigellosis	29	1.87e-35	3.15e-33	Green
Renal cell carcinoma	19	3.11e-18	3.48e-16	Yellow
Colorectal cancer	12	1.09e-9	9.17e-8	Blue
Ras signaling pathway	3	0.00213	0.143	Orange
Autophagy - animal	4	0.0104	0.581	Purple
MAPK signaling pathwa	2	0.0352	1	Cyan
Apelin signaling pathwa	2	0.0438	1	Magenta
Wnt signalina pathway	3	0.0819	1	Light Green

Module	Size	P-value	Color
<input checked="" type="checkbox"/> 0	100	4.55e-43	Red
<input type="checkbox"/> 1	30	7.68e-09	Green
<input type="checkbox"/> 2	33	7.9e-14	Yellow
<input type="checkbox"/> 3	23	9.17e-09	Blue
<input type="checkbox"/> 4	21	9.83e-05	Orange
<input type="checkbox"/> 5	23	1.81e-09	Purple
<input type="checkbox"/> 6	17	7.3e-07	Cyan
<input type="checkbox"/> 7	16	5.31e-06	Magenta
<input type="checkbox"/> 8	15	2.29e-05	Light Green
<input type="checkbox"/> 9	13	0.00545	Pink
<input type="checkbox"/> 10	15	7.43e-07	Dark Green
<input type="checkbox"/> 11	13	0.000528	Purple
<input type="checkbox"/> 12	13	5.74e-06	Brown
<input type="checkbox"/> 13	11	0.00101	Yellow

Current Selections

Hypertrophic cardiomyopathy (HCM)

- HIST2H2AC
- HIST1H2BA
- H2AFX
- HIST1H4A
- HIST1H4A

Explore gene regulation

Database Selection

Input list(s) ?

Gene (51)

Database Selection

Databases are organized under different tabs. Please choose proper database(s) for network creation based on your analysis objectives. Multiple types of networks will be merged (based on shared nodes) and customized in the next page

Protein-protein miRNA-gene Metabolite-protein **TF-gene**

TRRUST TF-gene interactions constructed using text mining, followed by manual curation (updated on 01/04/2022)

ENCODE TF-gene interactions derived from ENCODE CHIP-seq data (updated on 01/04/2022)

JASPAR TF-gene interactions derived from transcription factor binding profiles (updated on 01/04/2022)

Submit

Individual Omics Networks

Each network is created independently by searching input list against a selected database. The network usually contains several disconnected subnetworks.

Input Type	Network Type	Sizes (node# - edge# - seed#)	Browse	Download	Delete
Gene	PPI	449 - 489 - 45	🏠	↓	🗑️
Gene	miRNA-gene	597 - 687 - 39	🏠	↓	🗑️
Gene	TF-gene	62 - 57 - 20	🏠	↓	🗑️

<< < 1 > >>

Command History Save

```
1. dataset<-Init.Data()
2. dataset<-PrepareInputList(dataset,"Your input list", "hsa", "gene", "entrez");
3. dataset<-QueryNet(dataset, "gene", "innate", "gene")
4. CreateGraph()
5. dataset<-QueryNet(dataset, "mir", "mirtarbase", "gene")
6. CreateGraph()
7. dataset<-QueryNet(dataset, "tf", "trrusted", "gene")
8. CreateGraph()
```

