

# Quick Start Guide

Target discovery knowledgebase platform

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*Overview of the start page*

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## ***Summary of all the options provided on the platform to construct the network visualization and tutorial videos***

*Construct network visualization by genes*

By protein name

Search by Multiple proteins

1 Seed Genes

MAPT,STX6,EIF2AK3,MOBP,DCTN1,LRRK2

OR

Choose File No file chosen

2 Disease Map

PSP

Order

Zero

Interaction Type:

PPI Interaction

Min interaction score:

High (0.7)

3 Submit

The first option to construct the network visualization can be achieved by providing the gene names or [Ensembl](#) IDs.

1. You can either type into the **Seed Genes** textbox or upload a txt file.
2. Choose preferable options for **Disease Map, Order, Interaction Type** and **Min Interaction score**.
3. Click **Submit**.

## Construct network visualization by a network

Upload a file

Custom Upload

1

Select File Type

CSV

Upload a csv

Choose Files

No file chosen

2

Submit

First and second column consist of valid ENSG ids

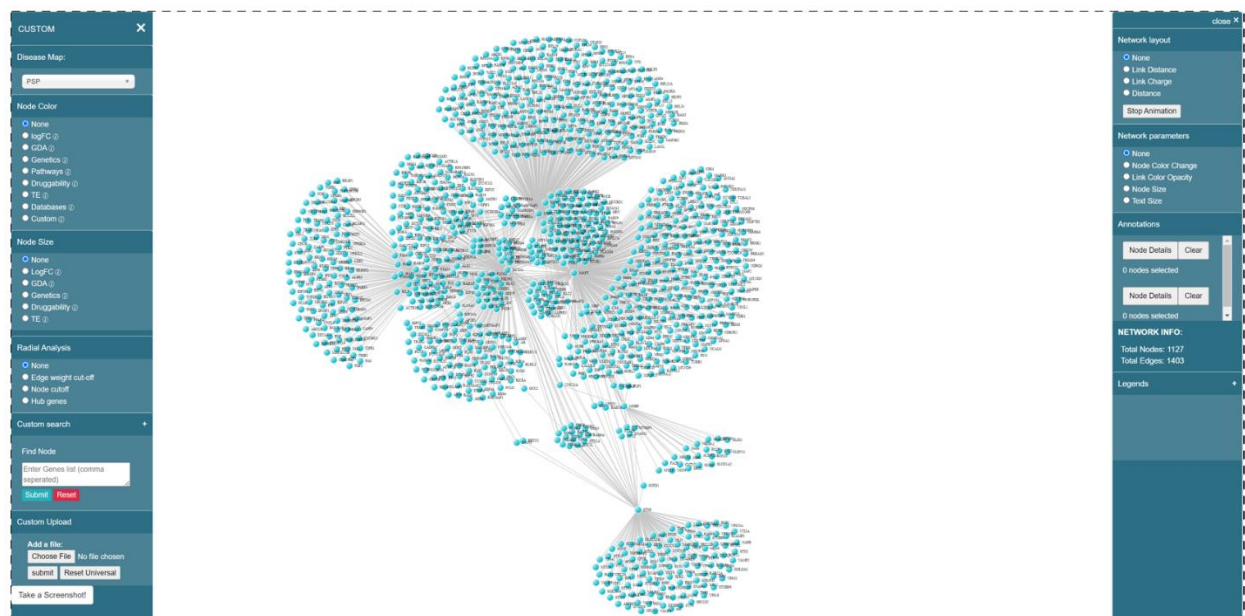
	A	B	C
1	Node1	Node2	Score
2	ENSG00000083520	ENSG00000039123	0.999
3	ENSG00000108883	ENSG00000174231	0.999
4	ENSG00000010810	ENSG00000176105	0.999

Third column consist of weight/score between both genes

The second option to construct the network visualization can be achieved by providing the network file.

1. You can choose to upload a **CSV** or **JSON** file. An example format is provided.
2. Click **Submit**.

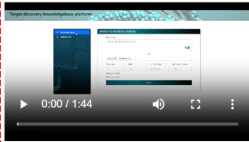
After constructing the network, a network visualization shows up



## Tutorials

Watch Tutorial Video

1




**Basic Overview of Platform**

Welcome to our tool, an Interactive Network Visualization tool. Please watch the video to see how to generate the network visualization.

