

The image features a dark background with a network graph of miRNAs. Nodes are represented by small squares (light blue) and circles (orange). Lines connect the nodes, forming a complex web. Three specific nodes are highlighted with labels: 'hsa-mir-369-5p' at the top right, 'hsa-mir-29b-3p' in the middle left, and 'hsa-mir-23a-3p' at the bottom right. A large, semi-transparent blue rectangle is centered over the graph, containing the title text.

# miRNet Tutorial Network Creation

# Goal for this tutorial

- Perform data filtering on the interaction table
- Perform nodes management on the original network

# Initial interaction table

miRNA Upload > Interaction Table

For cattle (*B. taurus*), chicken (*G. gallus*) and helminth (*S. mansoni*), the result will be mainly composed of interaction data predicted using miRanda. You can use the "Data Filter" to filter the results based on the miRanda scores to keep more confident predictions.

[Data Filter](#)
[Reset](#)
[Download](#)

miRNA ↕	Link	Tissue	Target:Gene ↕	Link	Method ↕	Literature	
<input type="text"/>	<a href="#">miRBase</a>	Kidney	<input type="text"/>	<a href="#">Entrez</a>	Sequencing	<a href="#">20371350</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	ACVR2B	<a href="#">Entrez</a>	Sequencing	<a href="#">20371350</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	AP1G1	<a href="#">Entrez</a>	PAR-CLIP	<a href="#">20371350, 23592263</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	AMD1	<a href="#">Entrez</a>	Sequencing	<a href="#">20371350</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	XIAP	<a href="#">Entrez</a>	Sequencing	<a href="#">20371350</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	BIRC5	<a href="#">Entrez</a>	Sequencing	<a href="#">20371350</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	APP	<a href="#">Entrez</a>	Sequencing	<a href="#">20371350, 72401</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	RHOA	<a href="#">Entrez</a>	Luciferase reporter assay//qPCR	<a href="#">28109909</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	ATM	<a href="#">Entrez</a>	Luciferase reporter assay//qPCR	<a href="#">20617180</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	ATP5B	<a href="#">Entrez</a>	qRT-PCR//Reporter assay//M	<a href="#">21291913</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	NKX3-2	<a href="#">Entrez</a>	HITS-CLIP	<a href="#">23824327</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	CCND1	<a href="#">Entrez</a>	Western blot	<a href="#">26286725</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	BCL9	<a href="#">Entrez</a>	Sequencing	<a href="#">20371350</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	PRDM1	<a href="#">Entrez</a>	Chromatin immunoprecipitation	<a href="#">26655851</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	ZFP36L2	<a href="#">Entrez</a>	PAR-CLIP	<a href="#">21572407, 20371350</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	CAPN2	<a href="#">Entrez</a>	Sequencing	<a href="#">20371350</a>	<a href="#">Delete</a>

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Click here to perform data filtering
Click here to delete individual interaction.
Search items by keywords
The experimental methods for validation. ( For *S.mansoni* is miRanda score)

# Perform Data Filtering

The screenshot shows the 'Data Filter Dialog' window. The 'Target Column:' dropdown is open, showing options: 'Method', 'miRNA', 'Target', 'Method', and 'Literature'. The 'Value Criterion:' dropdown is set to 'Matching'. The 'Action' section has 'Remove' selected with a radio button. A 'Submit' button is at the bottom.

Step 1 : Choose a target column which you want to perform the filter.

The screenshot shows the 'Data Filter Dialog' window. The 'Target Column:' dropdown is set to 'Method'. The 'Value Criterion:' dropdown is open, showing options: '(Character) Containing', '(Character) Matching', '(Character) Containing', and '(Numerics) At least'. The 'Action' section has 'Keep' selected with a radio button. A 'Submit' button is at the bottom.