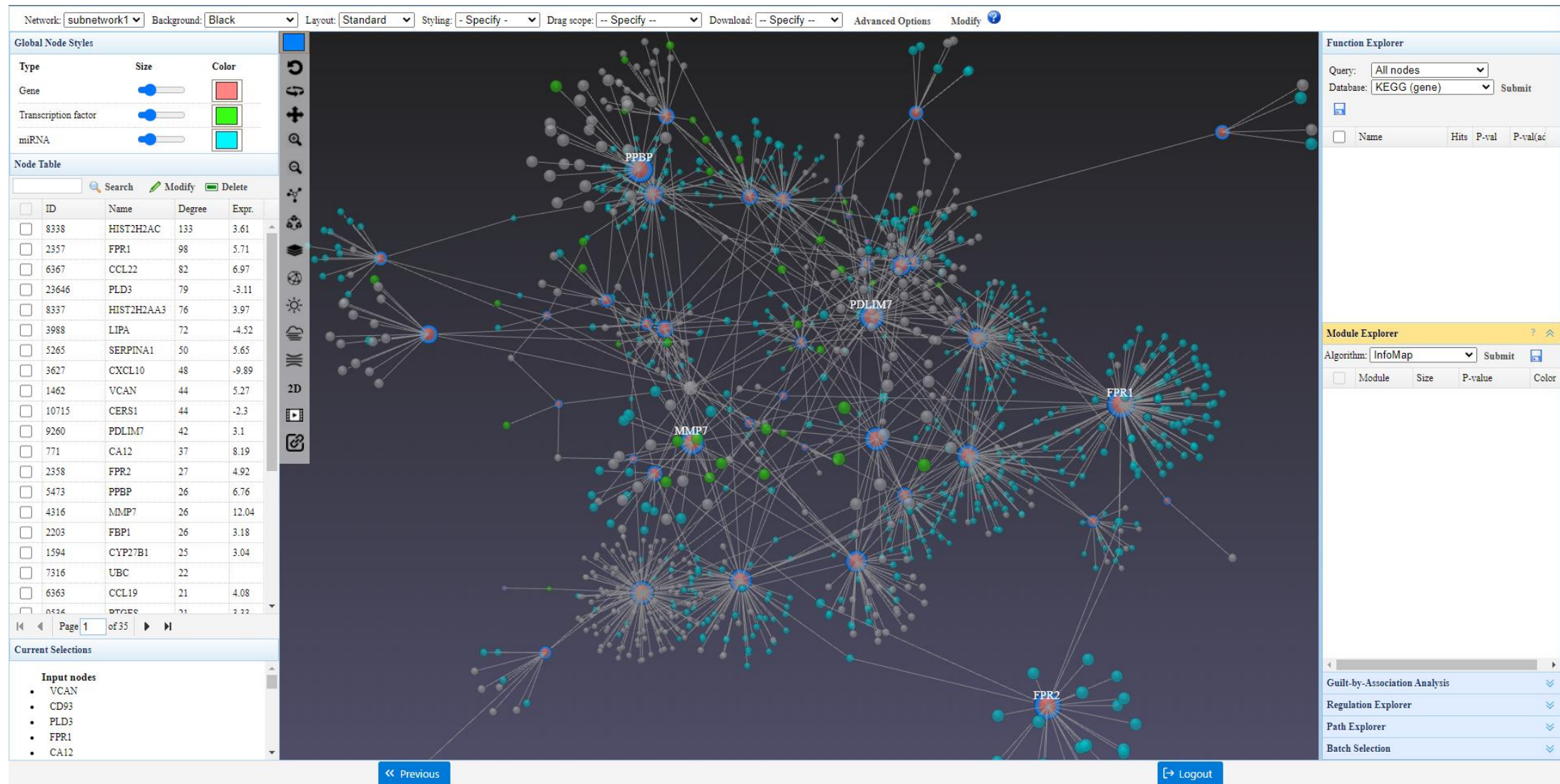
Individual omics networks are classified by input and network type. It is not possible to have multiple networks with same input and network type.

<< Previous Proceed >>

https://www.omicsnet.ca/Secure/DatabaseSelection.xhtml#acj_idt57 Xia Lab @ McGill University (last updated 2022-03-27)

- 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

Click on "Advanced Options" to open dialog

The screenshot displays a network visualization software interface. At the top, there are menu items: Network: subnetwork1, Background: Black, Layout: Standard, Styling: Size, Drag scope: -- Specify --, Download: -- Specify --, Advanced Options, and Modify. On the left, there is a 'Global Node Styles' panel with sliders for Type (Gene, Transcription factor, miRNA), Size, and Color. Below it is a 'Node Table' with columns for ID, Name, Degree, and Expr. The central area shows a 3D perspective layered layout of a network with nodes and edges. On the right, there is a 'Function Explorer' panel with a query input and a 'Submit' button. An 'Advanced Options' dialog box is open, showing tabs for Highlighting, Module Extraction, Layer, Sphere, and Back. The 'Layer' tab is selected, and it contains options for Coloring (Color: #000000), Type (Shapes: Grid), and a 'Submit' button. Below these options, there is a section for 'Set vertical position of highlighted nodes in layered view:' with a list of instructions.