2

**Network Analysis**

Our tool allows you to analyze the network. Please watch the video to see how to achieve it.



You can also check the tutorial videos for quick hands-on.

1. The first video is about the overall introduction of the platform, and the ways to construct the network visualization.
2. The second video is about how to utilize the platform to perform the network analysis.

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### Overview of the network analysis page

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**Summary of all the options provided on the platform to analyze the constructed network**

**The network visualization page contains the left panel and right panel**

**Left panel focuses on analysis of the network, while right panel focuses on network parameters modification**

#### Use Case 1

Switch to another disease map

Disease Map:

PSP

ALS

FTD

OI

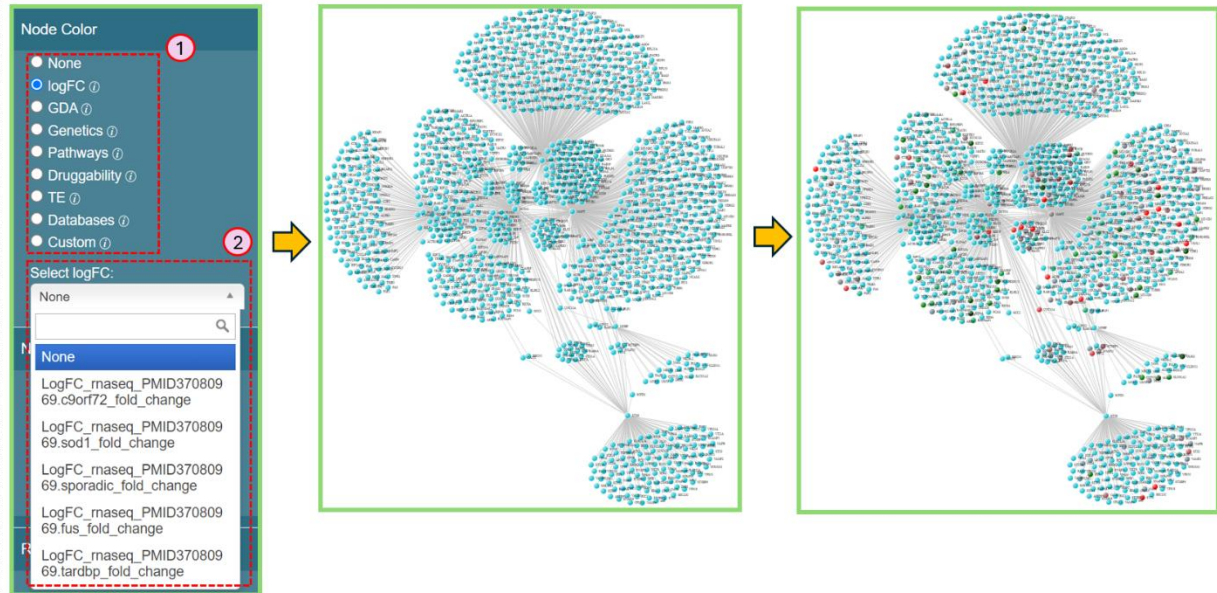
PSP

Sometimes you want to switch to another disease after generating the network visualization.

- Simply go to **Disease Map** and select different disease name you want to switch to.

## Use Case 2

### Change node color



The diagram illustrates the process of changing node color in a network visualization. It consists of three main parts: a control panel, an initial network graph, and a resulting network graph.

**Control Panel (Node Color):**

- 1. Choose a feature:** The 'Node Color' menu is shown with options: None, logFC (selected), GDA, Genetics, Pathways, Druggability, TE, Databases, and Custom.
- 2. Select the values for the feature you choose in step 1:** The 'Select logFC:' dropdown is shown with a search bar and a list of features: None, LogFC\_maseq\_P MID370809\_69.c9orf72\_fold\_change, LogFC\_maseq\_P MID370809\_69.sod1\_fold\_change, LogFC\_maseq\_P MID370809\_69.sporadic\_fold\_change, LogFC\_maseq\_P MID370809\_69.fus\_fold\_change, and LogFC\_maseq\_P MID370809\_69.tardbp\_fold\_change.

