

Cytoscape for Visualisation

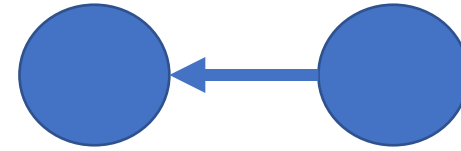


Cytoscape

- Analysing and visualising networks
 - Protein-Protein interactions
 - Gene coexpression
 - Functional Enrichments
- <https://github.com/cytoscape/cytoscape-tutorials/wiki>

Graphs/Networks

- Nodes connected by edges



- Nodes represent entities (genes, proteins, GO terms, nucleotides)
- Edges represent connections between the nodes (Pearson correlation, protein-protein interactions, the next base in a sequence)
- Can be directed or not

Cytoscape

- Load networks in various graph formats (sif, graphML, GML, BioPax)

Session: New Session

Control Panel

Network Style Select Annotation

Enter search terms for NDEx...

Drag network files here

Welcome to Cytoscape

Recent Sessions

- 5dpf_uninf_vs_5dpf_...
- 7dpf_uninf_hom_vs_...
- 7dpf_uninf_hom_vs_...
- 5dpf_uninf_hom_vs_...
- 5dpf_inf_hom_vs_5d...
- 3dpf_uninf_hom_vs_...

Sample Sessions

- Affinity Purification
- Import & Save
- Ivacaftor Coauthor
- Styles Demo
- TCGA Colorectal Can...
- Yeast Gene Interactio...
- Yeast Perturbation

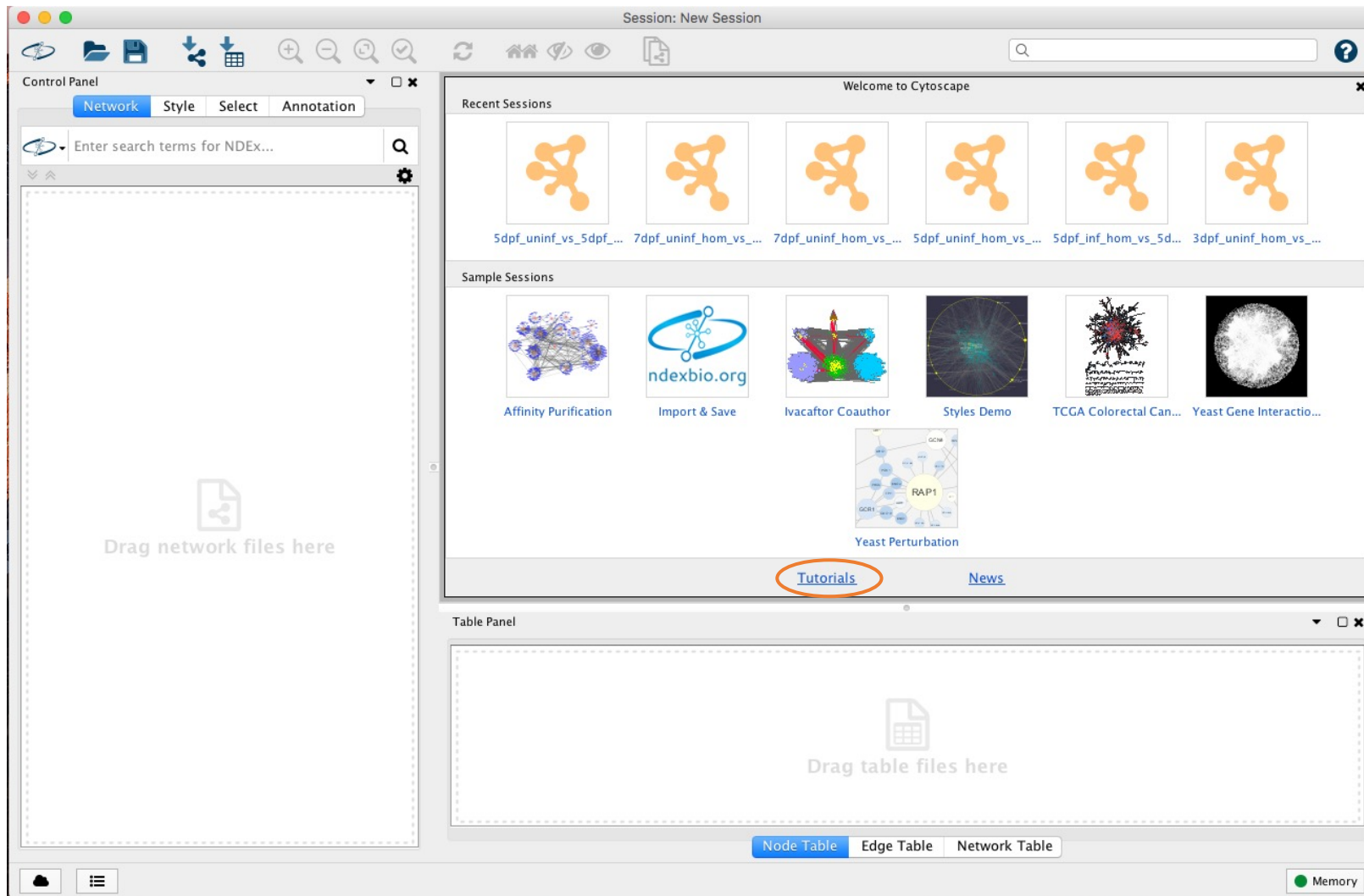
Tutorials News

Table Panel

Drag table files here

Node Table Edge Table Network Table

Memory



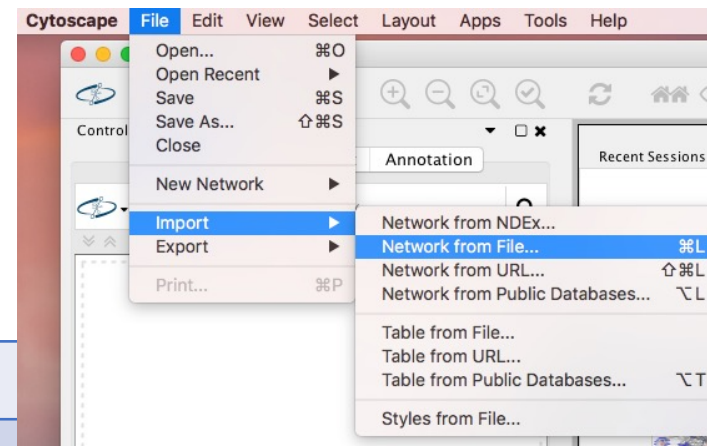
Loading Networks

- Simplest format is Simple interaction file (.sif)
- columns are:
 - Source Node
 - relationship type
 - Target Node

ENSDARG00000099966	geneExprCor	ENSDARG00000095904
ENSDARG00000099966	geneExprCor	ENSDARG00000086425
ENSDARG00000099966	geneExprCor	ENSDARG000000104899
ENSDARG00000070656	geneExprCor	ENSDARG00000038066
ENSDARG00000070656	geneExprCor	ENSDARG00000019339
ENSDARG00000070656	geneExprCor	ENSDARG00000095743

Loading Networks

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ENSDARG00000099966	geneExprCor	
ENSDARG00000099966	geneExprCor	ENSDARG00000086425
ENSDARG00000099966	geneExprCor	ENSDARG00000104899
ENSDARG00000070656	geneExprCor	ENSDARG00000038066
ENSDARG00000070656	geneExprCor	ENSDARG00000019339
ENSDARG00000070656	geneExprCor	ENSDARG00000095743

Loading Networks

The screenshot displays a software interface for network visualization. The main window is titled "Session: New Session". The interface is divided into several panels:

- Control Panel:** Located on the left, it includes tabs for "Network", "Style", "Select", and "Annotation". Below these is a search bar labeled "Enter search terms for NDEx..." and a list of networks. One network is selected: "3dpf_uninf_hom_vs_3dpf_uninf_sib.sif" with 205 nodes and 1154 edges.
- Network View:** The central area shows a complex network graph with blue square nodes and black edges. The graph consists of several interconnected clusters. A smaller inset window in the bottom right of the network view shows a zoomed-in view of a specific cluster.
- Table Panel:** Located at the bottom, it displays a table with two columns: "shared name" and "name". The table contains several rows of data, all starting with "ENSDARG" followed by a unique identifier.

At the bottom of the interface, there are tabs for "Node Table", "Edge Table", and "Network Table", with "Node Table" currently selected. A "Memory" indicator is visible in the bottom right corner.

shared name	name
ENSDARG0000099...	ENSDARG...
ENSDARG0000012...	ENSDARG...
ENSDARG0000095...	ENSDARG...
ENSDARG0000086...	ENSDARG...
ENSDARG0000104...	ENSDARG...
ENSDARG0000070...	ENSDARG...
ENSDARG0000038...	ENSDARG...