ID	Name	Degree	Expr.
<input type="checkbox"/>	8338 HIST2H2AC	133	3.61
<input type="checkbox"/>	2357 FPR1	98	5.71
<input type="checkbox"/>	6367 CCL22	82	6.97
<input type="checkbox"/>	23646 PLD3	79	-3.11
<input type="checkbox"/>	8337 HIST2H2AA3	76	3.97
<input type="checkbox"/>	3988 LIPA	72	-4.52
<input type="checkbox"/>	5265 SERPINA1	50	5.65
<input type="checkbox"/>	3627 CXCL10	48	-9.89
<input type="checkbox"/>	1462 VCAN	44	5.27
<input type="checkbox"/>	10715 CERS1	44	-2.3
<input type="checkbox"/>	9260 PDLIM7	42	3.1
<input type="checkbox"/>	771 CA12	37	8.19
<input type="checkbox"/>	2358 FPR2	27	4.92
<input type="checkbox"/>	5473 PPBP	26	6.76
<input type="checkbox"/>	4316 MMP7	26	12.04
<input type="checkbox"/>	2203 FBP1	26	3.18
<input type="checkbox"/>	1594 CYP27B1	25	3.04
<input type="checkbox"/>	7316 UBC	22	
<input type="checkbox"/>	6363 CCL19	21	4.08
<input type="checkbox"/>	8334 PRKCE	21	2.32

Advanced Options

Advanced options to modify the appearance of the rectangular mesh(es) of multi-layered layout

----- Coloring -----

Color: #000000

----- Type -----

Shapes: Grid

Submit

Set vertical position of highlighted nodes in layered view:

1. Highlight a set of nodes.

Current Selections

- Input nodes
 - VCAN
 - CD93
 - PLD3
 - FPR1
 - CA12

In "Layer" tab, you can customize the floor color and type

Change node size

Select Node size option to open dialog

Network: subnetwork1 Background: Black Layout: Standard Styling: Size Drag scope: -- Specify -- Download: -- Specify -- Advanced Options Modify

Global Node Styles

Type	Size	Color
Gene	<input type="range"/>	<input type="color" value="#f08080"/>
Transcription factor	<input type="range"/>	<input type="color" value="#00ff00"/>
miRNA	<input type="range"/>	<input type="color" value="#00ffff"/>

Node Table

ID	Name	Degree	Expr.
<input type="checkbox"/>	8338 HIST2H2AC	133	3.61
<input type="checkbox"/>	2357 FPR1	98	5.71
<input type="checkbox"/>	6367 CCL22	82	6.97
<input type="checkbox"/>	23646 PLD3	79	-3.11
<input type="checkbox"/>	8337 HIST2H2AA3	76	3.97
<input type="checkbox"/>	3988 LIPA	72	-4.52
<input type="checkbox"/>	5265 SERPINA1	50	5.65
<input type="checkbox"/>	3627 CXCL10	48	-9.89
<input type="checkbox"/>	1462 VCAN	44	5.27
<input type="checkbox"/>	10715 CERS1	44	-2.3
<input type="checkbox"/>	9260 PDLIM7	42	3.1
<input type="checkbox"/>	771 CA12	37	8.19
<input type="checkbox"/>	2358 FPR2	27	4.92
<input type="checkbox"/>	5473 PPBP	26	6.76
<input type="checkbox"/>	4316 MMP7	26	12.04
<input type="checkbox"/>	2203 FBP1	26	3.18
<input type="checkbox"/>	1594 CYP27B1	25	3.04
<input type="checkbox"/>	7316 UBC	22	
<input type="checkbox"/>	6363 CCL19	21	4.08
<input type="checkbox"/>	6524 PTCE	21	2.22

Function Explorer

Query: All nodes Database: KEGG (gene) Submit

Name	Hits	P-val	P-val(ac)
------	------	-------	-----------

Module Explorer

Algorithm: InfoMap Submit

Module	Size	P-value	Color
--------	------	---------	-------

Current Selections

- Input nodes
 - VCAN
 - CD93
 - PLD3
 - FPR1
 - CA12

Node Size dialog:

Node scope: All nodes

Node size: Increase ++

Submit

Tip: You can keep clicking on a node to increase its size

The node size can be scaled to one of these attributes

Node attribute: Degree

Submit

Manually increase/decrease node size

Node size can be scaled to certain node attribute

Previous Logout

Export current network

The screenshot displays a network visualization software interface. The central area shows a 3D network graph with nodes and edges. The nodes are color-coded by type: red for genes, green for transcription factors, and cyan for miRNAs. The graph is viewed from a perspective that shows three horizontal planes. A 'Download' menu is open, showing options: PNG, SIF, JSON, GraphML, Edge list(.txt), and GIF animation. The 'Global Node Styles' panel on the left allows for adjusting the size and color of different node types. Below it is a 'Node Table' with columns for ID, Name, Degree, and Expr. The 'Current Selections' panel at the bottom left lists input nodes: VCAN, CD93, PLD3, FPR1, and CA12. On the right side, there are panels for 'Function Explorer' and 'Module Explorer'. The 'Function Explorer' has a query field set to 'All nodes' and a database dropdown set to 'KEGG (gene)'. The 'Module Explorer' has an algorithm dropdown set to 'InfoMap'. At the bottom of the interface, there are 'Previous' and 'Logout' buttons.

ID	Name	Degree	Expr.	
<input type="checkbox"/>	8338	HIST2H2AC	133	3.61
<input type="checkbox"/>	2357	FPR1	98	5.71
<input type="checkbox"/>	6367	CCL22	82	6.97
<input type="checkbox"/>	23646	PLD3	79	-3.11
<input type="checkbox"/>	8337	HIST2H2AA3	76	3.97
<input type="checkbox"/>	3988	LIPA	72	-4.52
<input type="checkbox"/>	5265	SERPINA1	50	5.65
<input type="checkbox"/>	3627	CXCL10	48	-9.89
<input type="checkbox"/>	1462	VCAN	44	5.27
<input type="checkbox"/>	10715	CERS1	44	-2.3
<input type="checkbox"/>	9260	PDLIM7	42	3.1
<input type="checkbox"/>	771	CA12	37	8.19
<input type="checkbox"/>	2358	FPR2	27	4.92
<input type="checkbox"/>	5473	PPBP	26	6.76
<input type="checkbox"/>	4316	MMP7	26	12.04
<input type="checkbox"/>	2203	FBP1	26	3.18
<input type="checkbox"/>	1594	CYP27B1	25	3.04
<input type="checkbox"/>	7316	UBC	22	
<input type="checkbox"/>	6363	CCL19	21	4.08
<input type="checkbox"/>	8526	PTEN	21	2.22

- Input nodes
 - VCAN
 - CD93
 - PLD3
 - FPR1
 - CA12

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

Load network using network file

OmicsNet 2.0 -- multi-omics data integration via knowledge-based networks

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Project Overview

Objectives Click on a panel below to start

Intuitive network visualization in 2D or 3D space		A Graph File [network visualization]	
Link microbiome, SNPs or MS peaks to knowledge framework			SNP List [variants to genes]
Systems analysis of one or more list(s) of molecules	Gene List [protein-protein interactions]		miRNA List [miRNA-gene interactions]
			Metabolite List [metabolite reactions]

Upload a Graph File

Data file No file chosen

Use example data

None

[A small network \(.json\)](#)

