

eXamine: Exploring annotated modules in networks

Supplemental Text

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1 Introduction

This case study demonstrates how to use eXamine to study an annotated module in Cytoscape. The module that we study has 17 nodes and 18 edges and occurs within the KEGG mouse network consisting of 3863 nodes and 29293 edges. The module is annotated with sets from four different categories: (1) KEGG pathways and the GO categories (2) molecular process, (3) biological function and (4) cellular component. To perform this use case, you need to download the following three files.

1. `edges.txt`: contains the edges of the KEGG mouse network.

<https://raw.githubusercontent.com/ls-cwi/eXamine/master/data/edges.txt>

2. `nodes_induced.txt`: contains additional node annotation and set membership information for nodes that are part of the module.

https://raw.githubusercontent.com/ls-cwi/eXamine/master/data/nodes_induced.txt

3. `sets_induced.txt`: contains additional information on the sets such as a URL, a small description and an enrichment p -value.

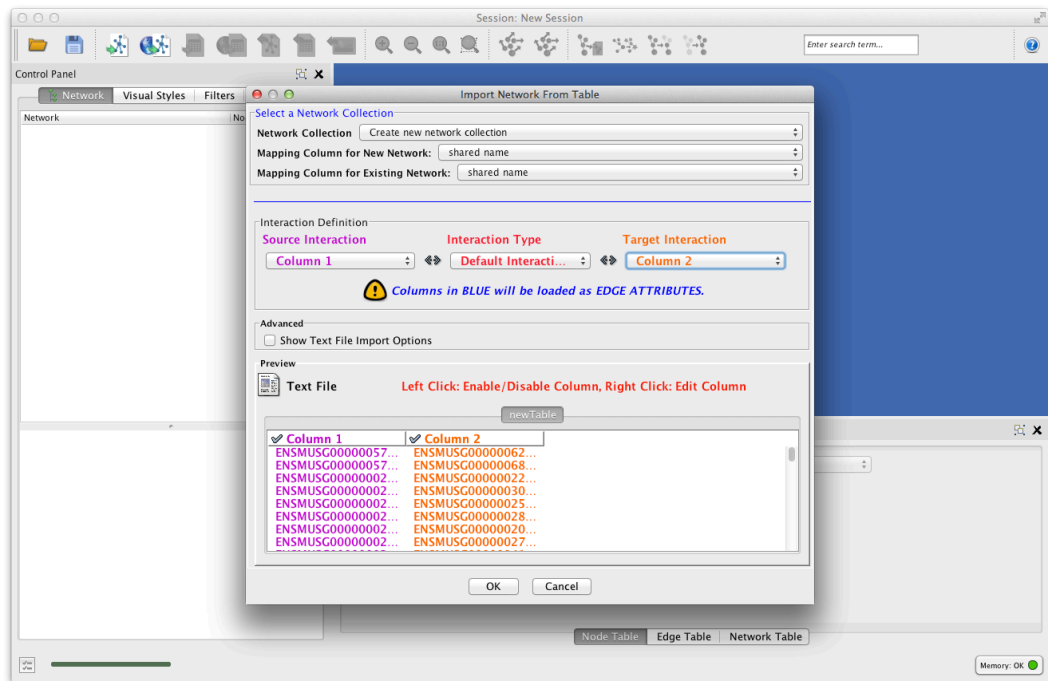
https://raw.githubusercontent.com/ls-cwi/eXamine/master/data/sets_induced.txt