Loading Networks

The screenshot displays a network visualization application window titled "Session: New Session". The interface is divided into several panels:

- Control Panel:** Located on the left, it includes tabs for "Network", "Style", "Select", and "Annotation". A search bar is present with the text "Enter search terms for NDEx...". Below it, a list shows "1 of 1 Network selected" with the file "3dpf_uninf_hom_vs_3dpf_uninf_sib.sif" selected.
- Main View:** The central area displays a network graph with nodes represented by blue rounded rectangles and edges as black lines. Nodes are labeled with IDs such as ENSDARG00000105586, ENSDARG0000009660, ENSDARG00000035559, ENSDARG0000012261, ENSDARG0000009966, ENSDARG0000007996, ENSDARG0000004044, ENSDARG00000086425, ENSDARG00000104644, ENSDARG00000058328, ENSDARG00000055838, ENSDARG00000095046, ENSDARG00000033440, ENSDARG00000024277, and ENSDARG00000000000. A small inset graph in the bottom right shows a broader view of the network structure.
- Table Panel:** Located at the bottom, it contains a table with two columns: "shared name" and "name". The table lists several ENSDARG IDs, with some truncated.
- Bottom Bar:** Includes a "Table Panel" header, a toolbar with icons for settings, table management, and a function $f(x)$, and tabs for "Node Table", "Edge Table", and "Network Table". A "Memory" indicator is visible in the bottom right corner.

Add extra node/edge information

- Extra node information can be imported from a file containing a column that matches the node names

Gene ID	GeneName	log2fc	adjp
ENSDARG00000099966	polr2a	0.773509255	1.32E-49
ENSDARG00000070656	si:ch211-69g19.2	-0.583759051	2.25E-15
ENSDARG00000038066	kpna2	-0.520683514	5.79E-14
ENSDARG00000037551	pm20d1.1	2.334699018	6.79E-11

Add extra node/edge information

- Extra node information can be imported from a file containing a column that matches the node names

Gene ID	GeneName	log2fc	adjp
ENSDARG00000099966	polr2a	0.773509255	1.32E-49
ENSDARG00000070656	si:ch211-69g19.2		2.25E-15
ENSDARG00000038066	kpna2		5.79E-14
ENSDARG00000037551	pm20d1.1		6.79E-11

Cytoscape File Edit View Select Layout Apps Tools Help

- Open... ⌘O
- Open Recent ▶
- Save ⌘S
- Save As... ⌘⇧S
- Close
- New Network ▶
- Import ▶
 - Network from NDEx...
 - Network from File... ⌘L
 - Network from URL... ⌘⇧L
 - Network from Public Databases... ⌘⇧L
 - Table from File... ⌘T
 - Table from URL...
 - Table from Public Databases... ⌘⇧T
- Export
- Print... ⌘P

Annotation Recent Sessions

Click on a column to edit it.

Gene ID	GeneName	log2fc	adjp
ENSDARG00000099966	polr2a	0.773509255	1.32E-49
ENSDARG00000070656	si:ch211-69g19.2		2.25E-15
ENSDARG00000038066	kpna2		5.79E-14
ENSDARG00000037551	pm20d1.1		6.79E-11

Meaning: 785513 6.79094625076733e-1

Data Type: 391158 2.2605168978616e-1

53485 4.27154668735411e-1

List Delimiter: [ab] [1] [123] [1.0] [y/n]

Advanced Options... Cancel OK

Add extra node/edge information

The screenshot displays a network visualization software interface. The main window shows a network graph with blue square nodes and black edges. The interface includes a Control Panel on the left with tabs for Network, Style, Select, and Annotation. Below the Control Panel is a search bar and a list of networks. The Table Panel at the bottom displays a table with columns for shared name, name, GeneNan, log2fc, and adjp. The table contains several rows of data, including gene names like polr2a, eftud2, prpf31, prpf3, CR9318, si:ch211, and kpna2, along with their corresponding log2fc and adjp values.

Control Panel

Network Style Select Annotation

Enter search terms for NEx...

1 of 1 Network selected

3dpf_uninf_hom_vs_3dpf_uninf_sib.sif

3dpf_uninf_hom_vs_3dpf_uninf_sib.sif 205 1154

Table Panel

shared name	name	GeneNan	log2fc	adjp
ENSDARG00000099...	ENSDARG...	polr2a	0.77350...	1.31750...
ENSDARG00000012...	ENSDARG...	eftud2	0.43041...	7.06488...
ENSDARG00000095...	ENSDARG...	prpf31	0.47628...	4.21870...
ENSDARG00000086...	ENSDARG...	prpf3	0.46136...	4.21870...
ENSDARG00000104...	ENSDARG...	CR9318...	2.66209...	0.00525...
ENSDARG00000070...	ENSDARG...	si:ch211...	-0.5837...	2.25336...
ENSDARG00000038...	ENSDARG...	kpna2	-0.5206...	5.78969...

Node Table Edge Table Network Table

Memory

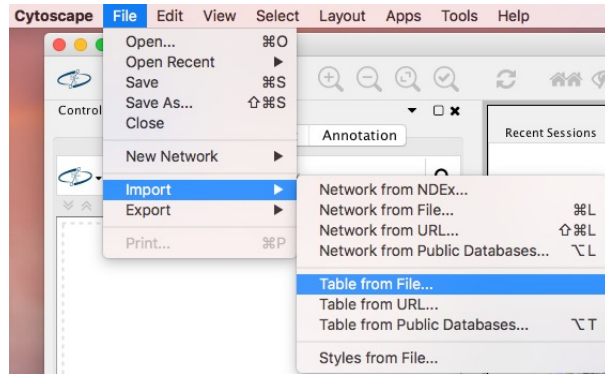
Add extra node/edge information

- Extra edge information can be imported in the same way

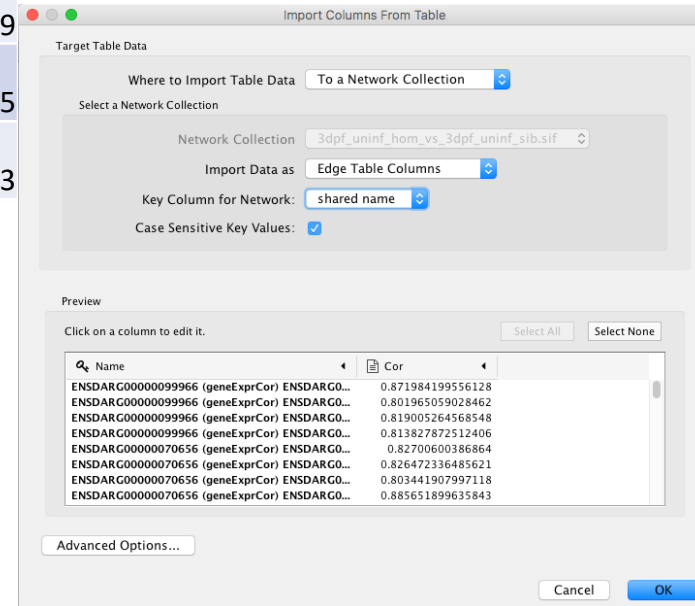
Name	Cor
ENSDARG00000099966 (geneExprCor) ENSDARG00000012261	0.8719842
ENSDARG00000099966 (geneExprCor) ENSDARG00000095904	0.801965059
ENSDARG00000099966 (geneExprCor) ENSDARG00000086425	0.819005265
ENSDARG00000099966 (geneExprCor) ENSDARG000000104899	0.813827873

Add extra node/edge information

- Extra edge information can be imported in the same way



Name	Cor
ENSDARG00000099966 (geneExprCor) ENSDARG00000012261	0.8719842
ENSDARG00000099966 (geneExprCor) ENSDARG00000095904	0.801965059
ENSDARG00000099966 (geneExprCor) ENSDARG00000086425	0.819005265
ENSDARG00000099966 (geneExprCor) ENSDARG000000104899	0.813827873



Add extra node/edge information

The screenshot displays a software interface for network analysis. The main window shows a network graph with blue square nodes and black edges. The interface includes a top toolbar with various icons, a search bar, and a 'Control Panel' on the left. The 'Control Panel' has tabs for 'Network', 'Style', 'Select', and 'Annotation'. Below these tabs is a search field and a list of networks. The selected network is '3dpf_uninf_hom_vs_3dpf_uninf_sib.sif' with 205 nodes and 1154 edges. The 'Table Panel' at the bottom displays a table of data for the selected network.

shared name	shared interaction	name	interaction	Cor
ENSDARG000000099...	geneExprCor	ENSDARG...	geneExprCor	0.87198...
ENSDARG000000099...	geneExprCor	ENSDARG...	geneExprCor	0.80196...
ENSDARG000000099...	geneExprCor	ENSDARG...	geneExprCor	0.81900...
ENSDARG000000099...	geneExprCor	ENSDARG...	geneExprCor	0.81382...
ENSDARG000000070...	geneExprCor	ENSDARG...	geneExprCor	0.82700...
ENSDARG000000070...	geneExprCor	ENSDARG...	geneExprCor	0.82647...
ENSDARG000000070...	geneExprCor	ENSDARG...	geneExprCor	0.80344...

