

PRL-3 roles in metastasis: a workflow to extract reduced pathways from signaling maps.

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Background

The pathway analysis was performed using the BiNoM (version 2.5) plugin in cytoscape (version 2.7). The objective was to extract the paths that are between the PRL-3 protein and the different phenotypes that lead to metastasis.

It is recommended to use both versions of the software for this task.

Link to cytoscape: <https://cytoscape.org/download.html>

Link to BiNoM: <https://binom.curie.fr/>

Process

1. First, a session in Cytoscape is open and xml file of the map is loaded. Using the import function from the BiNoM plugin. In the menu Plugins>BiNoM 2.5>BiNoM I/O>Import CellDesigner Document from file...

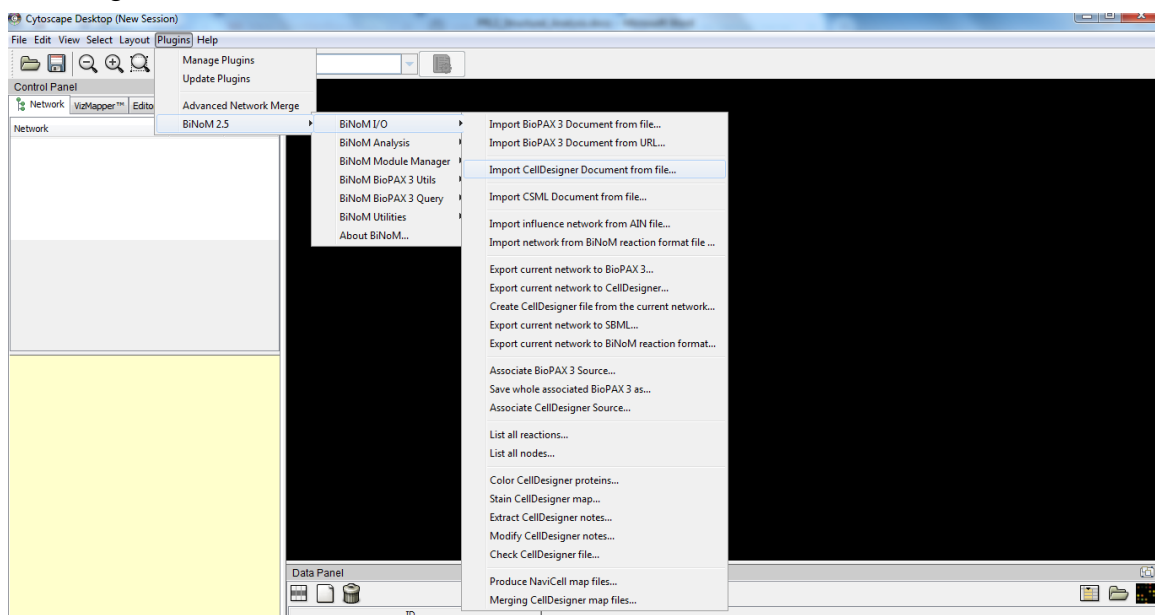


Figure 1 Importing CellDesigner file

2. Once loaded, select the whole network and proceed to do the pathway analysis. In the menu Plugins>BiNoM 2.5>BiNoM Analysis>Path Analysis...