2 Use case

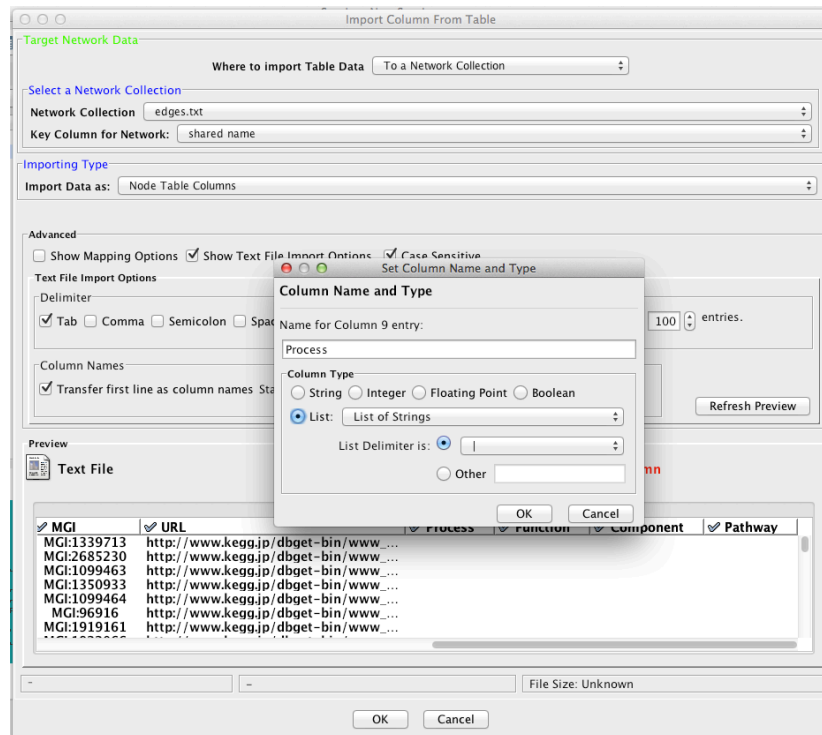
2.1 Importing edges and node annotation

In the following we give instructions for importing the edges and the node based annotation. Note that it is important to ensure that set-membership information is imported as ‘List of String’ type.

1. Start Cytoscape and close the Welcome screen.
2. Import the network defined in `edges.txt` via File → Import → Network → File...
 - (a) Set ‘Source Interaction’ to ‘Column 1’ and ‘Target Interaction’ to ‘Column 2’.



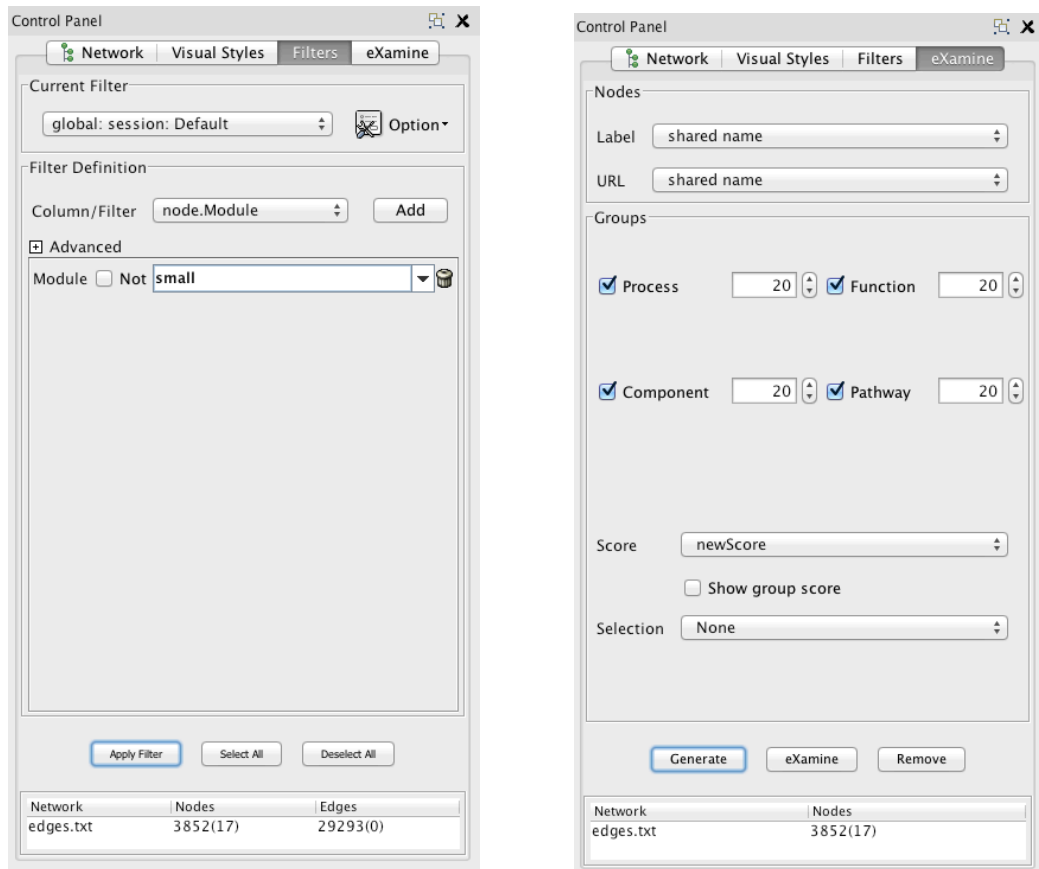
3. Import node annotation in `nodes_induced.txt` via File → Import → Table → File...
 - (a) Click on ‘Show Text File Import Options’.
 - (b) Click on ‘Transfer first line as column names’.
 - (c) Scroll all the way to the right in the table, so that the columns Process, Function, Component and Pathway are visible.
 - (d) Now right click on the column header ‘Process’.
 - (e) Set the column type to ‘List of Strings’ with ‘|’ as the delimiter and press OK.
 - (f) Repeat (d) and (e) for columns Function, Component and Pathway.
 - (g) Press OK.