At the bottom of the interface, there are tabs for 'Node Table', 'Edge Table', and 'Network Table', with 'Edge Table' currently selected. A 'Memory' indicator is visible in the bottom right corner.

Add styles to nodes

The screenshot displays a network visualization application window titled "Session: New Session". The interface is divided into several panels:

- Control Panel:** Contains tabs for "Network", "Style", "Select", and "Annotation". The "Style" tab is active, showing a "default" style. The "Properties" section includes:
 - Border Paint:** A color selection box.
 - Border Width:** A numeric input set to 0.0.
 - Fill Color:** A color selection box currently set to blue.
 - Column:** A dropdown menu set to "log2fc".
 - Mapping Type:** A dropdown menu set to "Continuous Mapping".
 - Current Mapping:** A color gradient bar ranging from -4.29 (blue) to 4.29 (red).
 - Height:** A numeric input set to 35.0.
 - Image/Chart 1:** A selection box.
 - Label:** A selection box.
 - Label Color:** A color selection box.
 - Label Font Size:** A numeric input set to 12.
 - Shape:** A selection box.
 - Size:** A selection box.
 - Transparency:** A numeric input set to 255.
 - Width:** A numeric input set to 75.0.
- Network View:** A central area showing a network graph with nodes colored according to the "log2fc" mapping. A smaller inset view shows a different style for the same network.
- Table Panel:** A data table at the bottom right, titled "3dpf_uninf_hom_vs_3dpf_uninf_sib.sif". It has columns for "shared name", "name", "GeneNan", "log2fc", and "adjp".

shared name	name	GeneNan	log2fc	adjp
ENSDARG00000099...	ENSDARG... polr2a	0.77350...	1.31750...	
ENSDARG00000012...	ENSDARG... eftud2	0.43041...	7.06488...	
ENSDARG00000095...	ENSDARG... prpf31	0.47628...	4.21870...	
ENSDARG00000086...	ENSDARG... prpf3	0.46136...	4.21870...	
ENSDARG00000104...	ENSDARG... CR9318...	2.66209...	0.00525...	
ENSDARG00000070...	ENSDARG... si:ch211...	-0.5837...	2.25336...	
ENSDARG00000038...	ENSDARG... kpna2	-0.5206...	5.78969...	

At the bottom of the interface, there are tabs for "Node Table", "Edge Table", and "Network Table", with "Node Table" selected. A "Memory" indicator is visible in the bottom right corner.

Add styles to nodes

The screenshot displays a network visualization application window titled "Session: New Session". The interface is divided into several panels:

- Control Panel:** Located on the left, it has tabs for "Network", "Style", "Select", and "Annotation". The "Style" tab is active, showing a "default" style. The "Properties" section includes:
 - Border Paint: [Color swatch]
 - Border Width: 0.0
 - Fill Color: [Color swatch]
 - Height: 35.0
 - Image/Chart 1: [Image swatch]
 - Label: [Color swatch]
 - Column: GeneName
 - Mapping Type: Passthrough Mapping
 - Label Color: [Color swatch]
 - Label Font Size: 12
 - Shape: [Shape swatch]
 - Size: [Value]
 - Transparency: 255
 - Width: 75.0
 - Lock node width and height
- Network View:** The central area shows a network graph with nodes colored in red and blue. A search bar is located at the top right of this panel.
- Table Panel:** Located at the bottom, it displays a table of node data. The table has columns for "shared name", "name", "GeneName", "log2fc", and "adjp".

shared name	name	GeneName	log2fc	adjp
ENSDARG00000099...	ENSDARG...	polr2a	0.77350...	1.31750...
ENSDARG00000012...	ENSDARG...	eftud2	0.43041...	7.06488...
ENSDARG00000095...	ENSDARG...	prpf31	0.47628...	4.21870...
ENSDARG00000086...	ENSDARG...	prpf3	0.46136...	4.21870...
ENSDARG00000104...	ENSDARG...	CR9318...	2.66209...	0.00525...
ENSDARG00000070...	ENSDARG...	si:ch211...	-0.5837...	2.25336...
ENSDARG00000038...	ENSDARG...	kpna2	-0.5206...	5.78969...

At the bottom of the interface, there are tabs for "Node Table", "Edge Table", and "Network Table", with "Node Table" currently selected. A "Memory" indicator is visible in the bottom right corner.

Add styles to nodes

The screenshot displays a network visualization application with a control panel on the left and a network graph on the right. The control panel is titled "Control Panel" and has tabs for "Network", "Style", "Select", and "Annotation". The "Style" tab is active, showing a "default" style. The "Properties" section includes various settings for nodes, such as "Border Paint", "Border Width", "Fill Color", "Height", "Image/Chart 1", "Label", "Label Color", "Label Font Size", "Shape", "Size", "Transparency", and "Width". The "Label" property is currently set to "GeneName". The network graph shows a complex network of nodes and edges. The nodes are labeled with gene names and identifiers, including "hoxc1a", "prpf3", "CABZ01085177.1", "tp53", "mettl16", "bmb", "prpf31", "ism7", "snrp2", "snrpd2", "eftud2", "polr2a", "CT583723.2", "no14la", "BX255967.1", and "3bc10.1". The graph is titled "3dpf_uninf_hom_vs_3dpf_uninf_sib.sif".

Table Panel

shared name	name	GeneName	log2fc	adjp
ENSDARG00000113...	ENSDARG...	si:dkey-...	1.70419...	0.00681...

Add styles to nodes

Session: New Session

Control Panel

Network Style Select Annotation

default

Properties

Def.	Map.	Byp.	Property	Value
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Border Paint	◀
0.0	<input type="checkbox"/>	<input type="checkbox"/>	Border Width	◀
<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Fill Color	◀
35.0	<input type="checkbox"/>	<input type="checkbox"/>	Height	◀
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Image/Chart 1	◀
<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Label	◀
<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	Label Color	◀
12	<input type="checkbox"/>	<input type="checkbox"/>	Label Font Size	◀
<input type="checkbox"/>	<input checked="" type="checkbox"/>	<input type="checkbox"/>	Shape	◅

