
Community Detection APplication and Service

Release 1.10.0

May 15, 2020

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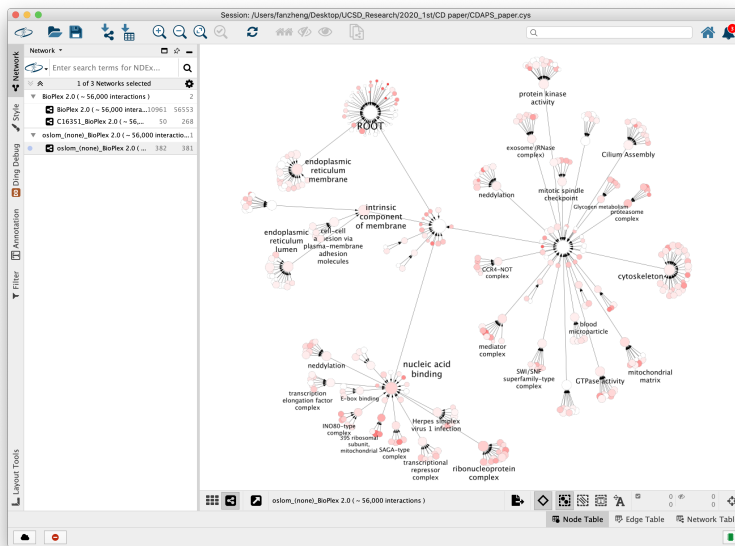
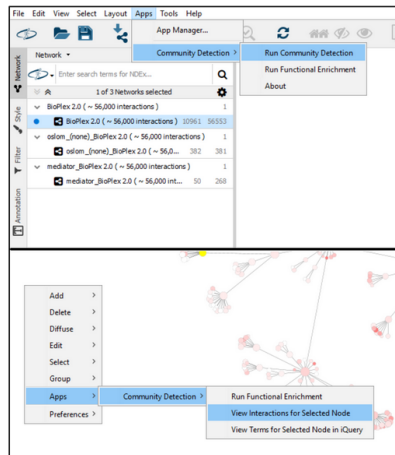
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Community Detection Application and Service (CDAPS)

CDAPS performs multiscale community detection and functional enrichment for network analysis through a service-oriented architecture. These features are provided by integrating popular community detection algorithms and enrichment tools. All the algorithms and tools run remotely on a dedicated server.

Currently supported features:

- Community detection algorithms: Louvain, Infomap, OSLOM, CliXO
- Functional enrichment tools: g:Profiler, Enrichr, iQuery



Feature Requests and Reporting Bugs

The CDAPS GitHub issue tracker can be used to report a bug or request a feature.

To Report a bug:

- Go to <https://github.com/cytoscape/cy-community-detection/issues>
- Click on *New Issue*
- Write a short description of the issue. It is very helpful to provide a series of steps that can be taken to reproduce the issue.
- If possible attach a session file (.cys) or example input files.
- Enter App version, Cytoscape version and operating system.
- Click on *Submit new issue*

Manuscript in preparation

2.1 Installation

- Cytoscape minimum version 3.7 is required.

Install Cytoscape

Download and install the latest version of Cytoscape at
<http://www.cytoscape.org/download.php>.

Install CyCommunityDetection

- Open Cytoscape
- In the main menu select **Apps > App Manager**
- In the App Manager select **CyCommunityDetection** in the list of All Apps and click the Install button.

CyCommunityDetection can also be installed from the Cytoscape App Store at
<http://apps.cytoscape.org/apps/cycommunitydetection>

2.2 What's New

2.2.1 Version 1.10.0

- Added new menu option *App -> Community Detection -> Settings* that lets caller easily change CDAPS REST server. UD-1066
- Added message letting user know using weight column in Community Detection dialog is an advanced parameter. UD-988
- In Community Detection dialog replaced **About** button with info icon next to algorithm selection dropdown. UD-987

Bug fixes

- Fixed bug where changes to properties under *Edit -> Properties -> CyCommunityDetection* were not being loaded. UD-986