2.2 Importing set annotation

In this subsection we describe how to import the set based annotations. In order to do so, eXamine needs to generate group nodes for each of the sets present in the module. Before doing so we need to select nodes present in the module; these nodes have the value 'small' in column 'Module'. We do this using Cytoscape's filter functionality.

1. Go to the 'Filters' pane in the 'Control panel'.
2. Select the column 'node.Module' and press 'Add'.
3. Select 'small' in the combo box.
4. Press 'Apply Filter'.
5. Now remove the filter by clicking on the recycle bin.



Now that we have selected the nodes of the module, we can proceed to generating group nodes for each set.

6. Go to the 'eXamine' pane in the 'Control panel'.
7. Select all four categories 'Process', 'Function', 'Component' and 'Pathway'.
8. Press 'Generate'.
9. Wait until the task 'Generate groups' is done (should take just a few seconds).

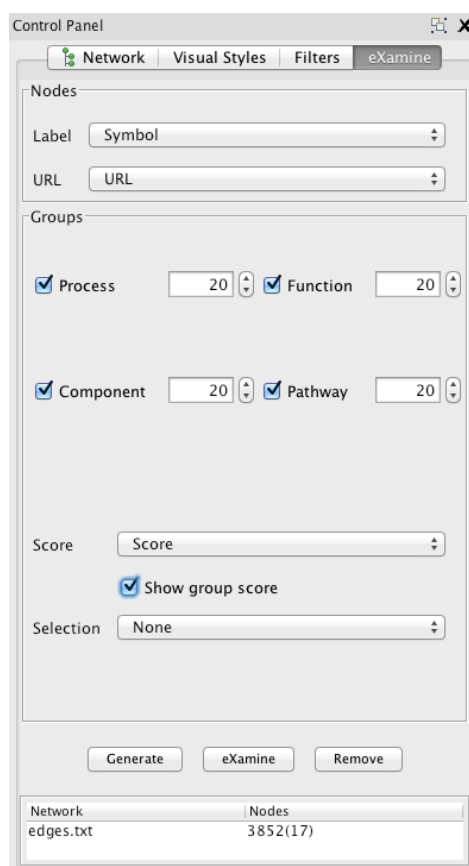
The next step is to import the set-based annotation.

10. Import node annotation in `sets_induced.txt` via File → Import → Table → File...
 - (a) Click on 'Show Text File Import Options'.
 - (b) Click on 'Transfer first line as column names'.
 - (c) Press OK.