Column: log2fc

Mapping Type: Continuous Mapping

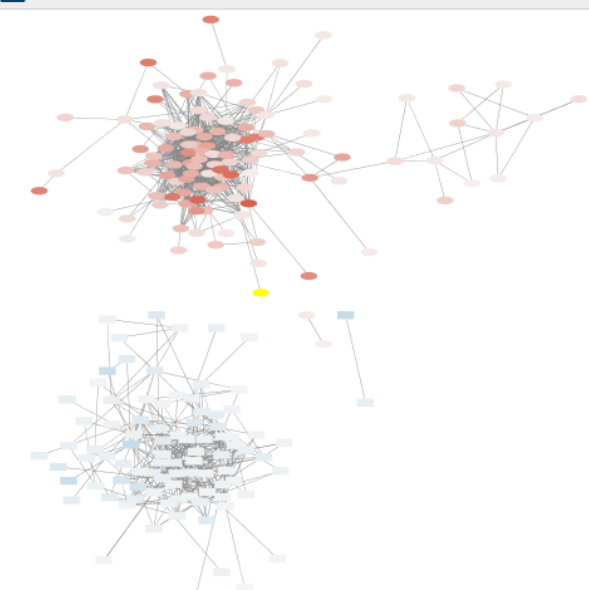
Current Mapping: -1.20 4.29

Size: ⓘ ◀

255 Transparency ◀

75.0 Width ◀

Node Edge Network



3dpf_uninf_hom_vs_3dpf_uninf_sib

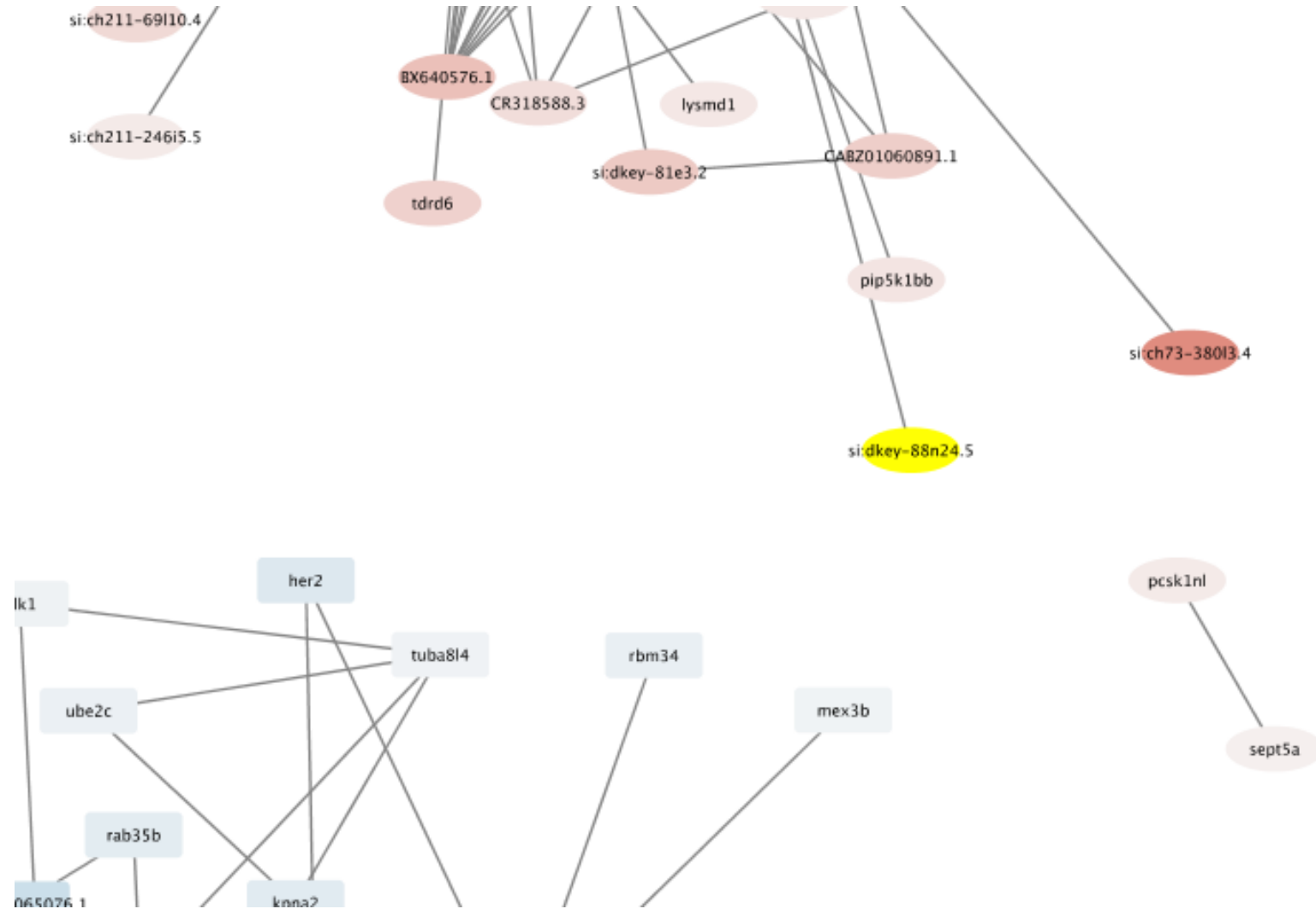
Table Panel

shared name	name	GeneNar	log2fc	adjp
ENSDARG00000113...	ENSDARG...	si:key-...	1.70419...	0.00681...

Node Table Edge Table Network Table

Memory

Add styles to nodes

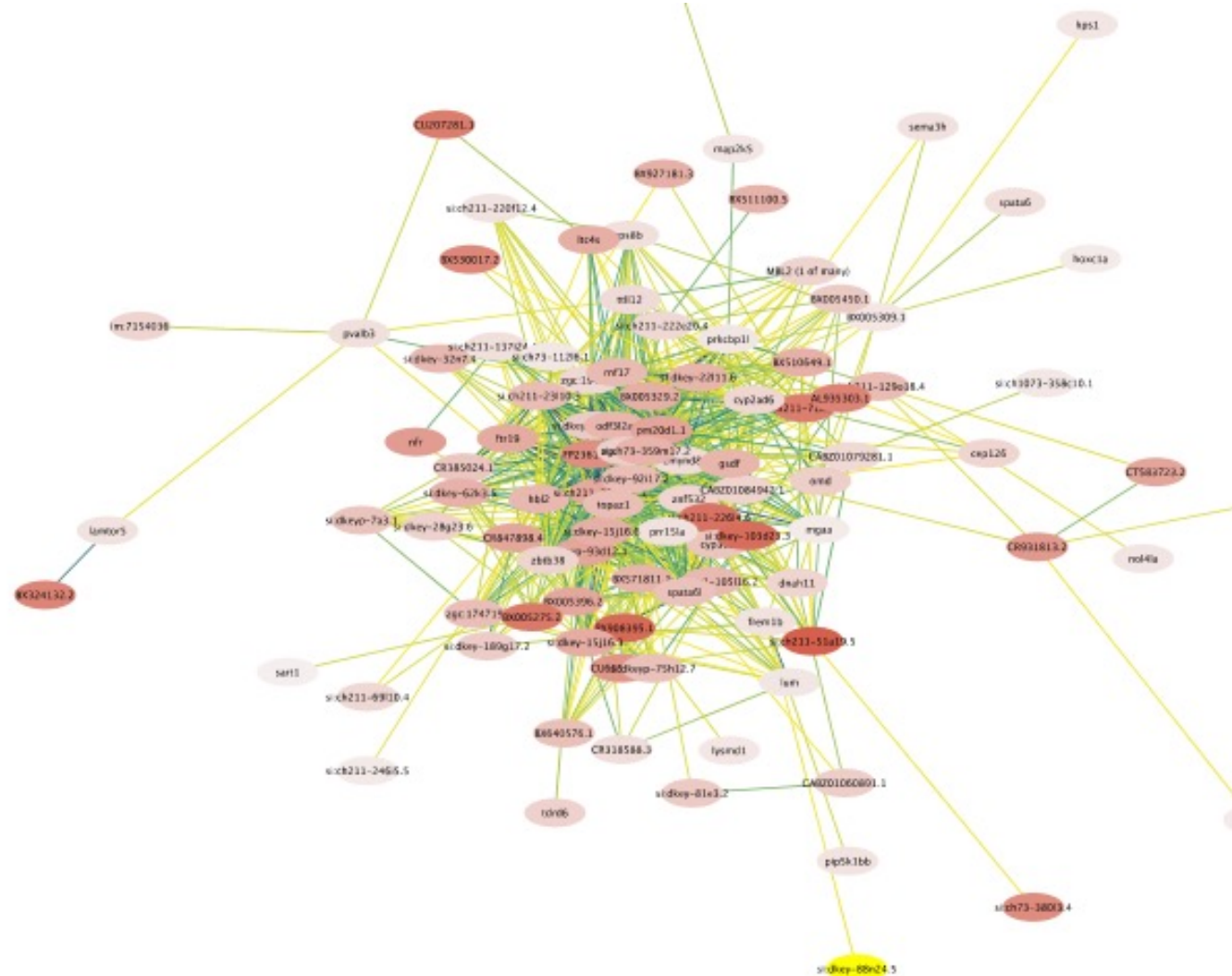


Add styles to edges

The screenshot displays a network visualization application window titled "Session: New Session". The interface is divided into several panels:

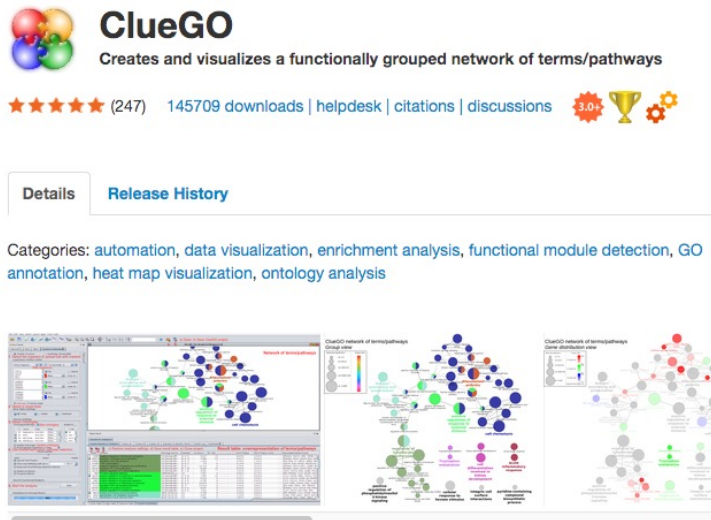
- Control Panel:** Located on the left, it has tabs for "Network", "Style", "Select", and "Annotation". The "Style" tab is active. It shows a dropdown menu set to "default" and a "Properties" section with sub-tabs "Def.", "Map.", and "Byp.". The "Color (Unselected)" property is selected, showing a "Column" of "Cor" and a "Mapping Type" of "Continuous Mapping". A color gradient bar is visible under "Current Mapping". Other properties listed include Label, Label Color, Label Font Size (set to 10), Line Type, Source Arrow Shape (set to None), Source Arrow Unselected Paint, Stroke Color (Unselected), Target Arrow Shape (set to None), Target Arrow Unselected Paint, Transparency (set to 255), and Width (set to 2.0).
- Network View:** The central area shows a network graph with nodes and edges. The nodes are colored in a gradient from yellow to red, and the edges are yellow. There are two distinct clusters of nodes.
- Table Panel:** Located at the bottom, it displays a table with columns: "shared name", "name", "GeneNan", "log2fc", and "adjp". The first row of data is: ENSDARG00000113..., ENSDARG..., sid:key-..., 1.70419..., 0.00681....
- Bottom Bar:** Contains tabs for "Node Table", "Edge Table", and "Network Table", with "Node Table" selected. A "Memory" indicator is visible in the bottom right corner.