2.2.2 Version 1.0

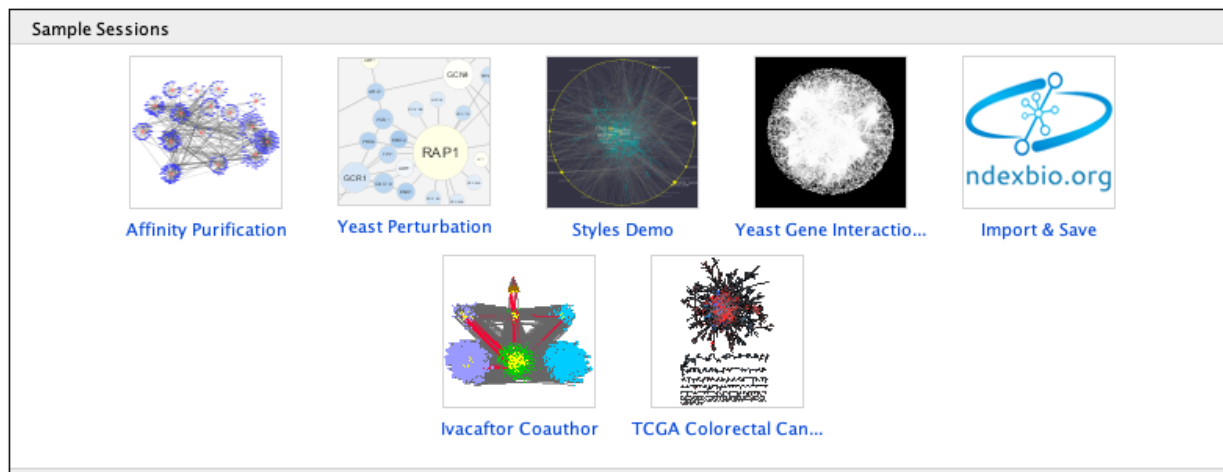
- First release

2.3 Quick Tutorial

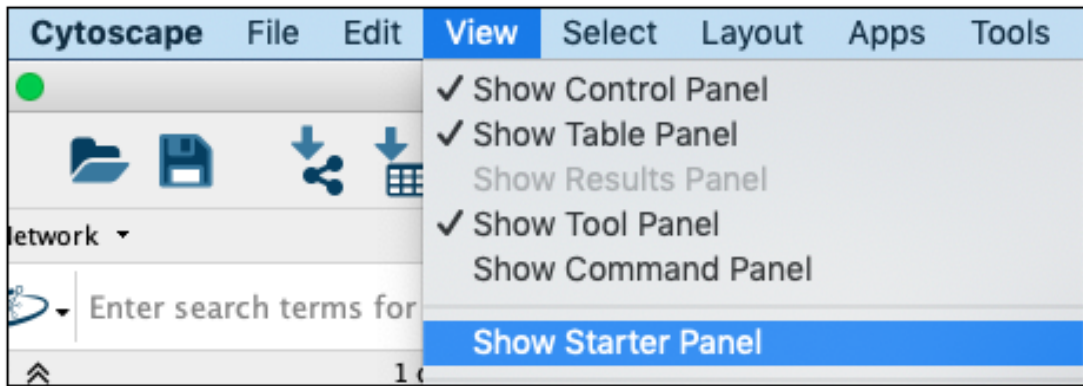
2.3.1 Open a network

To run Community Detection, a network must be loaded in Cytoscape.

From within Cytoscape click on **Affinity Purification** network on the starter panel:

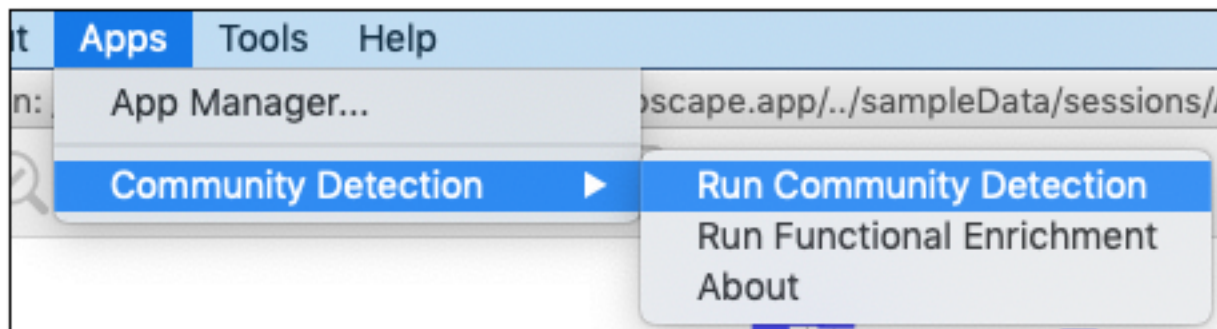


If **not** displayed, the **Starter Panel** can be displayed by invoking the menu option **View -> Show Starter Panel**.



