



miRNet 2.0 Tutorial 1

Starting from a list of microRNAs with
multiple targets



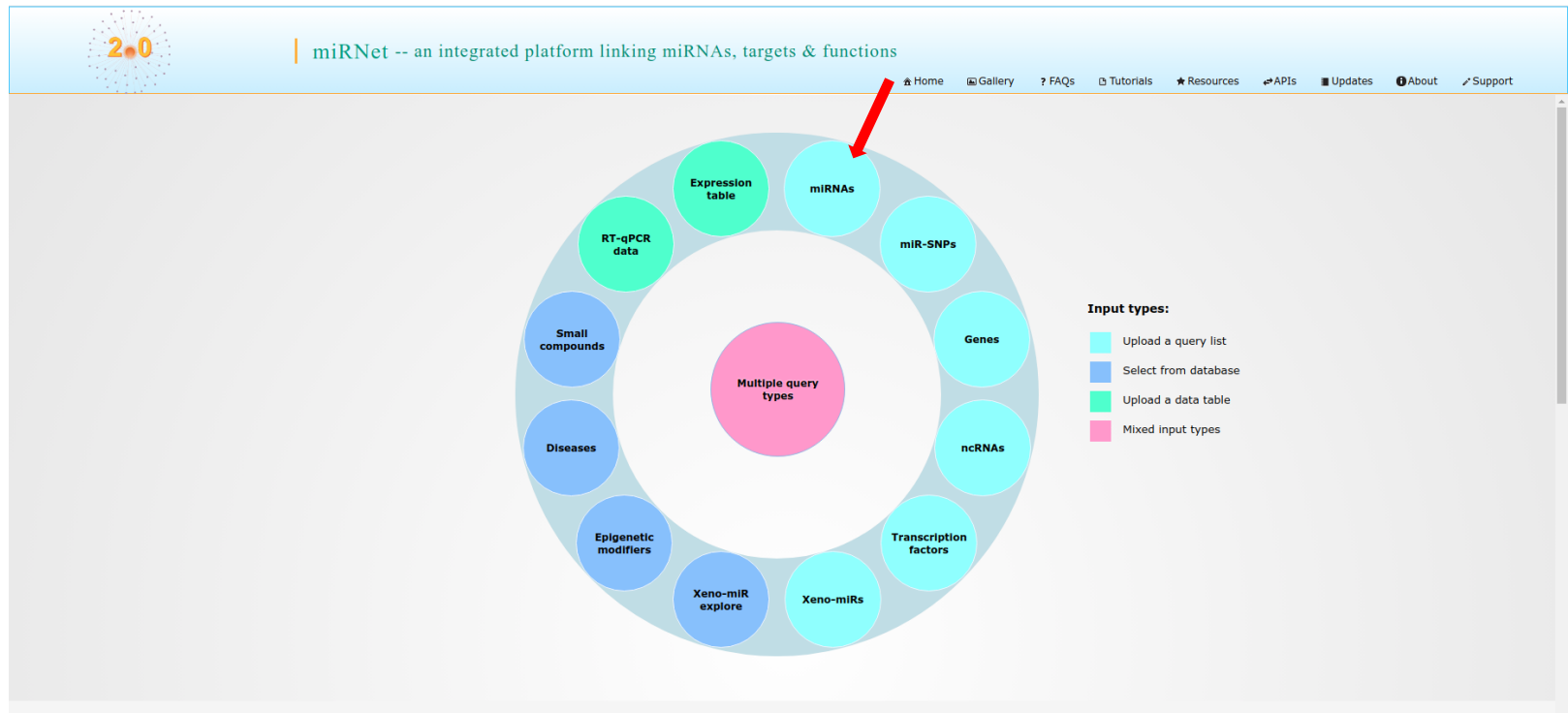
Computer and browser requirements

- A modern web browser with JavaScript enabled
 - Supported browsers include Chrome, Safari, Firefox, and Internet Explorer 9+
- For best performance and visualization, use:
 - Latest version of Google Chrome
 - A computer with at least 4GB of physical RAM
 - A 15-inch screen or bigger (larger is better)

Goals for this tutorial

- How to create a tripartite network from a list of miRNAs
- Network customization and visual exploration

Choose a module



Go to the miRNet home page (www.mirnet.ca) and click "miRNAs" to enter the module