Add styles to edges



ClueGO

- Cytoscape App for visualising functional enrichments
 - GO/KEGG/Reactome etc.
 - <http://www.ici.upmc.fr/cluego/cluegoDocumentation.shtml>
- Groups terms to identify non-redundant terms



ClueGO
Creates and visualizes a functionally grouped network of terms/pathways

★★★★★ (247) 145709 downloads | [helpdesk](#) | [citations](#) | [discussions](#) 3.0+

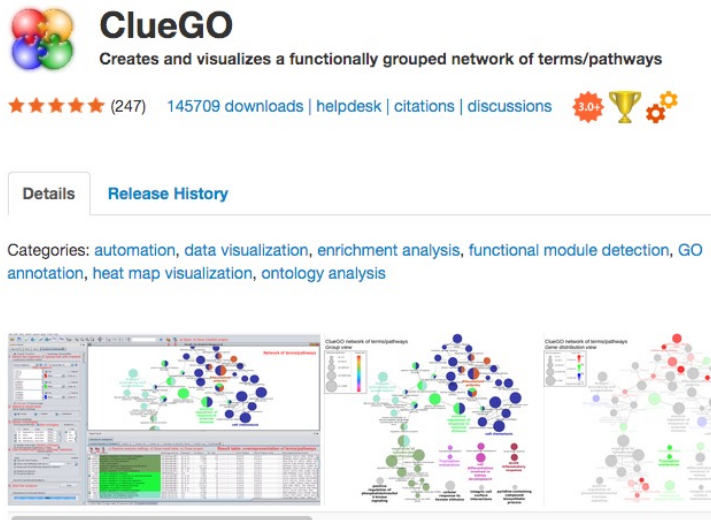
Details **Release History**

Categories: [automation](#), [data visualization](#), [enrichment analysis](#), [functional module detection](#), [GO annotation](#), [heat map visualization](#), [ontology analysis](#)

The screenshot displays the ClueGO software interface. It features a central network visualization of terms, with nodes represented by colored circles and edges connecting them. The interface includes a sidebar with various controls and a main window showing the network. Below the network, there are two smaller panels showing different views of the network, including a heat map and a list of terms.

ClueGO

- Cytoscape App for visualising functional enrichments
 - GO/KEGG/Reactome etc.
 - <http://www.ici.upmc.fr/cluego/cluegoDocumentation.shtml>
- Groups terms to identify non-redundant terms



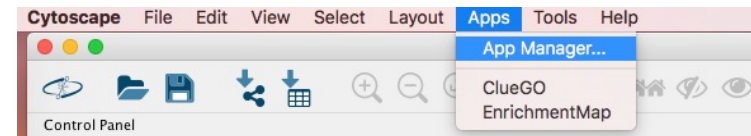
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Details **Release History**

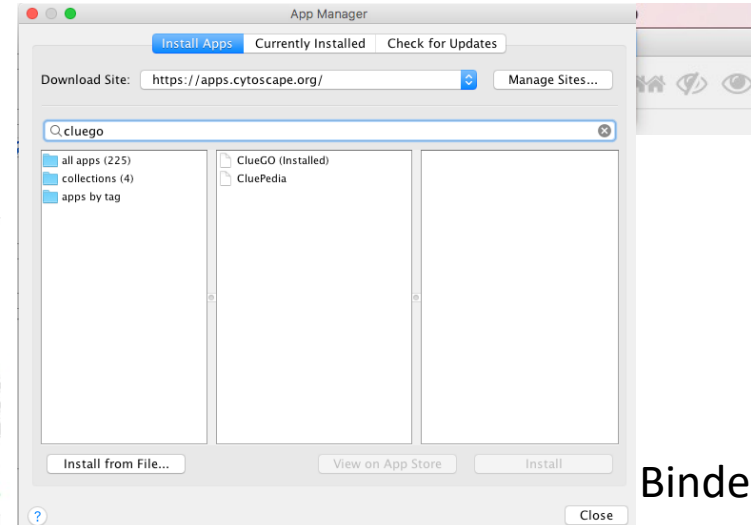
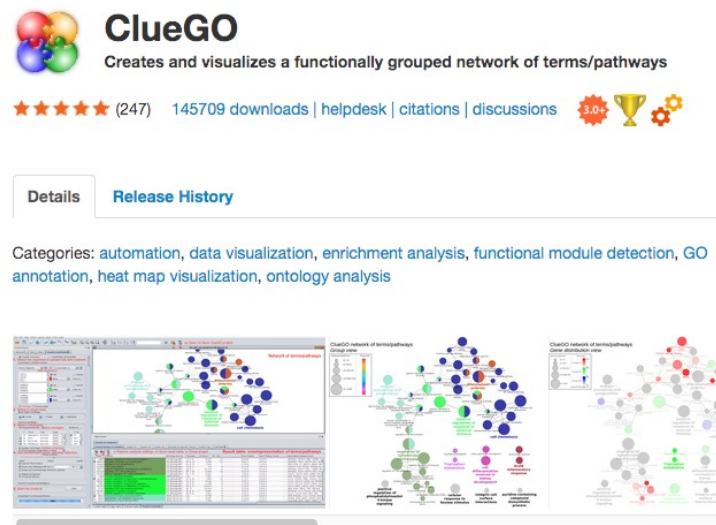
Categories: [automation](#), [data visualization](#), [enrichment analysis](#), [functional module detection](#), [GO annotation](#), [heat map visualization](#), [ontology analysis](#)

The screenshot shows the ClueGO application interface. It features a network visualization of terms, with nodes representing terms and edges representing relationships. The interface includes a control panel on the left and a main window displaying the network. The network is composed of various colored nodes and connecting lines, representing functional groupings of terms.



ClueGO

- Cytoscape App for visualising functional enrichments
 - GO/KEGG/Reactome etc.
 - <http://www.ici.upmc.fr/cluego/cluegoDocumentation.shtml>
- Groups terms to identify non-redundant terms



Bindea et al. 2009

ClueGO

The screenshot shows the Cytoscape software interface with the ClueGO application manager open. The ClueGO application manager is a window titled "Session: New Session" and contains a "Welcome to Cytoscape" message. It features a search bar, a "Recent Sessions" section with five thumbnails (including "Styles Demo.cys", "inf_5dpf_hom_vs_sib...", "3dpf_uninf_hom_vs_...", "5dpf_inf_hom_vs_5d...", and "5dpf_uninf_vs_5dpf_..."), and a "Sample Sessions" section with five thumbnails (including "Affinity Purification", "Import & Save", "Ivacaftor Coauthor", "Styles Demo", and "TCGA Colorectal Can..."). Below the sample sessions are two more thumbnails for "Yeast Gene Interactio..." and "Yeast Perturbation". At the bottom of the ClueGO window are links for "Tutorials" and "News".

The Cytoscape interface includes a menu bar (File, Edit, View, Select, Layout, Apps, Tools, Help) and a toolbar. The "Apps" menu is open, showing "App Manager...", "ClueGO", and "EnrichmentMap". The "Control Panel" is visible, showing "Network", "Style", "Select", "Annotation", and "ClueGO" tabs. The "ClueGO v2.5.5" panel is active, displaying "Analysis Mode" (ClueGO: Functional Analysis, CluePedia: Genes/miRNAs), "Check out CluePedia as well!" (To visualize Genes along with Pathways ->), "Load Marker List(s)" (Homo Sapiens [9606]), "Visual Style" (Groups), and "ClueGO Settings" (Ontologies/Pathways, Evidence, Network Specificity).

The "Table Panel" is visible at the bottom, showing a "Drag table files here" message and buttons for "Node Table", "Edge Table", and "Network Table". A "Memory" indicator is also present in the bottom right corner.