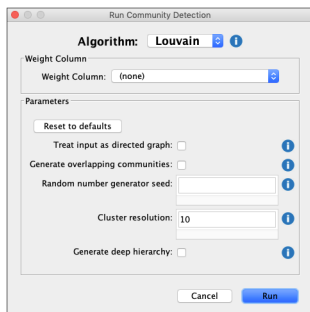
2.3.2 Run Community Detection

With the network loaded click on **Apps -> Community Detection -> Run Community Detection** menu option.

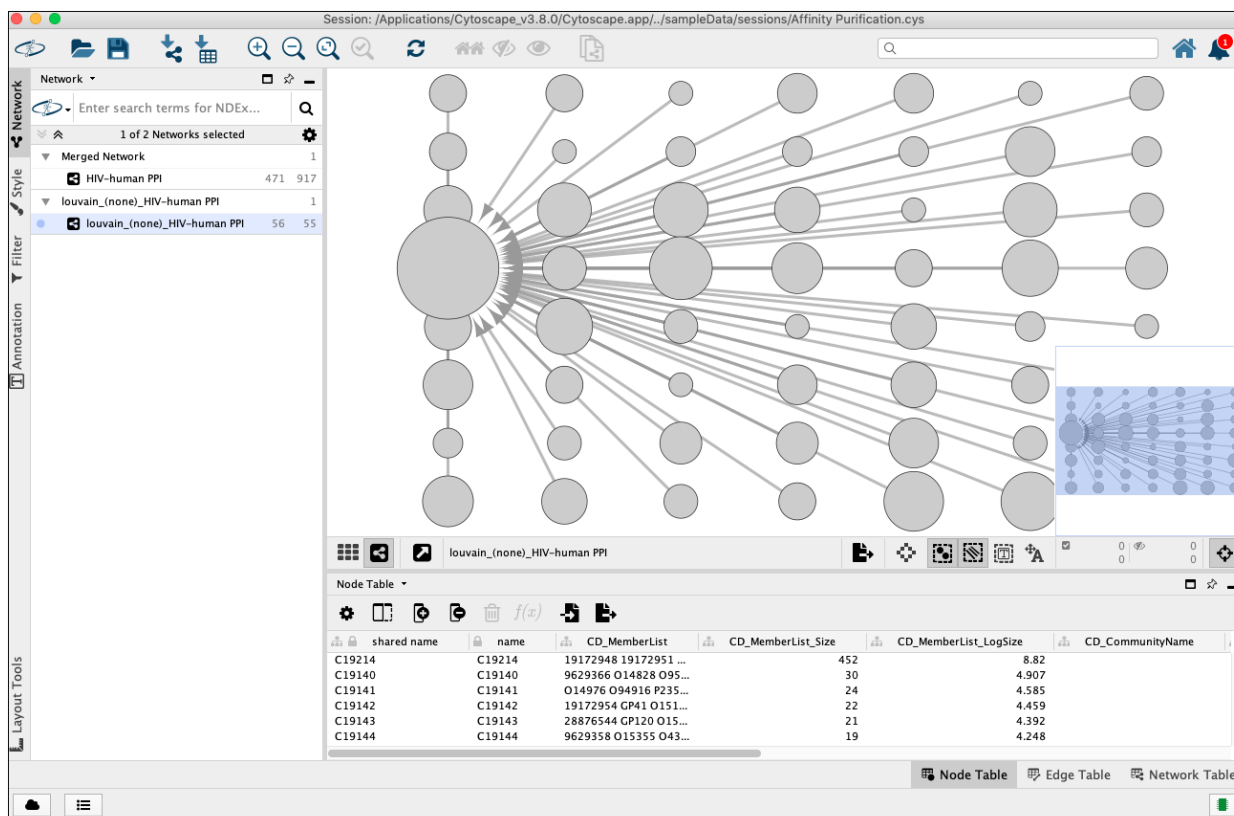


The above step will display a dialog seen below.

Select **Louvain** from algorithm dropdown and click **Run** button.