**Network Graphs:**

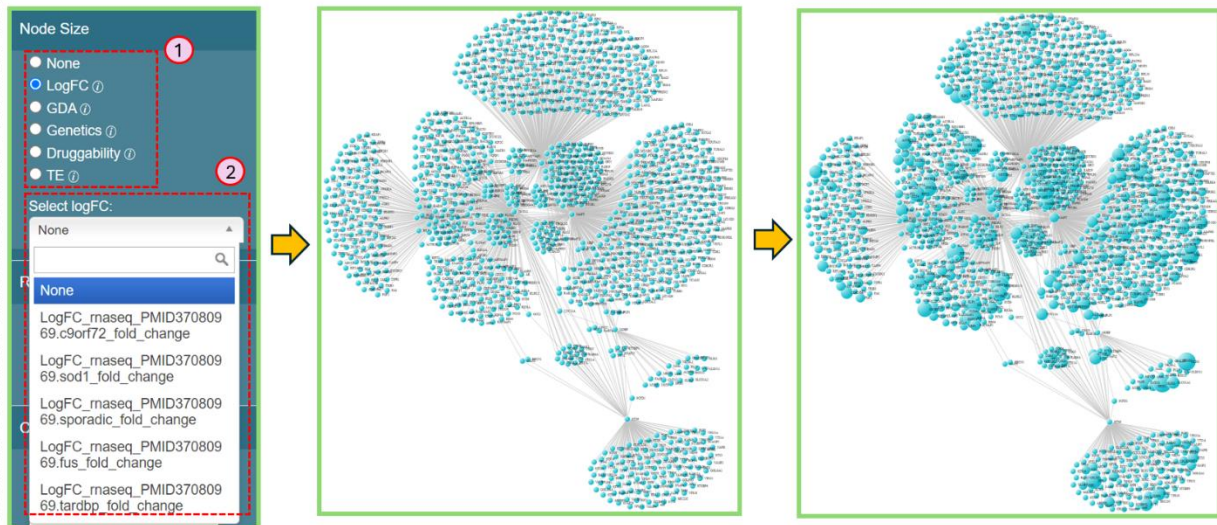
- The initial network graph shows nodes colored by default (light blue).
- The resulting network graph shows nodes colored based on the selected feature values (e.g., LogFC\_maseq\_P MID370809\_69.c9orf72\_fold\_change).

You can change the node color by selecting different feature values.

1. Choose a feature. You can hover on the info icon to check the explanation of a specific feature.
2. Select the values for the feature you choose in step 1.

## Use Case 3

### Change node size



The diagram illustrates the process of changing node size in a network visualization. It consists of three main parts: a control panel, an initial network graph, and a resulting network graph.

**Control Panel (Node Size):**

- 1. Choose a feature:** The 'Node Size' menu is shown with options: None, LogFC (selected), GDA, Genetics, Druggability, and TE.
- 2. Select the values for the feature you choose in step 1:** The 'Select logFC:' dropdown is shown with a search bar and a list of features: None, LogFC\_maseq\_P MID370809\_69.c9orf72\_fold\_change, LogFC\_maseq\_P MID370809\_69.sod1\_fold\_change, LogFC\_maseq\_P MID370809\_69.sporadic\_fold\_change, LogFC\_maseq\_P MID370809\_69.fus\_fold\_change, and LogFC\_maseq\_P MID370809\_69.tardbp\_fold\_change.

**Network Graphs:**

- The initial network graph shows nodes of uniform size.
- The resulting network graph shows nodes sized based on the selected feature values (e.g., LogFC\_maseq\_P MID370809\_69.c9orf72\_fold\_change).