ClueGO

Cytoscape File Edit View Select Layout Apps Tools Help

Session: New Session

Control Panel

Network Style Select Annotation ClueGO

ClueGO v2.5.5

Analysis Mode
ClueGO: Functional Analysis Preselected Functions
CluePedia: Genes/miRNAs

Check out CluePedia as well!
To visualize Genes along with Pathways -> [App Store](#)

Load Marker List(s)
Homo Sapiens [9606] # Automatic #
File Network

Visual Style
 Groups Significance

ClueGO Settings

Ontologies/Pathways

...	Name	#	Date	Shape
<input type="checkbox"/>	C... Huma...	5...	04.09....	
<input type="checkbox"/>	C... CORU...	3...	04.09....	
<input type="checkbox"/>	C... Chrom...	2...	27.02....	
<input checked="" type="checkbox"/>	GO Biolog...	1...	27.02....	
<input type="checkbox"/>	GO Cellul...	2...	27.02....	
<input type="checkbox"/>	GO Immu...	1...	27.02....	

Evidence

Code
<input checked="" type="checkbox"/> All
<input type="checkbox"/> All_Experimental_(EXP_IDA...
<input type="checkbox"/> All_without_IEA
<input type="checkbox"/> EXP (Inferred from Experim...
<input type="checkbox"/> IBA (Inferred from Biologic...
<input type="checkbox"/> IBD (Inferred from Biologic...

Update Ontologies
Download New Organisms or Data

Network Specificity
Global Medium Detailed

Use GO Term Fusion
 Show only Pathways with pV ≤ 0.05000

Recent Sessions
Welcome to Cytoscape

Styles Demo.cys inf_5dpf_hom_vs_sib... 3dpf_uninf_hom_vs_... 5dpf_inf_hom_vs_5d... 5dpf_uninf_vs_5dpf_...

Sample Sessions
Affinity Purification Import & Save Ivacraft Coauthor Styles Demo TCGA Colorectal Can...
Yeast Gene Interactio... Yeast Perturbation

Tutorials News

Table Panel
Drag table files here

Node Table Edge Table Network Table

Memory

ClueGO

Cytoscape File Edit View Select Layout Apps Tools Help

Session: New Session

Control Panel

Network Style Select Annotation ClueGO

ClueGO v2.5.5

Analysis Mode

ClueGO: Functional Analysis Preselected Functions

CluePedia: Genes/miRNAs

Check out CluePedia as well!

To visualize Genes along with Pathways -> [App Store](#)

Load Marker List(s)

Homo Sapiens [9606] # Automatic #

File Network

Visual Style

Groups Significance

ClueGO Settings

Ontologies/Pathways

...	Name	#	Date	Shape
<input type="checkbox"/>	C... Huma...	5...	04.09...	
<input type="checkbox"/>	C... CORU...	3...	04.09...	
<input type="checkbox"/>	C... Chrom...	2...	27.02...	
<input checked="" type="checkbox"/>	GO Biolog...	1...	27.02...	
<input type="checkbox"/>	GO Cellul...	2...	27.02...	
<input type="checkbox"/>	GO Immu...	1...	27.02...	

Evidence

Code

- All
- All_Experimental_(EXP,IDA...
- All_without_IEA
- EXP (Inferred from Experim...
- IBA (Inferred from Biologic...
- IBD (Inferred from Biologic...

Update Ontologies

Download New Organisms or Data

Network Specificity

Global Medium Detailed

Use GO Term Fusion

Show only Pathways with pV ≤ 0.05000

Recent Sessions

Welcome to Cytoscape

Styles Demo.cys inf_5dpf_hom_vs_sib... 3dpf_uninf_hom_vs_... 5dpf_inf_hom_vs_5d... 5dpf_uninf_vs_5dpf_...

Sample Sessions

Affinity Purification Import & Save Ivacaftor Coauthor Styles Demo TCGA Colorectal Can... Yeast Gene Interactio... Yeast Perturbation

[Tutorials](#) [News](#)

Table Panel

Drag table files here

Node Table Edge Table Network Table

Memory

ClueGO

Cytoscape File Edit View Select Layout Apps Tools Help

Session: New Session

Control Panel

Network Style Select Annotation ClueGO

ClueGO v2.5.5

Analysis Mode

ClueGO: Functional Analysis Preselected Functions

CluePedia: Genes/miRNAs

Check out CluePedia as well!

To visualize Genes along with Pathways -> [App Store](#)

Load Marker List(s)

Danio rerio [7955] # Automatic #

File Network

Visual Style

Groups Significance

ClueGO Settings

Ontologies/Pathways

T...	Name	#	Date	Shape
<input type="checkbox"/>	Chr...Chromosom...2...		27.03.2019	El...
<input checked="" type="checkbox"/>	GO BiologicalPr... 1...		27.03.2019	El...
<input checked="" type="checkbox"/>	GO CellularCo... 1...		27.03.2019	El...
<input type="checkbox"/>	GO ImmuneSyst... 5...		27.03.2019	El...
<input checked="" type="checkbox"/>	GO MolecularF... 3...		27.03.2019	El...
<input checked="" type="checkbox"/>	KEGG/KEGG	1...	27.03.2019	

Evidence

Code
<input checked="" type="checkbox"/> All
<input type="checkbox"/> All_Experimental_(EXP,IDA,IP,I,IMP,I,GI,I,EP)
<input type="checkbox"/> All_without_IJA
<input type="checkbox"/> EXP (Inferred from Experiment)
<input type="checkbox"/> IBA (Inferred from Biological Aspect of Ancestor)
<input type="checkbox"/> IBD (Inferred from Biological Aspect of Descende...

Update Ontologies

Download New Organisms or Data

Network Specificity

Global Medium Detailed

Use GO Term Fusion

Show only Pathways with pV ≤ 0.05000

Recent Sessions

Welcome to Cytoscape

Styles Demo.cys inf_5dpf_hom_vs_sib... 3dpf_uninf_hom_vs_... 5dpf_inf_hom_vs_5d...

Sample Sessions

Affinity Purification Import & Save Ivacaftor Coauthor Styles Demo

Tutorials News

Table Panel

Drag table files here

Node Table Edge Table Network Table

Memory

ClueGO

Cytoscape File Edit View Select Layout Apps Tools Help

Session: New Session

Control Panel

Network Style Select Annotation ClueGO

ClueGO v2.5.5

Analysis Mode

ClueGO: Functional Analysis Preselected Functions

CluePedia: Genes/miRNAs

Check out CluePedia as well!

To visualize Genes along with Pathways -> [App Store](#)

Load Marker List(s)

Danio rerio [7955] # Automatic #

ENSDARG00000117609
ENSDARG00000117610
ENSDARG00000117812

File Network

Visual Style

Groups Significance

ClueGO Settings

Ontologies/Pathways

T...	Name	#	Date	Shape	El...
<input type="checkbox"/>	Chr... Chromosom...		27.03.2019	El...	
<input checked="" type="checkbox"/>	GO BiologicalPr...	1...	27.03.2019	El...	
<input checked="" type="checkbox"/>	GO CellularCo...	1...	27.03.2019	El...	
<input type="checkbox"/>	GO ImmuneSyst...	5...	27.03.2019	El...	
<input checked="" type="checkbox"/>	GO MolecularF...	3...	27.03.2019	El...	
<input checked="" type="checkbox"/>	KEGG KEGG	1...	27.03.2019		

Evidence

Code

- All
- All_Experimental_(EXP,IDA,IPI,IMP,IGI,IJP)
- All_without_IEA
- EXP (Inferred from Experiment)
- IBA (Inferred from Biological Aspect of Ancestor)
- IBD (Inferred from Biological Aspect of Descende...

Update Ontologies

Download New Organisms or Data

Network Specificity

Global Medium Detailed

Use GO Term Fusion

Show only Pathways with pV ≤ 0.05000

Welcome to Cytoscape

Recent Sessions

Styles Demo.cys inf_5dpf_hom_vs_sib... 3dpf_uninf_hom_vs_... 5dpf_inf_hom_vs_5d...