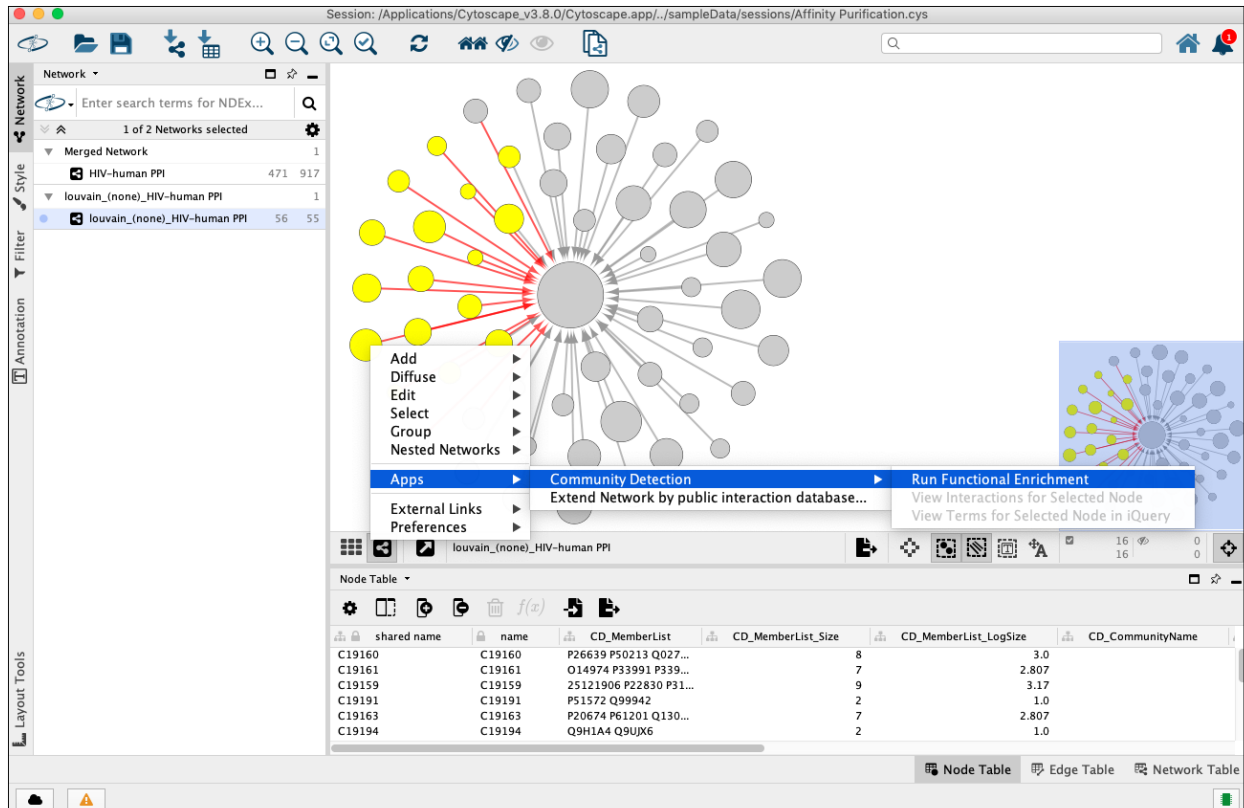
A new network/hierarchy should be generated as seen here (The current default layout will be used):



Each node in the network/hierarchy above represents a cluster with the members of that cluster set in the **CD_MemberList** node column