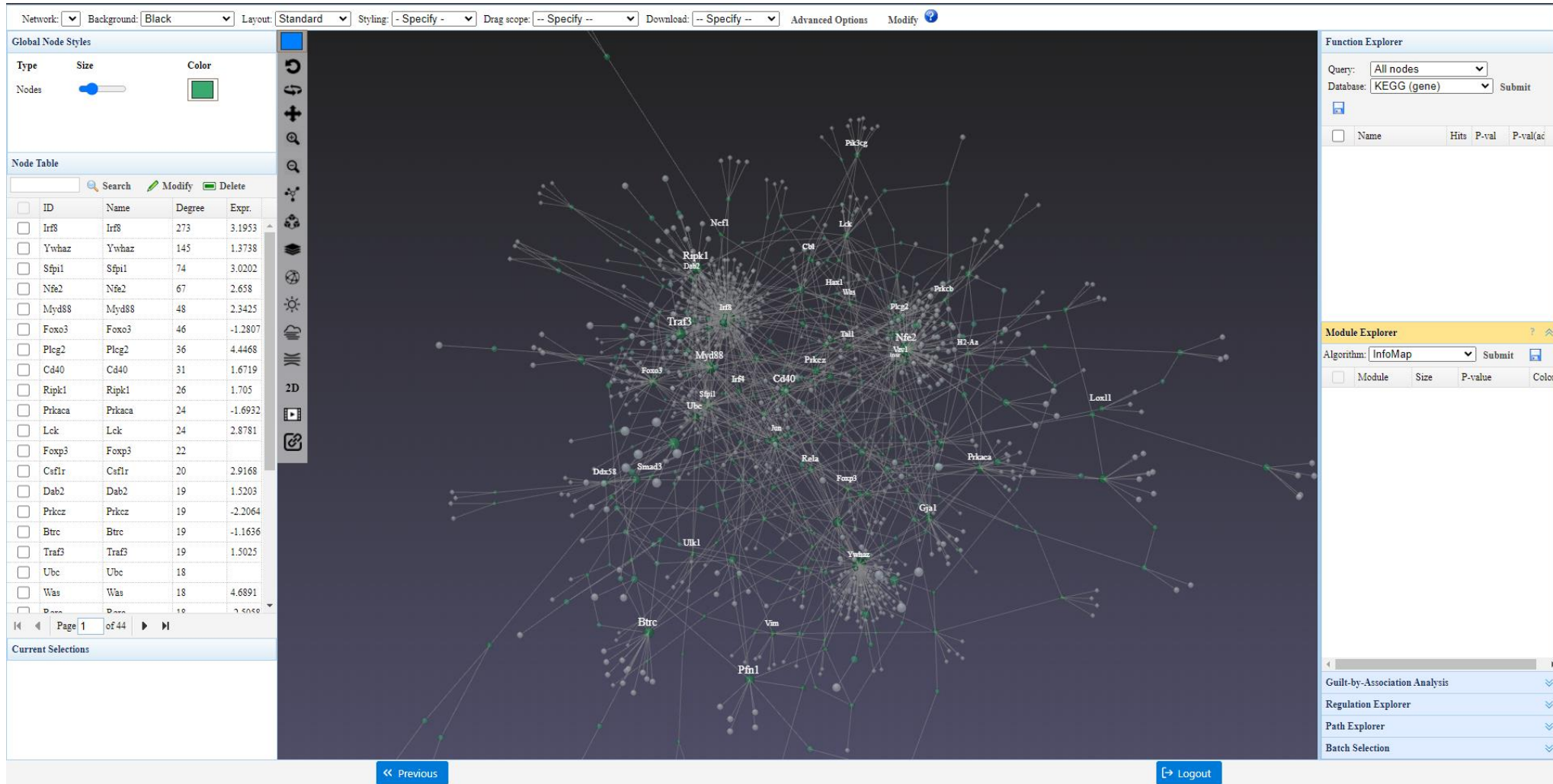
[A medium network \(.txt\)](#)

[A large network \(.graphml\)](#)

News & Updates

- Code refactoring and bug fixing based on user feedback (01/07/2022); **NEW**
- Added support for microbiome metabolite prediction based on comprehensive genome-scale metabolic models (GEMs) (12/20/2021); **NEW**
- Upgraded to PrimeFaces 11 (12/18/2021); **NEW**
- Added support for global annotation of untargeted metabolomics data based on the [NetID approach](#) (12/10/2021); **NEW**
- Code cleaning and interface updates (10/15/2021); **NEW**
- Added support for topological distributions in Network Tools (09/15/2021); **NEW**
- Users can now save an unique URL to share dynamic network with collaborators (08/12/2021); **NEW**

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 screenshot displays a network visualization software interface. The central area shows a dense network graph with nodes and edges. The edges are bundled, reducing visual occlusion. The interface includes several panels:

- Global Node Styles:** Controls for Type, Size, and Color.
- Node Table:** A table listing nodes with columns for ID, Name, Degree, and Expr. A callout box points to a bundling icon in the toolbar, stating "Click on this icon to apply bundling".
- Function Explorer:** A panel for querying the database (KEGG (gene)) and displaying results.
- Module Explorer:** A panel for exploring modules, with the InfoMap algorithm selected.

At the bottom, there are navigation buttons: "Previous" and "Logout".

ID	Name	Degree	Expr.
Myd88	Myd88	23425	2.3425
Foxo3	Foxo3	46	2.2807
Pleg2	Pleg2	36	4.4444
Cd40	Cd40	31	1.6719
Ripk1	Ripk1	26	1.705
Prkaca	Prkaca	24	-1.6932
Lck	Lck	24	2.8781
Foxp3	Foxp3	22	
Csflr	Csflr	20	2.9168
Dab2	Dab2	19	1.5203
Prkez	Prkez	19	-2.2064
Btrc	Btrc	19	-1.1636
Traf3	Traf3	19	1.5025
Ubc	Ubc	18	
Was	Was	18	4.6891
Panl	Panl	18	
Vim	Vim	18	

The End