Data input

The screenshot displays the miRNet web interface. At the top, there is a navigation bar with links for Home, Gallery, FAQs, Tutorials, Resources, and APIs. A notification box in the top right corner states: "OK A total of 9 unique items were uploaded. Click the Proceed button to proceed." The main content area is titled "Enter a list of miRNAs below:" and contains several input fields: "Organism" (set to "H. sapiens (human)"), "ID type" (set to "miRBase ID"), "Tissue (human only)" (set to "----Not specified----"), and "Targets" (set to "Selections"). Below these fields are checkboxes for "Include PPI (gene only)" and "Database selection". A list of miRNA IDs is provided, including hsa-mir-16-5p, hsa-mir-424-5p, hsa-mir-29c-3p, hsa-mir-29b-3p, hsa-mir-29a-3p, hsa-mir-149b-3p, hsa-mir-152-3p, hsa-mir-148a-3p, and hsa-mir-335-5p. A "Submit" button is located at the bottom of this section. A "Do You Know?" information box explains the miRNA ID format and provides additional context. A "Targets" dropdown menu is open, showing a list of target types: Genes (checked), lncRNAs (checked), circRNAs, Pseudogenes, sncRNAs, Diseases, Small molecules, Epigenetic modifiers, and Transcription factors. At the bottom of the page, there are "Try Examples" and "Proceed" buttons.

miRNet -- an integrated platform linking miRNAs, targets & functions

Home Gallery FAQs Tutorials Resources APIs

Upload

Enter a list of miRNAs below:

Organism: H. sapiens (human)

ID type: miRBase ID

Tissue (human only): ----Not specified----

Targets: Selections

Include PPI (gene only) Database selection

miRNA list (one entry per line)

Submit

Do You Know?

Please pay attention to the miRNA ID format. For miRBase ID, the format is "hsa-mir-1" (letters should be low-case) and for accession number is "MIMAT000001" (letters should be capital).

You can select one or multiple "Targets" to be included in the network, provided they have direct interactions with input miRNA list based on our knowledge

In addition, miRNet can automatically recognize different versions of miRBase IDs (v15-v22), as well as link pre-miRNAs to their mature forms.

Targets

Include PPI (gene only)

miRNA list (one entry per line)

Submit

Proceed

Try Examples

Selections

- Genes
- lncRNAs
- circRNAs
- Pseudogenes
- sncRNAs
- Diseases
- Small molecules
- Epigenetic modifiers
- Transcription factors

"Genes" and "lncRNAs" are selected in this analysis

Network creation

The screenshot shows the miRNet website interface. At the top, there is a navigation bar with links for Home, FAQs, Tutorials, Resources, Gallery, and APIs. The main content area is titled "Interaction Tables" and "Networks Created". A warning message in the top right corner states: "Warning: The network size is vary big. We recommend using appropriate Network Tool to reduce the size for better performance and experience." Below the warning, there is a "Network Tools" section with buttons for Degree Filter, Betweenness Filter, Shortest Path Filter, Update Network, Minimum Network, Steiner Forest Network, and Reset Network. The "Networks Created" section contains a table with the following data:

Networks	Nodes	Edges	Queries	
mirnet1	4857	6752	miRNA: 9;	± Download

At the bottom of the page, there are buttons for "Previous", "Downloads", and "Proceed".

We recommend that networks contain between 200-2000 nodes. This network is too big to be explored.

In order to prune this network down to a manageable size, you can choose an appropriate Network Tool.

Network trimming for better visualization

The screenshot shows the miRNet 2.0 interface. At the top, there is a navigation bar with a '2.0' logo and the text 'miRNet -- an integrated platform linking miRNAs, targets & functions'. A notification box in the top right corner says 'OK A total of 4365 was reduced.' The main content area is titled 'Network Builder' and contains several sections:

- Interaction Tables:** A section with a description and two rows of data. Each row has 'Download' and 'View' buttons. A blue callout box points to these buttons with the text: "You can also 'Download' or 'View' pair-wise interaction tables".
- Networks Created:** A section with a description and a table showing network statistics.
- Network Tools:** A vertical sidebar on the right containing several filter and action buttons. A blue callout box points to the 'Degree Filter' button with the text: "Use 'Degree Filter' to retain more 'hub' nodes (those with more connections)".

At the bottom of the interface, there are three buttons: 'Previous', 'Downloads', and 'Proceed'.