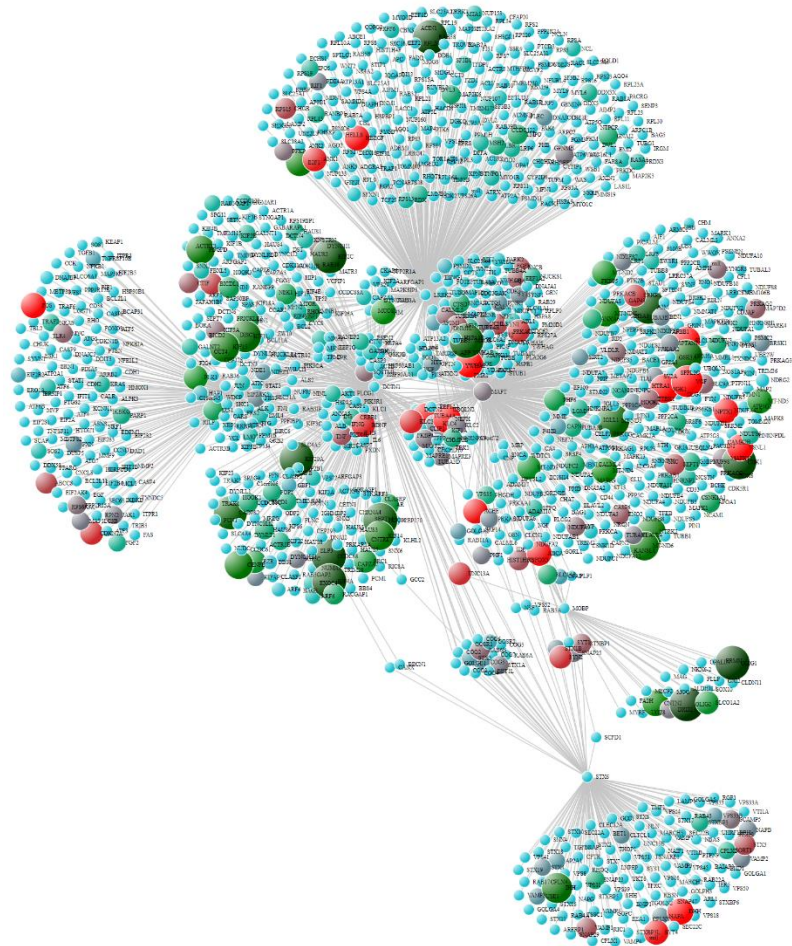
You can change the node size by selecting different feature values.

1. Choose a feature. You can hover on the info icon to check the explanation of a specific feature.
2. Select the values for the feature you choose in step 1.