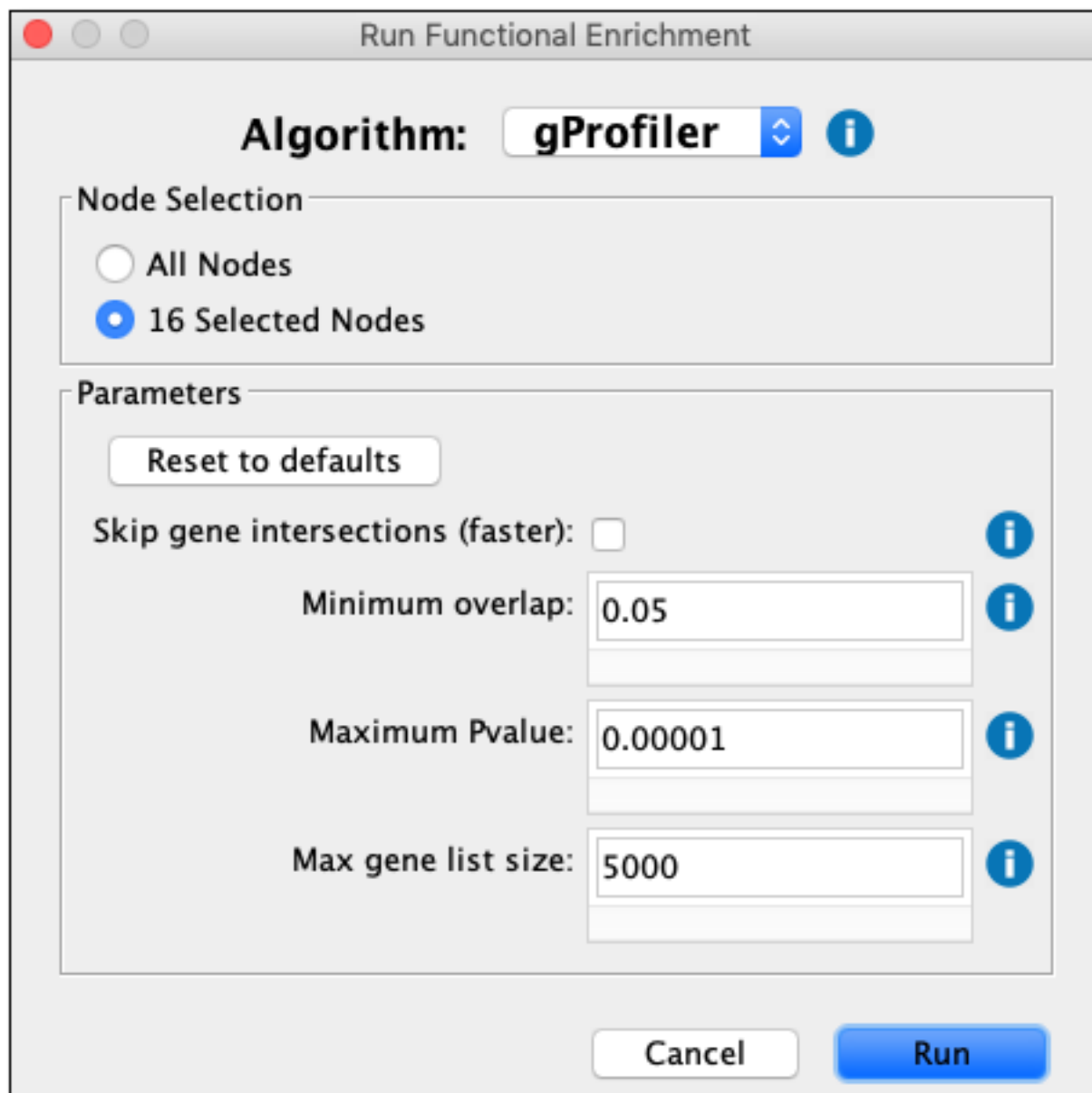
2.3.3 Perform Term Mapping

Using network/hierarchy generated above select a few nodes in the network view and then right click on a selected node to display the submenu and select **Apps -> Community Detection -> Run Functional Enrichment** as seen here:



The above step will display a dialog seen below:

Select **gProfiler** from algorithm dropdown and click **Run** button.



The image shows a 'Run Functional Enrichment' dialog box. At the top, the title bar says 'Run Functional Enrichment'. Below it, the 'Algorithm:' dropdown is set to 'gProfiler'. There are two sections: 'Node Selection' and 'Parameters'. In 'Node Selection', '16 Selected Nodes' is selected with a radio button. In 'Parameters', there is a 'Reset to defaults' button. Below it, 'Skip gene intersections (faster):' is an unchecked checkbox. 'Minimum overlap:' is a text input field with '0.05'. 'Maximum Pvalue:' is a text input field with '0.00001'. 'Max gene list size:' is a text input field with '5000'. Each of these three input fields has an information icon (i) to its right. At the bottom, there are 'Cancel' and 'Run' buttons.