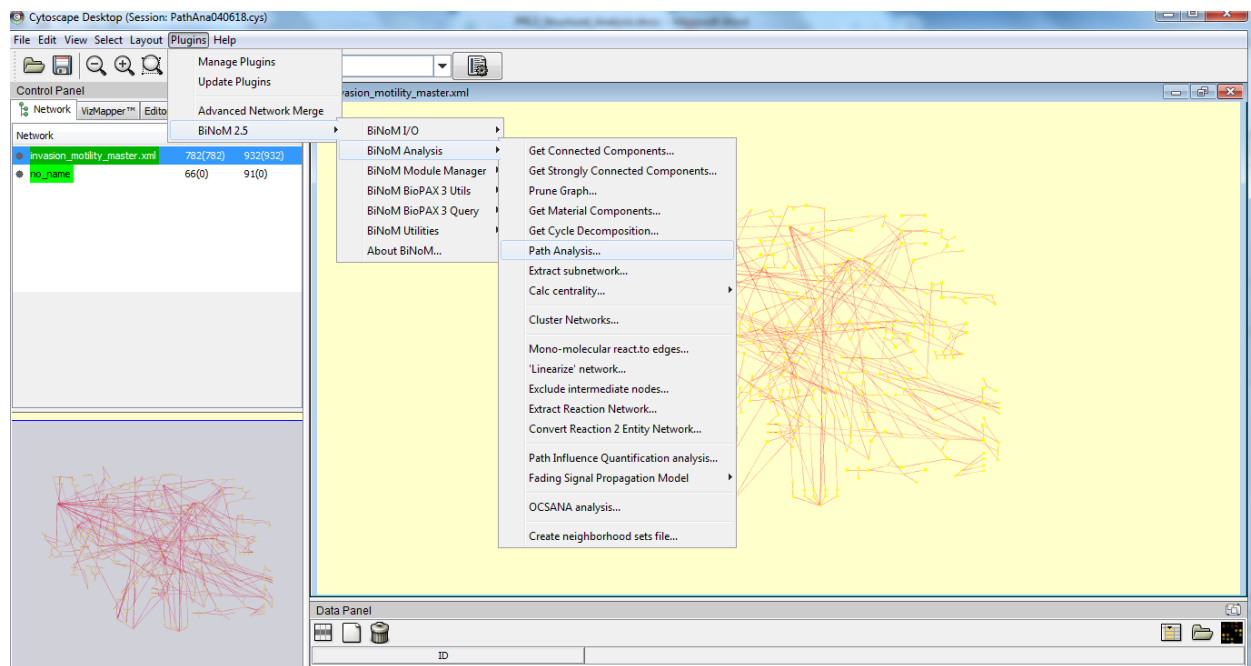


Figure 2 Selecting Path Analysis

3. After selecting path analysis, a dialogue will open; here you can define the source, the target and other parameters for the path analysis. In this example I will use PTP4A3 (PRL-3) as a source and EMT & motility as target.