2.3 Starting and using eXamine

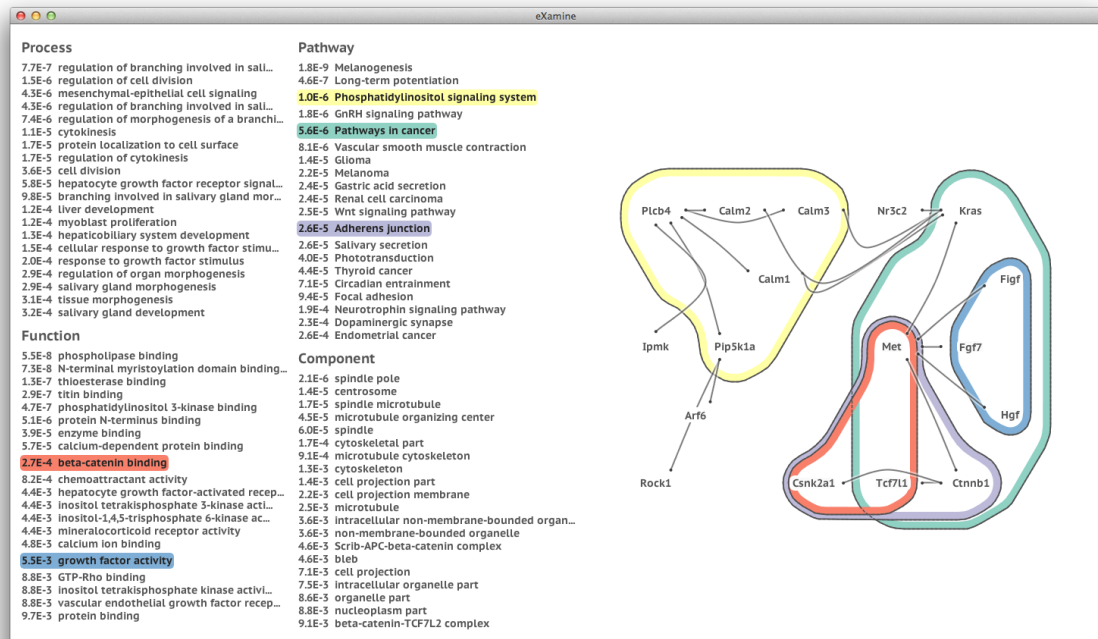
Next we describe how to start eXamine. Before doing so, make sure that the 17 nodes of the module are selected. If they are not, go to the previous sub section for instructions on how to select them.

1. Go to the 'eXamine' pane in the 'Control panel'.
2. Set 'Label' to 'Symbol'.
3. Set 'URL' to 'URL'.
4. Select all four categories 'Process', 'Function', 'Component' and 'Pathway'.
5. Set 'Score' to 'Score'.
6. Click on 'Show group score'.
7. Press 'eXamine' and maximize the new window that pops up.



In the eXamine window sets can be made active and additional information can be requested.

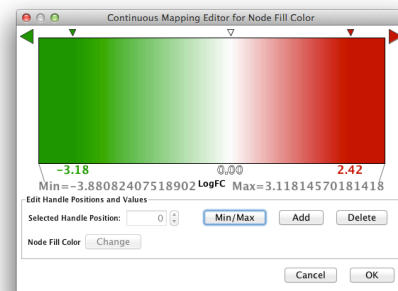
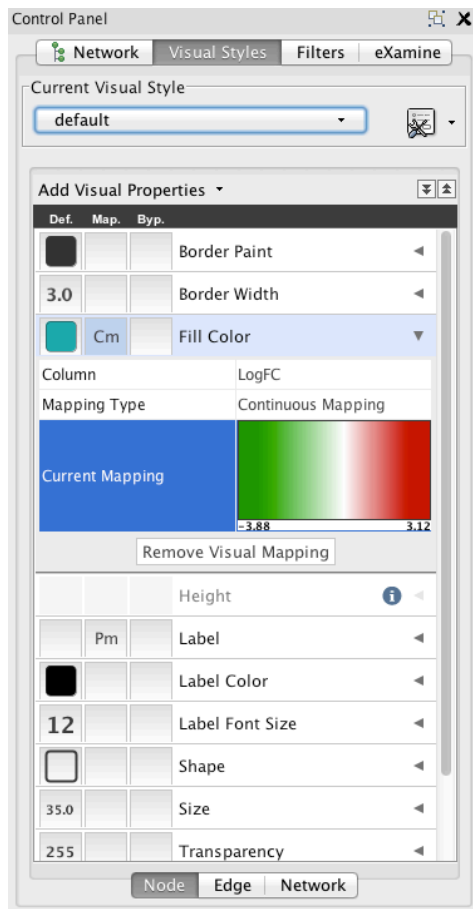
8. Select the GO terms 'beta-catenin binding', 'growth factor activity', and KEGG pathways 'Phosphatidylinositol signaling', 'Pathways in cancer', and 'Adherens junction'.



9. To adjust the set dominance of one the selected sets hover over either the set label or the corresponding contour and spin the mouse wheel.
10. Additional node information can be requested by Ctrl-clicking on a node.
11. Similarly Ctrl-clicking on a set gives additional information about that set.

To color the labels we need to set the node fill color.

12. Go to the 'Visual Styles' pane in the 'Control panel'.
13. Click on 'Fill Color'.
14. Set 'Column' to 'newScore' and 'Mapping Type' to 'Continuous Mapping'.
15. Double click on the color map.
16. Set the dialog box as follows.



17. Now the module looks as follows.