Sample Sessions

Affinity Purification Import & Save Ivacaftor Coauthor Styles Demo

Tutorials News

Table Panel

Drag table files here

Node Table Edge Table Network Table

Memory

ClueGO

The screenshot displays the Cytoscape ClueGO interface. The main window is titled "Cytoscape" and "Session: New Session". The interface is divided into several panels:

- Control Panel:** Contains various settings for ClueGO analysis. It includes a "Global" section with a "Use GO Term Fusion" checkbox and a "Show only Pathways with pV ≤" slider set to 0.05000. Below this are "Advanced Term/Pathway Selection Options" with "GO Tree Interval" (Min Level: 3, Max Level: 8) and "GO Term/Pathway Selection (#/% Genes)" (Cluster #1: 3, Min #Genes: 4,000). There is also a "GO Term/Pathway Network Connectivity (Kappa Score)" slider set to 0.4. The "Statistical Options" section includes "Enrichment (Right-sided hypergeometric test)", "Bonferroni step down", "pV Correction", "mid-P-values", and "Doubling". "Reference Set Options" includes "Selected Ontologies Reference Set", "Predefined IDs Reference Set", and "Custom Reference Set". "Grouping Options" and "Preferred Layout" (Set to "Prefuse Force Directed Layout") are also present. A "ClueGO Functional Analysis" section has a "Start" button.
- Recent Sessions:** A panel titled "Welcome to Cytoscape" showing a list of recent sessions with network visualizations. Sessions include "Styles Demo.cys", "inf_5dpf_hom_vs_sib...", "3dpf_uninf_hom_vs_...", and "5dpf_inf_hom_vs_5d...".
- Sample Sessions:** A panel showing sample sessions with network visualizations and labels: "Affinity Purification", "Import & Save", "Ivacaftor Coauthor", "Styles Demo", "Tutorials", and "News".
- Table Panel:** A panel titled "Table Panel" with a large dashed box and the text "Drag table files here". Below it are buttons for "Node Table", "Edge Table", and "Network Table".

The bottom right corner of the interface shows a "Memory" indicator with a green dot.

ClueGO

The screenshot displays the Cytoscape ClueGO interface. The main window is titled "Cytoscape" and "Session: New Session". The interface is divided into several panels:

- Control Panel:** Contains settings for ClueGO analysis. The "ClueGO" tab is active. Settings include:
 - Global: Use GO Term Fusion (unchecked), Show only Pathways with pV ≤ 0.05000 (checked).
 - Advanced Term/Pathway Selection Options: GO Tree Interval (Min Level: 3, Max Level: 8), GO Term/Pathway Selection (#/% Genes) (Cluster #1: 3, Min #Genes: 4,000 %Genes).
 - GO Term/Pathway Network Connectivity (Kappa Score): Score: 0.4.
 - Statistical Options: Enrichment (Dish-circled-hierarchical-test) (dropdown menu open showing Bonferroni, Bonferroni step down (checked), Benjamini-Hochberg, None), pV Correction (dropdown).
 - Reference Set Options: Selected Ontologies Reference Set (selected).
 - Grouping Options: (empty).
 - Preferred Layout: Select Layout: Prefuse Force Directed Layout (dropdown), Apply button.
 - ClueGO Functional Analysis: Start button.
- Recent Sessions:** Displays a list of recent sessions with thumbnails and names: Styles Demo.cys, inf_5dpf_hom_vs_sib..., 3dpf_uninf_hom_vs_..., 5dpf_inf_hom_vs_5d..., and an unlabeled session.
- Sample Sessions:** Displays a list of sample sessions with thumbnails and names: Affinity Purification, Import & Save (ndexbio.org), Ivacaftor Coauthor, Styles Demo, and RAP1.
- Table Panel:** A panel for displaying data tables. It contains a large dashed box with the text "Drag table files here". Below the box are buttons for "Node Table", "Edge Table", and "Network Table".

The interface also includes a search bar, a help icon, and a memory indicator at the bottom right.

ClueGO

Cytoscape File Edit View Select Layout Apps Tools Help

Session: New Session

Control Panel

Network Style Select Annotation ClueGO

Analysis Mode

ClueGO: Functional Analysis CluePedia: Genes/m

Preselected Functions

Check out CluePedia as well!

To visualize Genes along with Pathways ->

Load Marker List(s)

Danio rerio [7955]

ENSDARG00000117609 File Ne

ENSDARG00000117610

ENSDARG00000117812

Visual Style

Groups Significance

ClueGO Settings

Ontologies/Pathways

...	Name	#	Date	Shape
<input type="checkbox"/>	Ch...Chromo...2...		27.03.2...	
<input checked="" type="checkbox"/>	GO Biologic...1...		27.03.2...	
<input checked="" type="checkbox"/>	GO Cellular...1...		27.03.2...	
<input type="checkbox"/>	GO Immun...5...		27.03.2...	
<input checked="" type="checkbox"/>	GO Molecu...3...		27.03.2...	
<input checked="" type="checkbox"/>	KE...KEGG	1...	27.03.2...	

Evidence

Code
<input checked="" type="checkbox"/> All
<input type="checkbox"/> All_Experimental
<input type="checkbox"/> All_without_IEA
<input type="checkbox"/> EXP (Inferred from
<input type="checkbox"/> IBA (Inferred from
<input type="checkbox"/> IBD (Inferred from