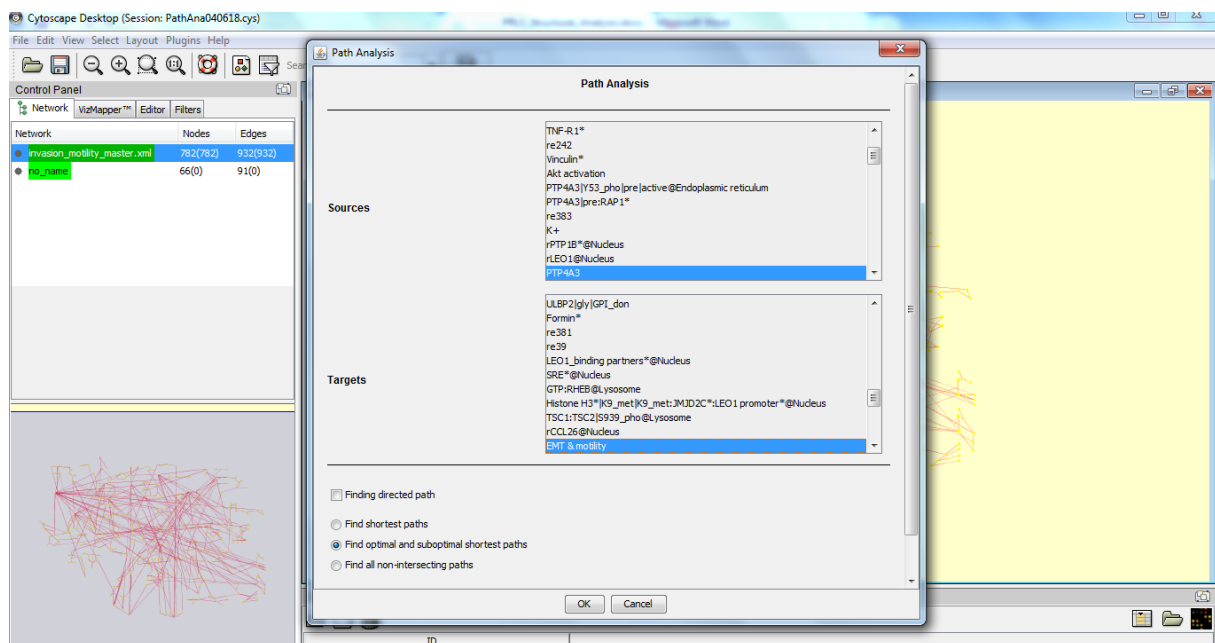


Figure 3 Path Analysis dialogue

- After the analysis is performed, the nodes that are part of the paths are highlighted. Then select the extract network option in the menu to create a new network using only the participants of the pathway of interest. In the menu Plugins>BiNoM 2.5>BiNoM Analysis>Extract subnetwork... (Figure 5)