Networks	Nodes	Edges	Queries	
mirnet1	492	1714	miRNA: 9;	± Download

Network Tools:

- Degree Filter
- Betweenness Filter
- Shortest Path Filter
- Update Network
- Minimum Network
- Steiner Forest Network
- Reset Network

Main functions in Network View

The screenshot displays the Network View interface with several key components highlighted by blue callout boxes:

- Top Menu Bar:** Located at the top of the browser window, containing navigation and utility links like Home, FAQs, Tutorials, Resources, Gallery, APIs, Updates, About, and Support.
- Viewer Tool:** A vertical toolbar on the left side of the network visualization area, providing tools for zooming, panning, and other navigation functions.
- Node Explorer:** A table on the left side listing network nodes with columns for ID, Degree, Betweenness, and Status. It includes search and delete options.
- Detail for the selected nodes:** A section at the bottom left showing the 'Current Selections' of the nodes currently highlighted in the network.
- Functional enrichment analysis:** A panel on the right side, labeled 'Function Explorer', which allows users to perform enrichment tests. It includes fields for Query (All genes), Algorithm (Hypergeometric test), and Database (KEGG), along with a Submit button and a table for results (Hits, Pval, Color).
- Advanced Features:** A panel at the bottom right, labeled 'Module Explorer', which provides options for algorithm selection (InfoMap) and a table for module analysis (Module, Size, P-value, Color).

The central network visualization shows a complex graph of nodes (represented by red and blue dots) and edges (gray lines) on a dark background. Several nodes are highlighted in cyan, indicating they are selected.

Customizing Network (I)

Change layout to Circular Bipartite/Tripartite

The screenshot displays a network visualization software interface. The main window shows a network graph with a circular bipartite/tripartite layout. The nodes are arranged in three concentric layers: a central zone of blue nodes (lncRNAs), a middle layer of green nodes (miRNAs), and an outer layer of red nodes (genes). The interface includes a Node Explorer table on the left, a Function Explorer panel on the right, and a Module Explorer panel at the bottom right. A callout box points to the layout menu, and another points to a highlighted node in the network.

Node Explorer

ID	Degree	Betweenness	Status
hsa-mir-29b-3p	239	22669.5	*
hsa-mir-29a-3p	238	22268.35	*
hsa-mir-29c-3p	238	22828.43	*
hsa-mir-148b-3p	188	18737.6	*
hsa-mir-148a-3p	185	17994.41	*
hsa-mir-152-3p	183	18133.36	*
hsa-mir-16-5p	175	20106.18	*
hsa-mir-335-5p	137	13943.91	*
hsa-mir-424-5p	131	9509.258	*
XIST	9	1677.923	
TUG1	9	1677.923	
KCNQ1OT1	9	1677.923	
NEAT1	9	1677.923	
DDX6	8	1495.235	
HCG18	8	1479.374	
STAG3L5P-PVI	8	1479.374	
PVT1	8	1479.374	
KDM6B	7	1273.528	
OIP5-AS1	7	1273.528	
SNHG20	7	1273.528	
CCND2	6	282.7629	
VEGFA	6	282.7629	
TXNIP	6	321.5322	
DICER1	6	904.2064	
CCNA2	6	1082.646	
PHACTR2	6	1082.646	

Function Explorer

Query: All genes
Algorithm: Hypergeometric test
Database: KEGG

Module Explorer

Algorithm: InfoMap

Module	Size	P-value	Color
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Current Selections

- hsa-mir-16-5p
- hsa-mir-29a-3p
- hsa-mir-29b-3p
- hsa-mir-148a-3p

You can highlight seed nodes here

A lncRNA-miRNA-gene competing endogenous RNA (ceRNA) network. The blue nodes (central zone) represent lncRNAs, green nodes (middle layer) represent miRNAs and red nodes (outer layer) represent genes.

You can customize background color, node shape and label, edge color and opacity

Customizing Network (II)

The screenshot displays the Network Builder interface. The main window shows a network visualization with nodes and edges. A callout box highlights the 'Node type' option in the 'Scope' dropdown menu. The Node Explorer table on the left lists various genes and miRNAs with their IDs, Degrees, Betweenness, and Status. The Function Explorer on the right shows the current query and algorithm settings.