Run Functional Enrichment

Algorithm: **gProfiler**

Node Selection

☐ All Nodes

☒ 16 Selected Nodes

Parameters

Reset to defaults

Skip gene intersections (faster): ☐

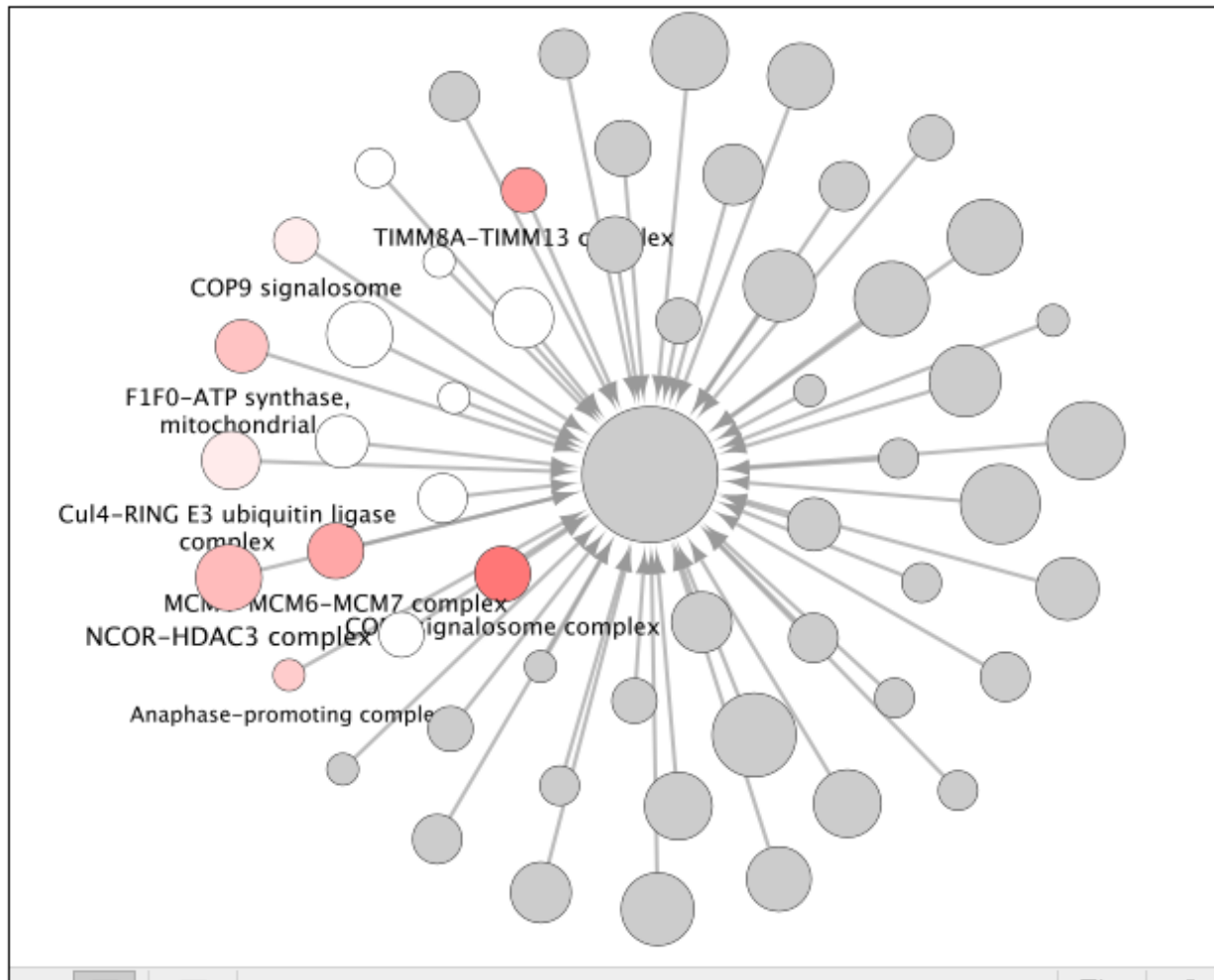
Minimum overlap: 0.05

Maximum Pvalue: 0.00001

Max gene list size: 5000

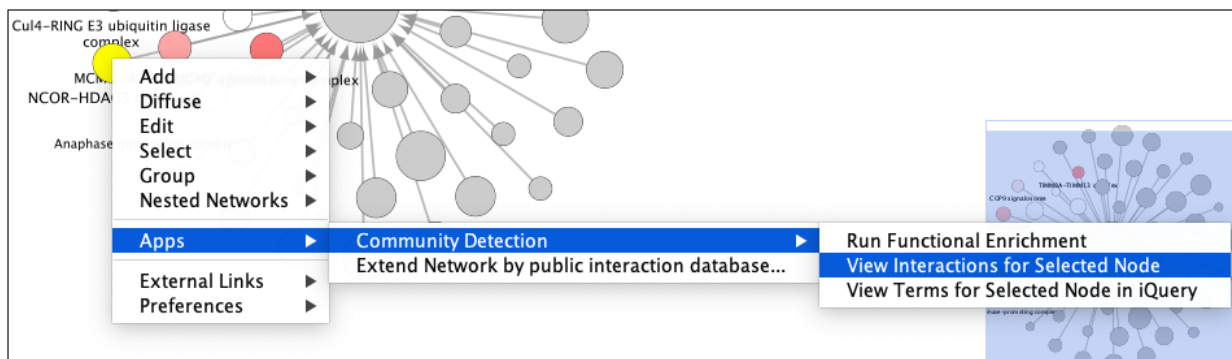
Cancel Run

gProfiler will be run and nodes will be named and colored according to overlap as seen here:

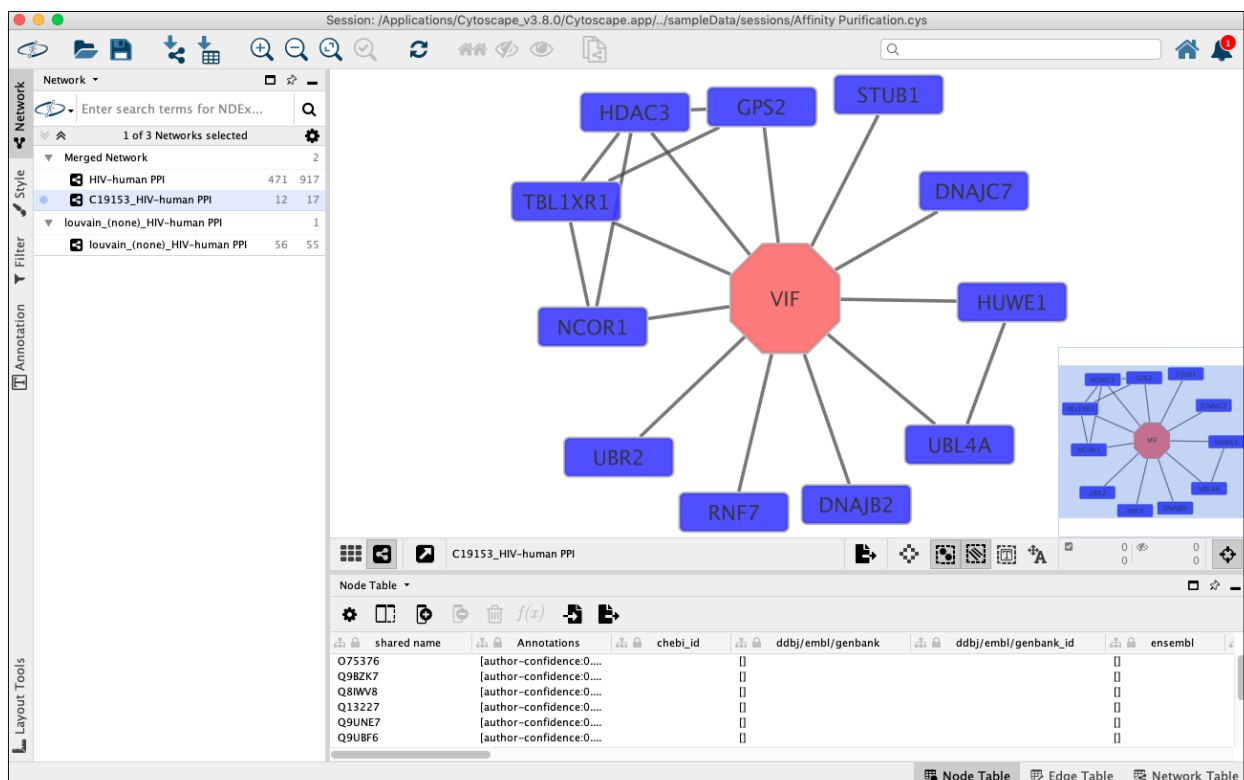


2.3.4 View Interactions

Using network/hierarchy generated above select a **single** node in the network view and then right click on the selected node to display the submenu and select **Apps -> Community Detection -> View Interactions for Selected Node**



Invoking this menu option will show all the nodes pertaining to this cluster in the parent network like as seen here:



2.3.5 Send terms in cluster to iQuery

2.4 Columns

This page describes the columns created by CDAPS in the network and node tables.

2.4.1 Network Columns

- Columns created in network table when invoking **Run Community Detection**

| Network Table | | | | | | |
|---------------|-----------|----------------------|------------------|---------------------|------------------------|-------------|
| shared name | name | __CD_OriginalNetwork | description | prov:wasDerivedFrom | prov:wasGeneratedBy | __Annotatio |
| Network | louval... | 259 | Original netw... | HIV-human PPI | App: CyCommunityDet... | [] |

- name - String in format:

Example:

- __CD_OriginalNetwork - SUID of parent network. (Bug Saving/reloading a Cytoscape session changes SUID and will cause **View Interactions for Selected Node** to fail)
- description - Contains string in this format:

Example:

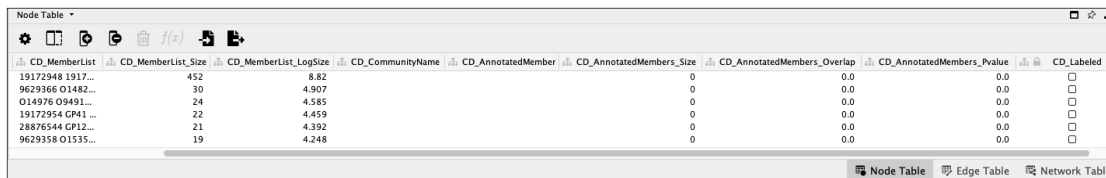
- prov:wasDerivedFrom - Name of parent network
- prov:wasGeneratedBy - Denotes version of CDAPS and algorithm used in this format:

Example:

2.4.2 Node Columns

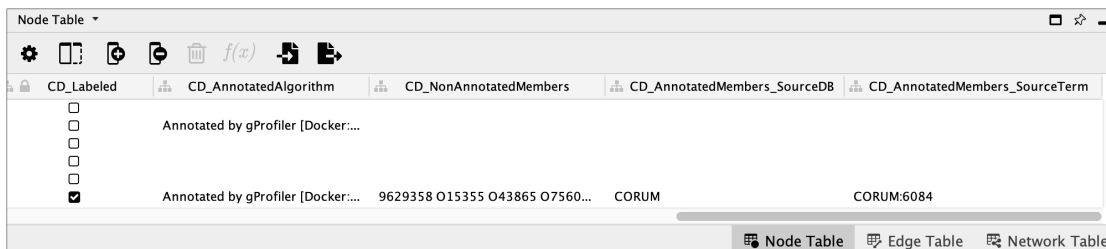
In the node table columns created by CDAPS are prefixed with CD_

- Columns created in node table when invoking **Run Community Detection**



| CD_MemberList | CD_MemberList_Size | CD_MemberList_LogSize | CD_CommunityName | CD_AnnotatedMember | CD_AnnotatedMembers_Size | CD_AnnotatedMembers_Overlap | CD_AnnotatedMembers_Pvalue | CD_Labeled |
|-------------------|--------------------|-----------------------|------------------|--------------------|--------------------------|-----------------------------|----------------------------|--------------------------|
| 19172948 1917... | 452 | 8.82 | | | 0 | 0.0 | 0.0 | <input type="checkbox"/> |
| 9629366 O1482... | 30 | 4.907 | | | 0 | 0.0 | 0.0 | <input type="checkbox"/> |
| O14976 O9491... | 24 | 4.585 | | | 0 | 0.0 | 0.0 | <input type="checkbox"/> |
| 19172954 CP41 ... | 22 | 4.459 | | | 0 | 0.0 | 0.0 | <input type="checkbox"/> |
| 28876544 CP12... | 21 | 4.392 | | | 0 | 0.0 | 0.0 | <input type="checkbox"/> |
| 9629358 O1535... | 19 | 4.248 | | | 0 | 0.0 | 0.0 | <input type="checkbox"/> |

- CD_MemberList - String of space delimited node names representing members of this cluster
- CD_MemberList_Size - Size of CD_MemberList
- CD_MemberList_LogSize - Log of CD_MemberList_Size
- CD_CommunityName - Name of community set by invocation of **Run Functional Enrichment**
- CD_AnnotatedMembers - String of space delimited node names used to set value in CD_CommunityName
- CD_AnnotatedMembers_Size - Size of CD_AnnotatedMembers
- CD_AnnotatedMembers_Overlap - CD_AnnotatedMembers_Size divided by CD_MemberList_Size
- CD_AnnotatedMembers_Pvalue - Pvalue obtained from term mapping algorithm invoked by **Run Functional Enrichment**
- CD_Labeled - Boolean denoting if CD_CommunityName was set to a value other than blank or (*none*)
- Columns created in node table when invoking **Run Functional Enrichment**



| CD_Labeled | CD_AnnotatedAlgorithm | CD_NonAnnotatedMembers | CD_AnnotatedMembers_SourceDB | CD_AnnotatedMembers_SourceTerm |
|-------------------------------------|------------------------------------|--------------------------------|------------------------------|--------------------------------|
| <input type="checkbox"/> | Annotated by gProfiler [Docker:... | | | |
| <input type="checkbox"/> | | | | |
| <input type="checkbox"/> | | | | |
| <input type="checkbox"/> | | | | |
| <input checked="" type="checkbox"/> | Annotated by gProfiler [Docker:... | 9629358 O15355 O43865 O7560... | CORUM | CORUM:6084 |

- CD_AnnotatedAlgorithm - Algorithm used to set value in CD_CommunityName in format:
Example:
- CD_NonAnnotatedMembers - String of space delimited node names **NOT** used by algorithm to set mapped term in CD_CommunityName
- CD_AnnotatedMembers_SourceDB Source database used by algorithm to set mapped term in CD_CommunityName
- CD_AnnotatedMembers_SourceTerm Id of mapped term set in CD_CommunityName