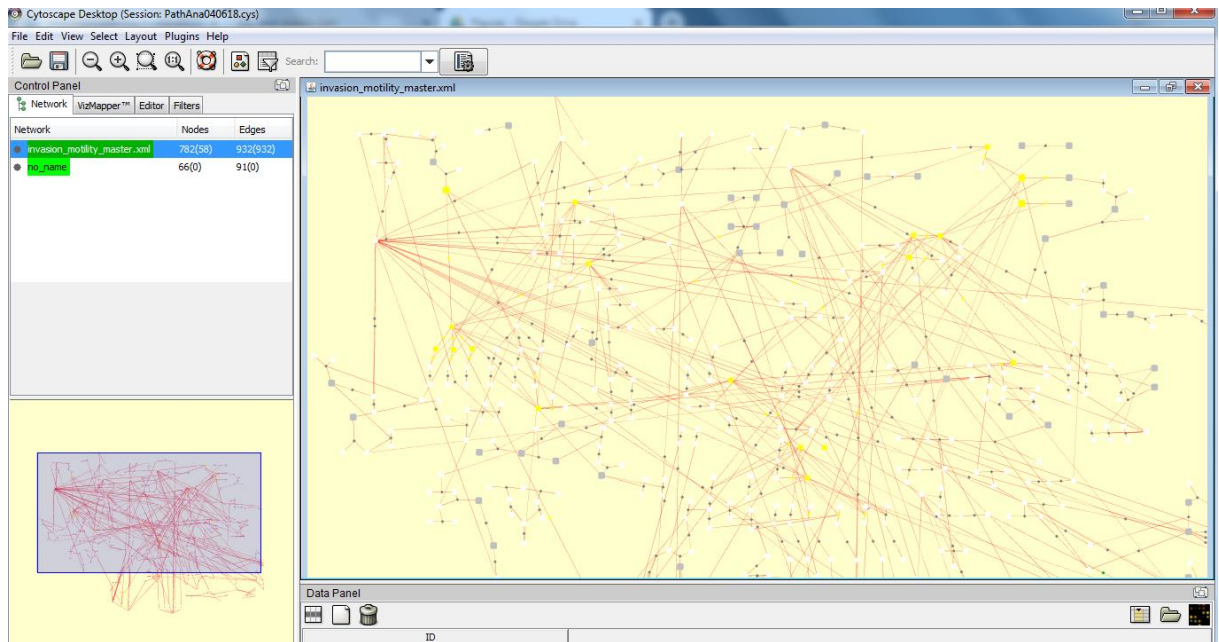


Figure 4 Path Analysis output

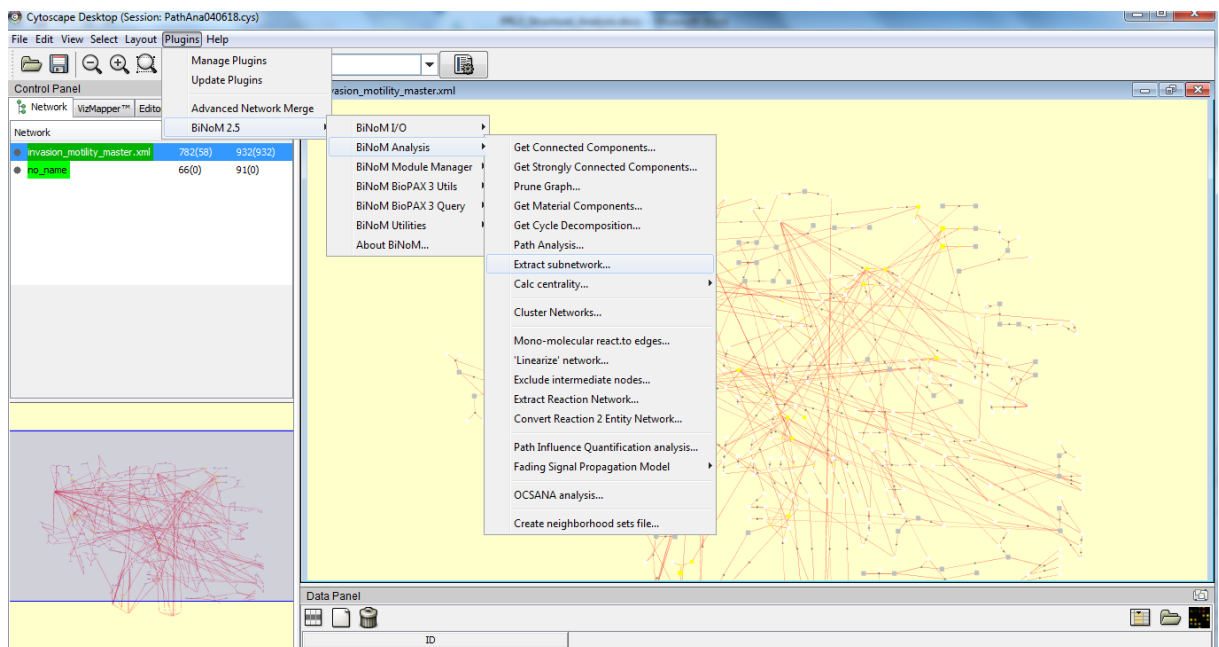


Figure 5 Selecting extract subnetwork

- Then a dialogue appears with the different options and parameters to extract the subnetwork.