ID	Degree	Betweenness	Status
hsa-mir-29b-3p	239	22669.5	*
hsa-mir-29a-3p	238	2268.35	*
hsa-mir-29c-3p	238	22828.43	*
hsa-mir-148b-3p	188	18737.6	*
hsa-mir-148a-3p	185	17994.41	*
hsa-mir-152-3p	183	18133.36	*
hsa-mir-16-5p	175	20106.18	*
hsa-mir-335-5p	137	13943.91	*
hsa-mir-424-5p	131	9509.258	*
XIST	9	1677.923	
TUG1	9	1677.923	
KCNQ1OT1	9	1677.923	
NEAT1	9	1677.923	
DDX6	8	1495.235	
HCG18	8	1479.374	
STAG3L5P-PV1	8	1479.374	
PVT1	8	1479.374	
KDM6B	7	1273.528	
OIP5-AS1	7	1273.528	
SNHG20	7	1273.528	
CCND2	6	282.7629	
VEGFA	6	282.7629	
TXNIP	6	321.5322	
DICER1	6	904.2064	
CCNA2	6	1082.646	
PHACTR2	6	1082.646	

Node Explorer

Function Explorer

Module Explorer

Current Selections

- Manual Selection
 - hsa-mir-16-5p
 - hsa-mir-29a-3p
 - hsa-mir-29b-3p

Xia Lab @ McGill (last updated 2020-03-13)

You can select "Node type" (new feature) under "Scope" and drag to a separate area to further investigate.

Module detection & highlighting

The screenshot displays the Network Viewer interface with a network graph. The graph consists of numerous nodes and edges, with several clusters highlighted in yellow and cyan. The interface includes a Node Explorer on the left, a Function Explorer on the right, and a Module Explorer at the bottom right. Two callout boxes provide instructions: one pointing to the Node Explorer table and another pointing to the Module Explorer table.

Node Explorer

ID	Degree	Betweenness	Status
hsa-mir-29b-3p	239	22669.5	*
hsa-mir-29a-3p	238	22268.35	*
hsa-mir-29c-3p	238	22828.43	*
hsa-mir-148b-3p	188	18737.6	*
hsa-mir-148a-3p	185	17994.41	*
hsa-mir-152-3p	183	18133.36	*
hsa-mir-16-5p	175	20106.18	*
hsa-mir-335-5p	137	13943.91	*
hsa-mir-424-5p	131	9509.258	*
XIST	9	1677.923	
TUG1	9	1677.923	
KCNQ1OT1	9	1677.923	
NEAT1	9	1677.923	
DDX6	8	1495.235	
HCG18	8	1479.374	
STAG3L5P-PV1	8	1479.374	
PVT1	8	1479.374	
KDM6B	7	1273.528	
OIP5-AS1	7	1273.528	
SNHG20	7	1273.528	
CCND2	6	282.7629	
VEGFA	6	282.7629	
TXNIP	6	321.5322	
DICER1	6	904.2064	
CCNA2	6	1082.646	
PHACTR2	6	1082.646	

Function Explorer

Name	Hits	Pval	Color
Pathways in cancer	38	1.42e-12	
Focal adhesion	27	1.21e-9	
Small cell lung cancer	15	4.83e-7	
Prostate cancer	15	0.00001	
Chronic myeloid leukemia	13	0.00005	
Glioma	12	0.00010	
Colorectal cancer	9	0.00303	
Epstein-Barr virus infection	12	0.00312	
p53 signaling pathway	10	0.00525	
Melanoma	10	0.00525	
ECM-receptor interaction	11	0.00571	
Cell cycle	13	0.0104	
HTLV-I infection	17	0.0104	
Wnt signaling pathway	14	0.0111	
Pancreatic cancer	9	0.00237	
ErbB signaling pathway	10	0.0028	
Acute myeloid leukemia	8	0.0029	
Endometrial cancer	7	0.00309	
Renal cell carcinoma	8	0.00373	

Module Explorer

Module	Size	P-value	Color
0	107	2.39e-22	
1	213	3.69e-77	
2	172	1.4e-49	

Current Selections

- module 1
 - hsa-mir-29a-3p
 - hsa-mir-29b-3p
 - hsa-mir-29c-3p

Modules are tightly clustered subnetworks with more internal connections than expected by chance in the whole network. Members within a module are likely to work together to perform a biological function.

Exploring Enriched Biological Functions

The screenshot displays the miRNet software interface. The central panel shows a network visualization with nodes and edges. A blue callout box points to the 'Function Explorer' panel on the right, which contains a table of enriched biological functions.