Step 2 : Choose the filter option, “Matching” is filtering by the exact words, “Containing” is filtering by keywords, “At least” is filtering by predicted score (only for *S.mansoni*)

The screenshot shows the 'Data Filter Dialog' window. The 'Target Column:' dropdown is set to 'Method'. The 'Value Criterion:' dropdown is set to '(Character) Containing'. The text input field contains 'CLIP'. The 'Action' section has 'Keep' selected with a radio button. A 'Submit' button is at the bottom.

Step 3 : Input the keywords and perform the filtering to keep or remove

# The table after performing data filter

miRNA Upload > Interaction Table

For cattle (*B. taurus*), chicken (*G. gallus*) and helminth (*S. mansoni*), the result will be mainly composed of interaction data predicted using miRanda. You can use the "Data Filter" to filter the results based on the miRanda scores to keep more confident predictions.

[Data Filter](#) [Reset](#) [Download](#)

miRNA ↕	Link	Tissue	Target:Gene ↕	Link	Method ↕	Literature ↕	Action
<input type="text"/>			<input type="text"/>				
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	AP1G1	<a href="#">Entrez</a>	PAR-CLIP//Sequencing	<a href="#">20371350</a> , <a href="#">23592263</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	AMD1	<a href="#">Entrez</a>	HITS-CLIP	<a href="#">23313552</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	APP	<a href="#">Entrez</a>	Luciferase reporter assay/P	<a href="#">20395292</a> , <a href="#">21172309</a> , <a href="#">2157240</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	NKX3-2	<a href="#">Entrez</a>	HITS-CLIP	<a href="#">23824327</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	ZFP36L2	<a href="#">Entrez</a>	PAR-CLIP	<a href="#">21572407</a> , <a href="#">20371350</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	CAPZB	<a href="#">Entrez</a>	PAR-CLIP	<a href="#">27292025</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	CCNF	<a href="#">Entrez</a>	PAR-CLIP	<a href="#">23592263</a> , <a href="#">26701625</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	CD81	<a href="#">Entrez</a>	PAR-CLIP	<a href="#">23592263</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	CDKN1A	<a href="#">Entrez</a>	PAR-CLIP	<a href="#">23592263</a> , <a href="#">22012620</a> , <a href="#">2670162</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	COX10	<a href="#">Entrez</a>	PAR-CLIP	<a href="#">23592263</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	CPS1	<a href="#">Entrez</a>	PAR-CLIP	<a href="#">23592263</a>	<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	DYNC1L12	<a href="#">Entrez</a>			<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	DSC1	<a href="#">Entrez</a>			<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	EIF4G2	<a href="#">Entrez</a>			<a href="#">Delete</a>
hsa-mir-101-3p	<a href="#">miRBase</a>	Kidney	ELAVL3	<a href="#">Entrez</a>			<a href="#">Delete</a>

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Only keep the method contains "CLIP"

Click "Proceed" to the network builder

# Pruning or Expanding Network Data

Home > Microarray Profiling > Interaction Table > Network Builder > Network Viewer

**Network Overview:**

Number of queries:	75
Number of nodes:	1185 (miRNAs: 1142, Targets: 43)
Number of edges:	1738

In some cases, multiple isolated networks will be generated, with a big 'continent' containing most of queries, and several small 'islands' containing one or a few queries. You can select one or more networks for visual analysis in the next step.

	Networks	Nodes	Edges	Queries	
<input checked="" type="checkbox"/>	mirnet1	1185	1738	43	± Download

**Network Tools:**

- Degree Filter
- Betweenness Filter
- Shortest Path Filter
- Update Network
- Reset Network