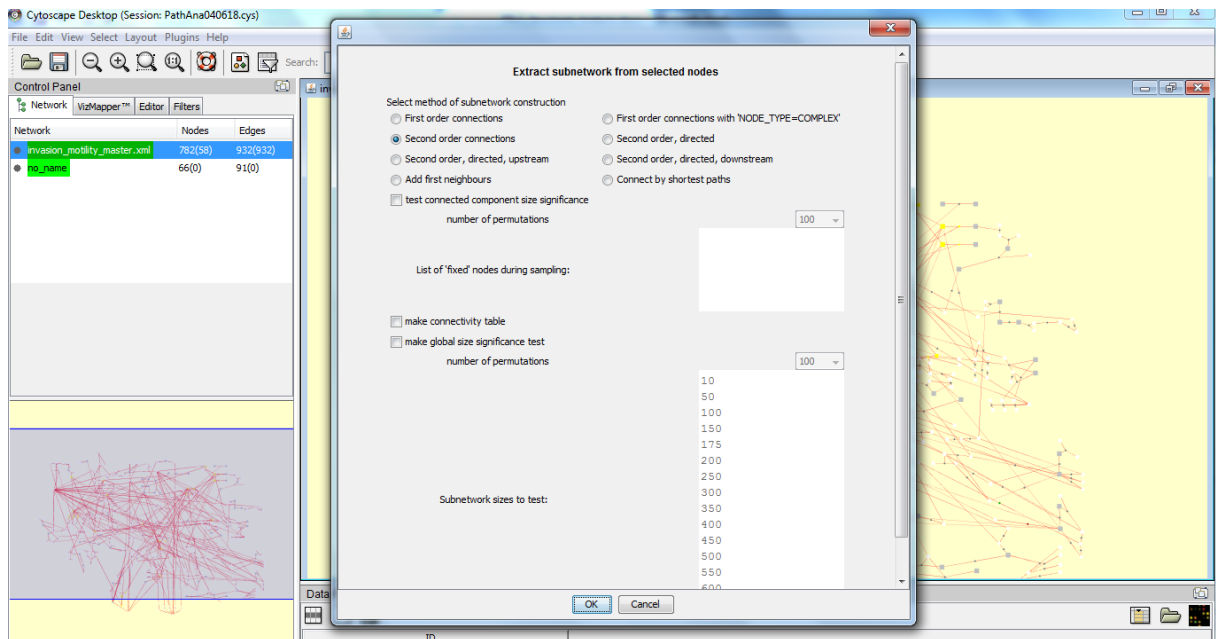


Figure 6 Menu to extract the subnetwork

- Then the extracted network appeared as a new network.

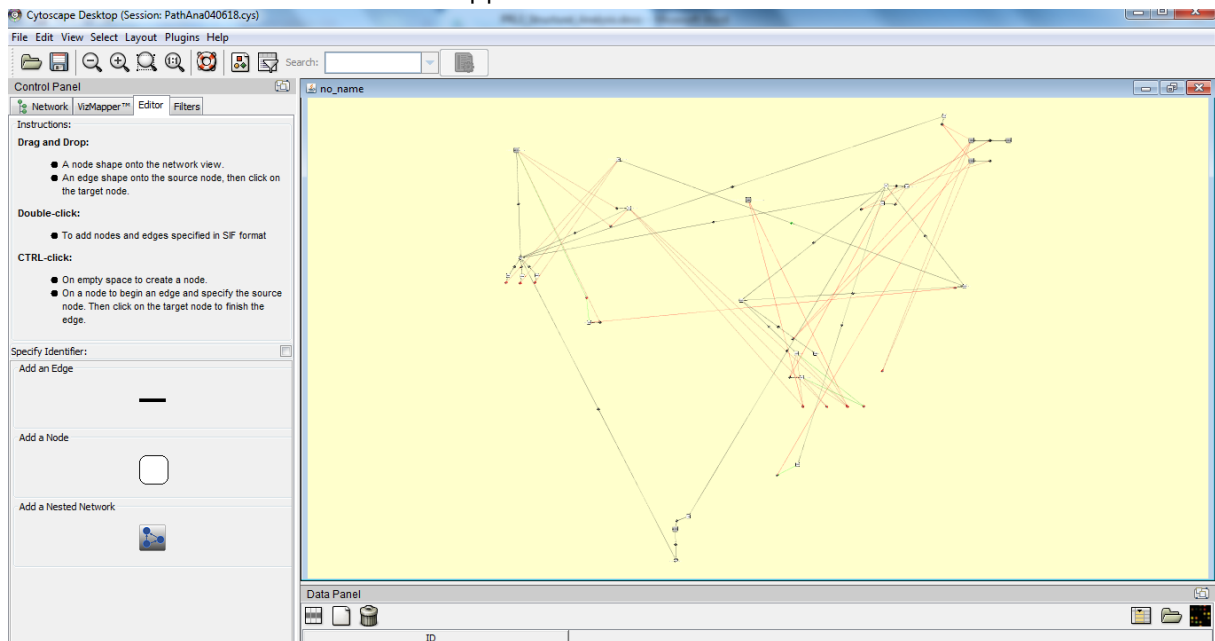


Figure 7 Extracted subnetwork