Function Explorer

Query: All genes
Algorithm: Hypergeometric test
Database: KEGG

Name	Hits	Pval	Color
Pathways in cancer	38	1.42e-12	Yellow
Focal adhesion	27	1.21e-9	Cyan
Small cell lung cancer	15	4.83e-7	Light Blue
Prostate cancer	15	0.000001	Light Blue
Chronic myeloid leukemia	13	0.000005	Light Blue
Glioma	12	0.000010	Light Blue
Colorectal cancer	9	0.000303	Light Blue
Epstein-Barr virus infection	12	0.000312	Light Blue
p53 signaling pathway	10	0.000525	Light Blue
Melanoma	10	0.000525	Light Blue
ECM-receptor interaction	11	0.000571	Light Blue
Cell cycle	13	0.00104	Light Blue
HTLV-I infection	17	0.00104	Light Blue
Wnt signaling pathway	14	0.00111	Light Blue
Pancreatic cancer	9	0.00237	Light Blue
ErbB signaling pathway	10	0.0028	Light Blue
Acute myeloid leukemia	8	0.0029	Light Blue
Endometrial cancer	7	0.00309	Light Blue
Renal cell carcinoma	8	0.00373	Light Blue

Module Explorer

Algorithm: InfoMap

Module	Size	P-value	Color
Module			

Current Selections

- Focal adhesion
 - CCND1
 - BCL2
 - CCND2

miRNet provides four query types (all genes, highlighted genes, all miRNAs, highlighted miRNAs), two enrichment algorithms (hypergeometric tests and empirical sampling), nine annotation libraries (three gene-set libraries and six miRNA-set libraries) for functional enrichment analysis.

Path of interactions between queries

The screenshot displays a network visualization tool interface. At the top, navigation links include Home, FAQs, Tutorials, Resources, Gallery, APIs, Updates, About, and Support. Below this is a control bar with options for Network (mirnet1), Background (Black), View (Grey), Layout (Concentric circle), Node (- Specify -), Edge (- Specify -), Scope (-- Specify --), and Download (-- Specify --). A View Options icon is also present.

Node Explorer

ID	Degree	Betweenness	Status
hsa-mir-16-5p	738	340262.6	*
hsa-mir-424-5p	560	146938.2	*
hsa-mir-335-5p	303	103361.9	*
hsa-mir-29a-3p	268	66780.75	*
hsa-mir-29b-3p	267	65641.85	*
hsa-mir-29c-3p	267	66393.15	*
hsa-mir-148b-3p	261	77345.88	*
hsa-mir-148a-3p	208	49527.76	*
hsa-mir-152-3p	188	39354.9	*
XIST	9	5996.356	
TUG1	9	5996.356	
KCNQ1OT1	9	5996.356	
NEAT1	9	5996.356	
DDX6	8	4162.324	
HCG18	8	5109.215	
STAG3L5P-PVI	8	5109.215	
PVT1	8	5109.215	
KDM6B	7	1978.416	
OIP5-AS1	7	1978.416	
SNHG20	7	1978.416	
CCND2	6	2438.4	
VEGFA	6	2438.4	
TXNIP	6	2479.233	
DICER1	6	2623.161	
CCNA2	6	1407.578	
PHACTR2	6	1407.578	

Function Explorer

Query: All genes
Algorithm: Hypergeometric test
Database: KEGG

Name	Hits	Pval	Color
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Module Explorer

Batch Selection

Path Finder

From KCNQ1OT1 To C1RL-AS1 Submit

- KCNQ1OT1->hsa-mir-424-5p->C1RL-AS1
- KCNQ1OT1->hsa-mir-16-5p->C1RL-AS1

Current Selections

- hsa-mir-424-5p
- KCNQ1OT1
- C1RL-AS1

To identify interaction partners between queries, click on "Path Finder"

Batch selection & highlighting

The screenshot displays the Network Viewer application interface. The main window shows a large network graph with nodes and edges. The interface includes several panels:

- Node Explorer:** A table listing nodes with columns for ID, Degree, Betweenness, and Status. The table is sorted by Betweenness.
- Function Explorer:** A panel for running queries, currently set to "All genes" and "Hypergeometric test" using the "KEGG" database.
- Batch Selection:** A panel for manually selecting nodes, containing a text input field with the following IDs: KCNQ10T1, C1RL-AS1, LINC00511, and LINC00174. There are "Highlight" and "Delete" buttons below the input field.
- Path Finder:** A panel for finding paths in the network.

The network graph shows a dense network of nodes, with a central cluster of nodes highlighted in blue and yellow. The nodes are arranged in a circular pattern, with a large orange border around the perimeter.

You can manually "Highlight" or "Delete" a list of nodes by using the "Batch Selection" feature

== END ==