Summary for the nodes of the network

Perform the network management

Click "Proceed" to the network viewer

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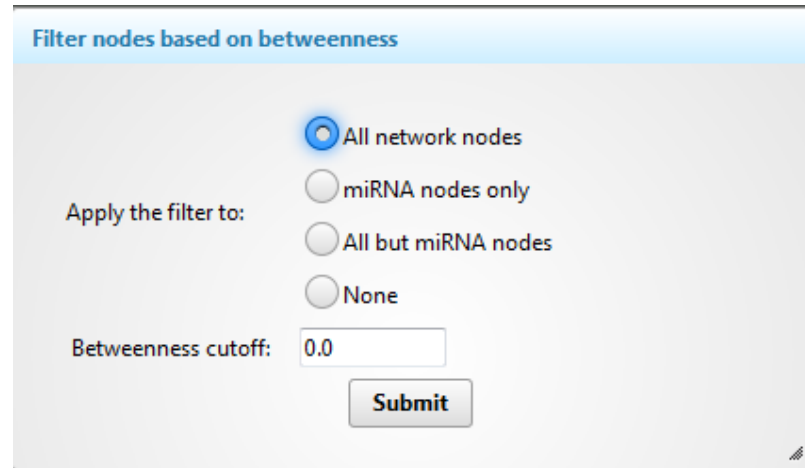
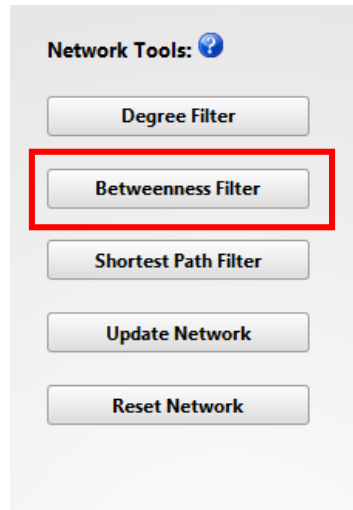
# Network tools

The image shows two parts of a web interface. On the left, a panel titled "Network Tools: ?" contains five buttons: "Degree Filter" (highlighted with a red box), "Betweenness Filter", "Shortest Path Filter", "Update Network", and "Reset Network". On the right, a panel titled "Filter nodes based on degree" contains the following options:

- Apply the filter to:
  - All network nodes
  - miRNA nodes only
  - All but miRNA nodes
  - None
- Degree cutoff:
- 

- The degree of a node is the number of connections it has to other nodes. Nodes with higher node degree act as hubs in a network.
- **Degree cutoff:** default 1.0, the minimal degree you want to choose.
- **All network nodes** : default option, choose all nodes in the network.
- **miRNA nodes only**: the degree filter will only perform in miRNA nodes.
- **All but miRNA nodes** : the degree filter will perform to other nodes except miRNA.
- **None**: Do not perform the filter.

# Network tools



- The **betweenness centrality** measures the number of shortest paths going through the node. It takes into consideration the global network structure. For example, nodes that occur between two dense clusters will have a high betweenness centrality even if their degree centrality values are not high.
- **Degree cutoff**: default 0.0 (all nodes), the minimal betweenness you want to choose.
- **All network nodes** : default option, choose all nodes in the network.
- **miRNA nodes only**: the betweenness filter will only perform in miRNA nodes.
- **All but miRNA nodes** : the betweenness filter will perform to other nodes except miRNA.
- **None**: Do not perform the filter.



# Network tools

The image shows a software interface for network analysis. On the left, a panel titled "Network Tools: ?" contains five buttons: "Degree Filter", "Betweenness Filter", "Shortest Path Filter" (highlighted with a red box), "Update Network", and "Reset Network". Two blue callout boxes point to the "Shortest Path Filter" and "Reset Network" buttons. The "Shortest Path Filter" callout says "Refresh network as new changes." and the "Reset Network" callout says "Reset the network to default." To the right, a sub-panel titled "Reduce connections between densely connected nodes" is shown. It has a heading "Apply the filter to:" followed by four radio button options: "All network nodes" (selected), "miRNA nodes only", "All but miRNA nodes", and "None". A "Submit" button is located at the bottom right of this sub-panel.

- **Shortest Path Filter** : If there are multiple paths that can link two nodes together, only one shortest path will be chose to reduce dense networks.
- **All network nodes** : default option, choose all nodes in the network.
- **miRNA nodes only**: the filter will only perform in miRNA nodes.
- **All but miRNA nodes** : the filter will perform to other nodes except miRNA.
- **None**: Do not perform the filter.

**==END==**