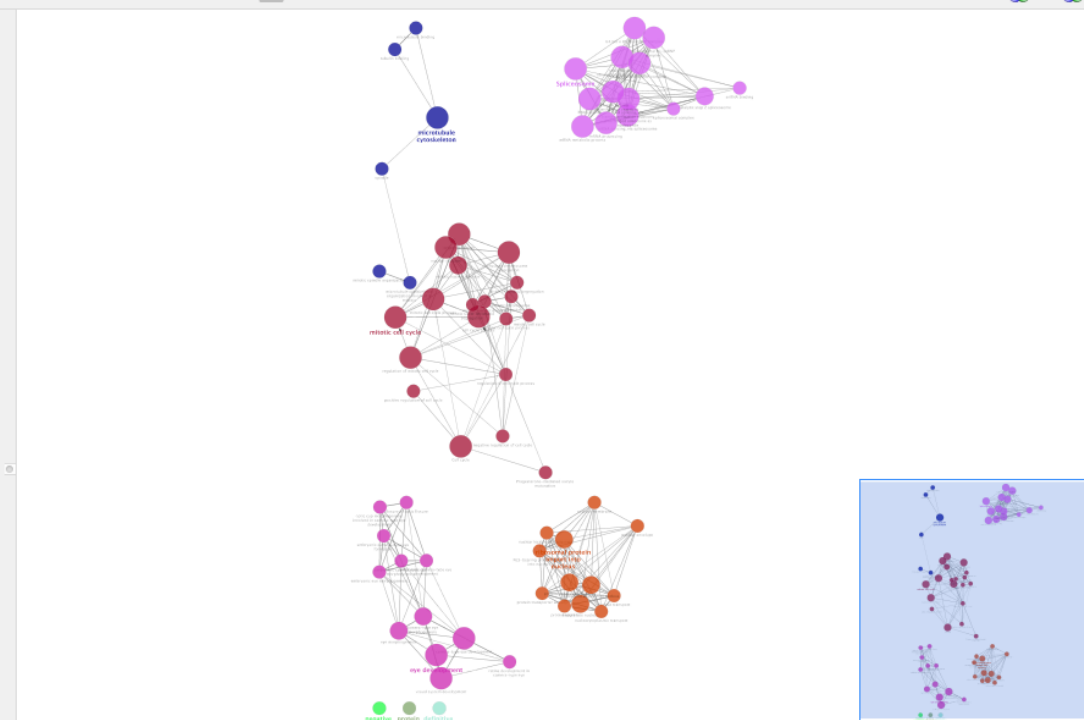
Update Ontologies

Download New Organisms or Data

Network Specificity

Global Medium Detailed

Use GO Term Fusion



Results for Analysis0

Table Panel

Results for Analysis0

ClueGO Results (Cluster #1) Cluster #1 ClueGO Log

Node Table Edge Table Network Table ClueGO

Memory

ClueGO

Cytoscape File Edit View Select Layout Apps Tools Help

Session: New Session

microtubule cytoskeleton

Cell cycle

Spliceosome

ribosomal protein import into nucleus

negative regulation of neurogenesis

protein sumoylation

definitive hemopoiesis

eye development

Results for Analysis0

Table Panel

Results for Analysis0

ClueGO Results (Cluster #1) Cluster #1 ClueGO Log

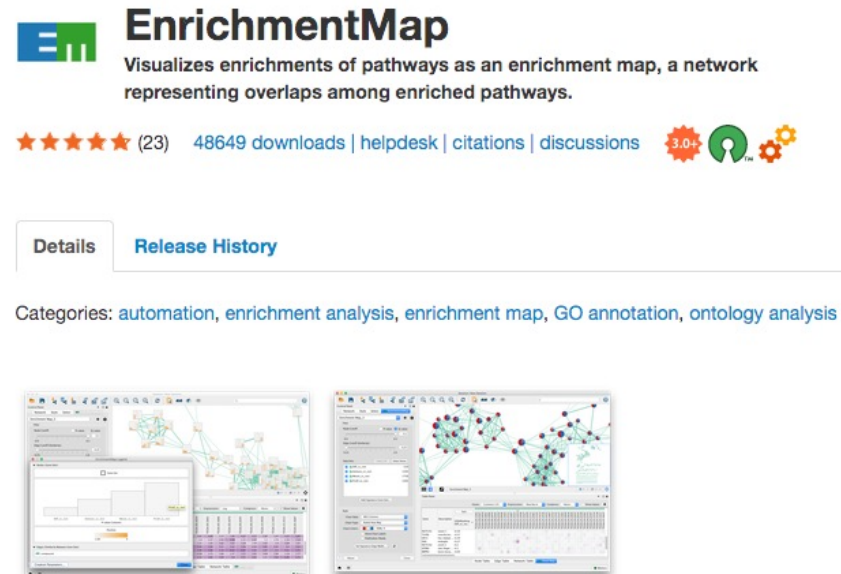
GOID	GO Term	Ontology Source	Term PValue	Term PValue Corrected with...	Group PValue	Selection
<input checked="" type="checkbox"/> KEGG:0...	cell cycle	KEGG_27.03.2019	1.3 E-7	1.3 E-5	1.6 E-9	
<input type="checkbox"/> KEGG:0...	progesterone-mediated oocyte maturation	KEGG_27.03.2019	7.1 E-4	4.2 E-2	1.6 E-9	
<input type="checkbox"/> GO:002...	cell cycle process	GO_BiologicalProcess-EBI-U...	3.7 E-9	4.0 E-7	1.6 E-9	
<input type="checkbox"/> GO:005...	meiotic cell cycle	GO_BiologicalProcess-EBI-U...	7.8 E-4	4.3 E-2	1.6 E-9	
<input type="checkbox"/> GO:000...	mitotic cell cycle	GO_BiologicalProcess-EBI-U...	4.6 E-10	5.1 E-8	1.6 E-9	
<input type="checkbox"/> GO:190...	meiotic cell cycle process	GO_BiologicalProcess-EBI-U...	1.3 E-4	9.8 E-3	1.6 E-9	
<input type="checkbox"/> GO:009...	nuclear chromosome segregation	GO_BiologicalProcess-EBI-U...	5.1 E-6	4.7 E-4	1.6 E-9	
<input type="checkbox"/> GO:190...	mitotic cell cycle process	GO_BiologicalProcess-EBI-U...	3.3 E-9	3.6 E-7	1.6 E-9	

Node Table Edge Table Network Table ClueGO


Memory

Enrichment Map

- <https://enrichmentmap.readthedocs.io/en/latest>
- Inputs:
 - GSEA
 - DAVID/BINGO/Great
 - Generic



EnrichmentMap
Visualizes enrichments of pathways as an enrichment map, a network representing overlaps among enriched pathways.

★★★★★ (23) 48649 downloads | [helpdesk](#) | [citations](#) | [discussions](#) 

Details [Release History](#)

Categories: [automation](#), [enrichment analysis](#), [enrichment map](#), [GO annotation](#), [ontology analysis](#)

Generic Input Files

Enrichments

GeneSetID	Description	p.Val	FDR	Phenotype
GO:0000070	mitotic sister chromatid segregation	6.83E-04	0.04165	1.38041
GO:0000278	mitotic cell cycle	4.64E-10	5.10E-08	7.29235
GO:0000280	NA	3.62E-07	NA	4.43731

GeneSets

GeneSetID	Description	Genes					
GO:0000070	mitotic sister chromatid segregation	bub1	incenp	nusap1	pds5a	ran	
GO:0000278	mitotic cell cycle	aspm	atoh7	bmb	bub1	ccna2	...
GO:0000280	NA	bub1	ccna2	ccnd1	ccne2	incenp	...

Expression

name	description	uninf_3dpf_wt_rep1	uninf_3dpf_wt_rep2
slc35a5	ENSDARG000000000001	36.28229146	33.4323
ccdc80	ENSDARG000000000002	75.50639034	113.155
nrf1	ENSDARG000000000018	305.9479712	281.174

Ranks

name	rank
slc35a5	0.946000588
ccdc80	0.987509859
nrf1	0.646467578

Enrichment Map

Create Enrichment Map

Data Sets:

- Common Files (included in all data sets)
- uninf_5dpf (Generic/gProfiler)
- uninf_3dpf (Generic/gProfiler)

* Name: uninf_5dpf

* Analysis Type: Generic/gProfiler

* Enrichments: 9/deseq2/enrichment_map/uninf_5dpf_hom_vs_sib.EM-Ph.tsv

* GMT: 019/deseq2/enrichment_map/uninf_5dpf_hom_vs_sib.EM.gmt

Ranks: i-course-2019/deseq2/enrichment_map/uninf_5dpf_expr.rnk

Expressions: n-course-2019/deseq2/enrichment_map/uninf_5dpf_expr.txt

Classes:

Phenotypes: Positive: UP Negative: DOWN

Network Name: Use Default uninf_5dpf

Number of Nodes (gene-set filtering)

Filter genes by expressions:

FDR q-value cutoff: 0.1

p-value cutoff: 1.0

NES (GSEA only): All

Filter by minimum experiments:

Minimum experiments: 3

Number of Edges (gene-set similarity filtering)

Data Set Edges: Automatic

Cutoff: 0.375

Metric: Jaccard

Scientific Notation Show Advanced Options

Reset Cancel Build

<https://enrichmentmap.readthedocs.io/en/latest/Parameters.html>

Enrichment Map

Control Panel

Annotation: **EnrichmentMap**

uninf_5dpf

Filter

Node Cutoff: P-value Q-value

0.0 | 0.1 | 0.1

Edge Cutoff (Similarity):

0.375 | 1.0 | 0.375

Data Sets:

Select All Select None

- uninf_3dpf 66
- uninf_5dpf 69

Add Signature Gene Sets...

Style

Chart Data: Q-value (FDR) Columns

Chart Type: Radial Heat Map

Chart Colors: RdBu-3

Show Chart Labels

Publication-Ready

Set Signature Edge Width...

About Close

Table Panel

shared name	name	EnrichmentMap	EnrichmentMap	EnrichmentMap	EnrichmentMap
		Name	GS_DESCR	GS_Type	
GO:0016925	GO:00169...	GO:0016925	protein sumoylation	ENR	GO:
GO:0062023	GO:00620...	GO:0062023	collagen-containing ex...	ENR	GO:
GO:0022402	GO:00224...	GO:0022402	cell cycle process	ENR	GO:
GO:0048513	GO:00485...	GO:0048513	animal organ developm...	ENR	GO:

Node Table Edge Table Network Table Heat Map

Memory

Enrichment Map

Cytoscape File Edit View Select Layout Apps Tools Help

Session: New Session

Control Panel

Annotation **EnrichmentMap**

uninf_5dpf

Filter

Node Cutoff: P-value Q-value

0.0 0.1

Edge Cutoff (Similarity):

0.375 1.0

Data Sets:

- uninf_3dpf 66
- uninf_5dpf 69

Add Signature Gene Sets...

- None --
- NES Columns
- P-value Columns
- Q-value (FDR) Columns
- Color by Data Set**

Style

Chart Data: Color by Data Set

Chart Type:

Chart Colors:

Show Chart Labels

Publication-Ready

Table Panel

shared name	name	EnrichmentMap Name	EnrichmentMap GS_DESCR	EnrichmentMap GS_Type	EnrichmentMap
GO:0016925	GO:00169...	GO:0016925	protein sumoylation	ENR	GO:
GO:0062023	GO:00620...	GO:0062023	collagen-containing ex...	ENR	GO:
GO:0022402	GO:00224...	GO:0022402	cell cycle process	ENR	GO:
GO:0048513	GO:00485...	GO:0048513	animal organ developm...	ENR	GO:

Node Table Edge Table Network Table Heat Map

Memory

Enrichment Map

The screenshot shows the Cytoscape application window with a session titled "New Session". The interface includes a top menu bar (File, Edit, View, Select, Layout, Apps, Tools, Help), a toolbar with various icons, and a search bar. The main workspace displays a network graph with nodes and edges. A context menu is open over a node, listing options: "Create New Style...", "Copy Style...", "Rename Style...", "Remove Style", "Make Current Styles Default", and "Create Legend...".

The left sidebar contains the "Control Panel" with tabs for "Network", "Style", "Select", "Annotation", and "EnrichmentMap". The "Style" tab is active, showing a dropdown menu with "EM2_visual_style" selected. Below this is the "Properties" panel for the selected style, which includes a table with columns "Def.", "Map.", and "Byp." and various style attributes.

Def.	Map.	Byp.	Property
			Border Paint
1.0			Border Width
			Fill Color
			Height
			Image/Chart 1
			Label
			Label Color
12			Label Font Size
			Shape
40.0			Size
			Tooltip

The main workspace shows a network graph with nodes and edges. The nodes are colored in green and blue. The graph is titled "uninf_5dpf" in the bottom right corner. The bottom right corner also shows a "Table Panel" with a grid icon and a "1 0 0" display.