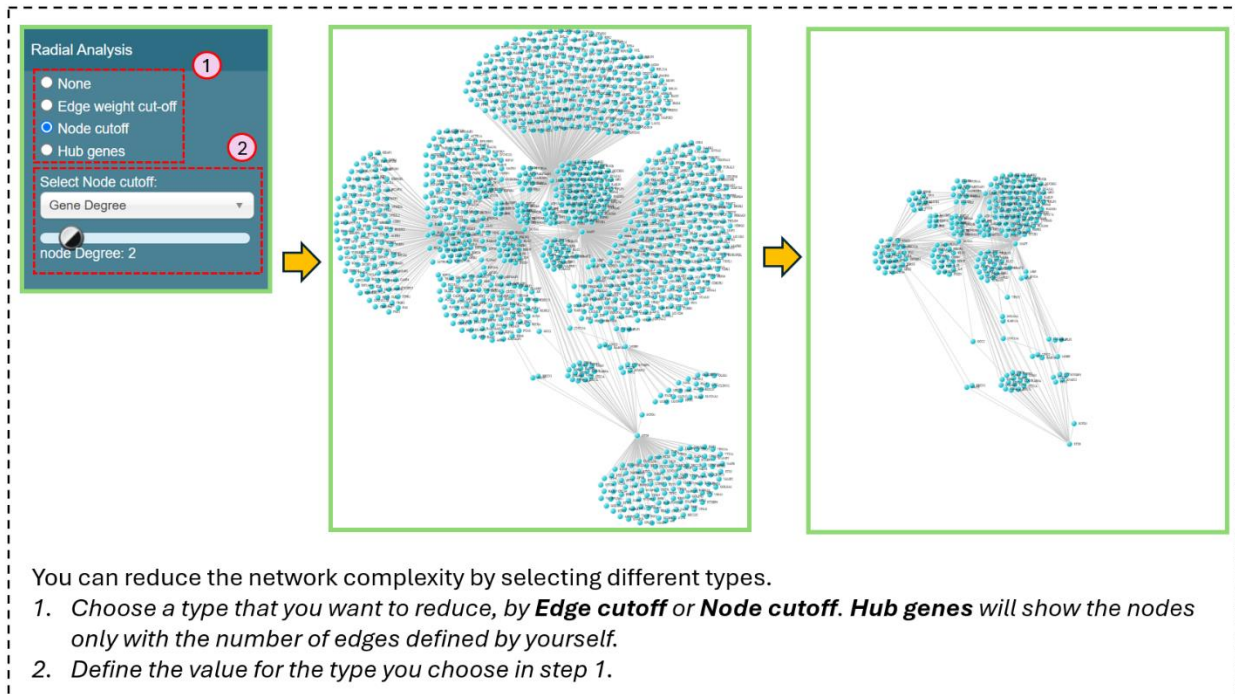
**Note:**

### Use Case 2 and 3 can be combined to change both node color and size



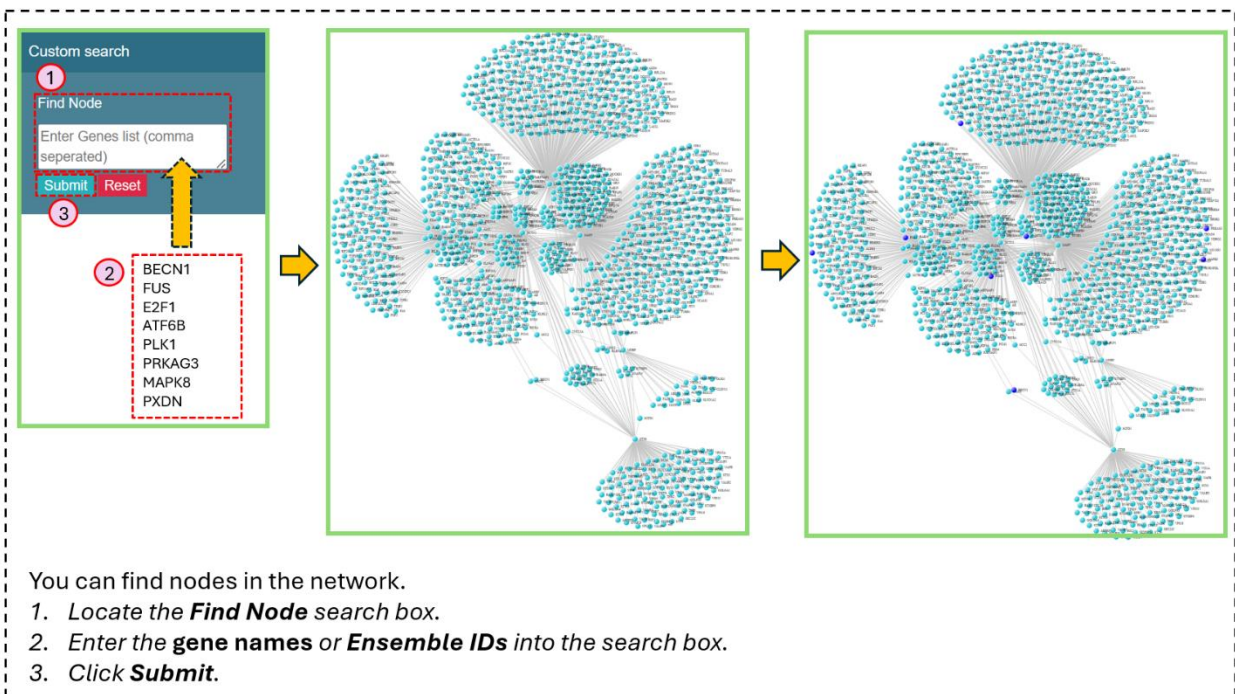
## Use Case 4

Radial analysis can help focus on a more precise level



## Use Case 5

Find node in the network



## Use Case 6

### Custom upload

**Custom Upload** 1

Add a file:

No file chosen

**Node Color** 2

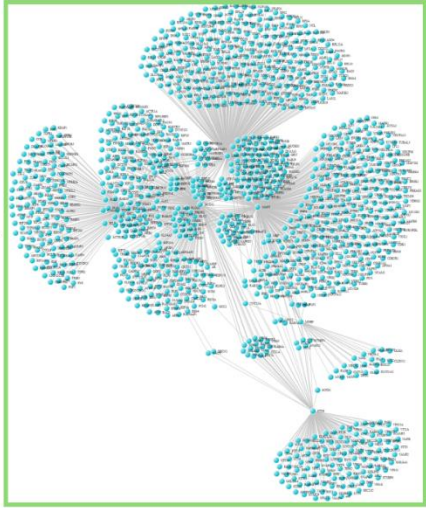
3

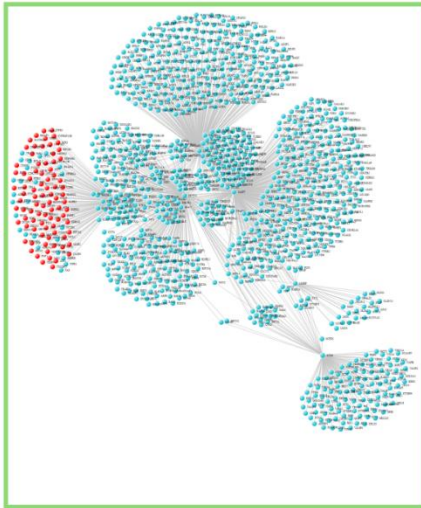
- ☐ None
- ☐ logFC (i)
- ☐ GDA (i)
- ☐ Genetics (i)
- ☒ Pathways (i)
- ☐ Druggability (i)
- ☐ TE (i)
- ☐ Databases (i)
- ☐ Custom (i)

**Select Pathway:** 4

Pathway\_test

➡


➡



You can upload your own customized data to analyze the network, instead of using the existing data.

1. Upload a **CSV** file with your own data, please refer to the **file format** below.
2. Click **Submit**.
3. Locate **Node Color** and select the corresponding feature name.
4. Select the name of your customized data.

### File format

For	Column Naming	Value range
LogFC	logFC_ <u>CustomName</u>	$[-\text{Inf}, +\text{Inf}]$
GDA	GDA_ <u>CustomName</u>	[0, 1]
Genetics	GWAS_ <u>CustomName</u>	[-1, 1]
Pathway	pathway_ <u>CustomName</u>	Binary
Druggability	druggability_ <u>CustomName</u>	[0, 1]
TE	TE_ <u>CustomName</u>	[0, +Inf], decimal
Database	database_ <u>CustomName</u>	Binary
Custom	custom_color_ <u>CustomName</u>	Red, green, blue, orange, yellow, black

The **table** above elaborates the naming convention, and the value ranges for all the supported features.

The **CSV file** on the right provides an example of what the real file looks like.

	A	B	C	D
1	ID	pathway_test	custom_color_test	logFC_test
2	WFS1	1	red	0.899996
3	PTEN	0	yellow	3.987554
4	SOS2	1	black	-0.57945
5	ABCC8	1	blue	0.566458
6	KEAP1	0	orange	1.246587
7	TRIB3	1	green	-6.2479



## Use Case 7

### Change network layout

**Network layout** 1

- None
- Link Distance
- Link Charge
- Distance

Stop Animation 2

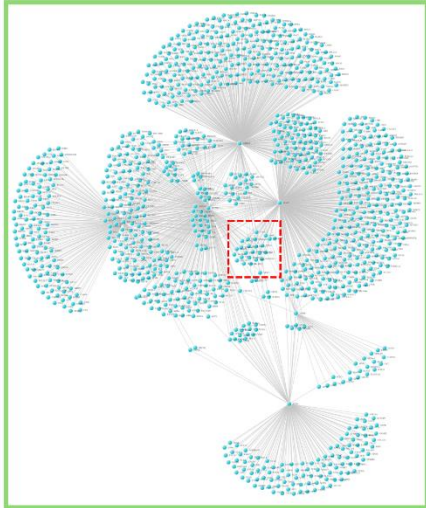
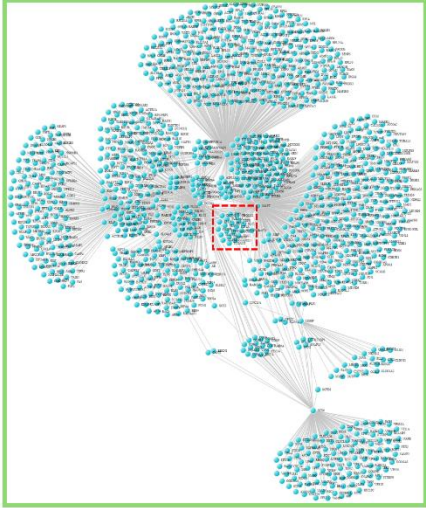
distance: 181

**Network parameters** 1

- None
- Node Color Change
- Link Color Opacity
- Node Size
- Text Size

**Annotations** 1

**NETWORK INFO:**  
Total Nodes: 1127  
Total Edges: 1403



You can make the clusters more readable.

1. Select **Distance** or other options.
2. Select the distance value to separate the nodes.

You can change basic parameters of the network.

1. Change the **Node Color**, **Link Opacity**, **Node Size** and **Text Size**.

You can get the basic information of your network.

1. Locate **NETWORK INFO** to check the node and edge counts.

