

Cytoscape for Visualisation

Cytoscape

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

Session: New Session

Control Panel

NetworkStyleSelectAnnotation

Enter search terms for NDEx...

Drag network files here

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](#)

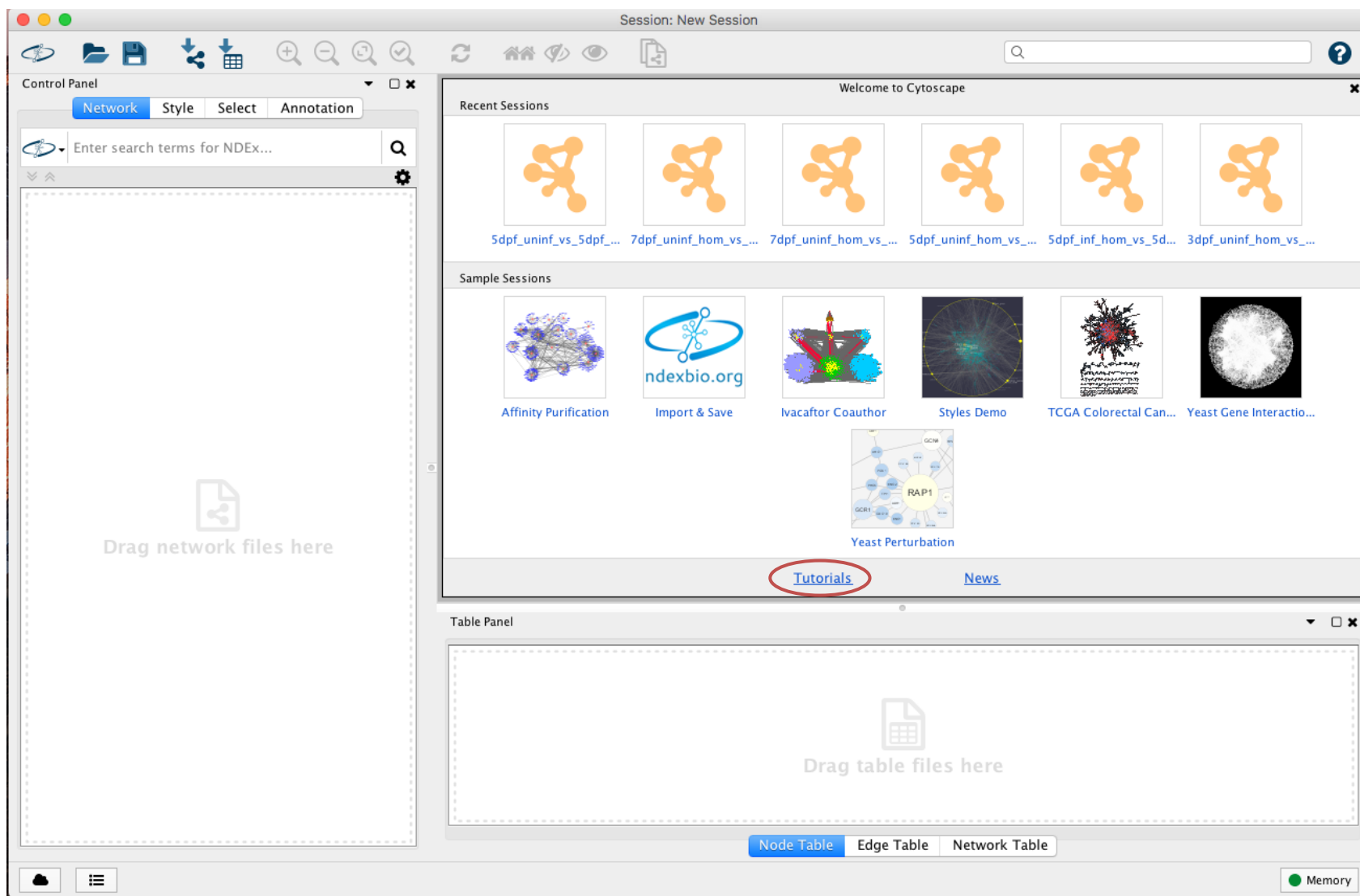
[News](#)

Table Panel

Drag table files here

Node TableEdge TableNetwork Table

Memory



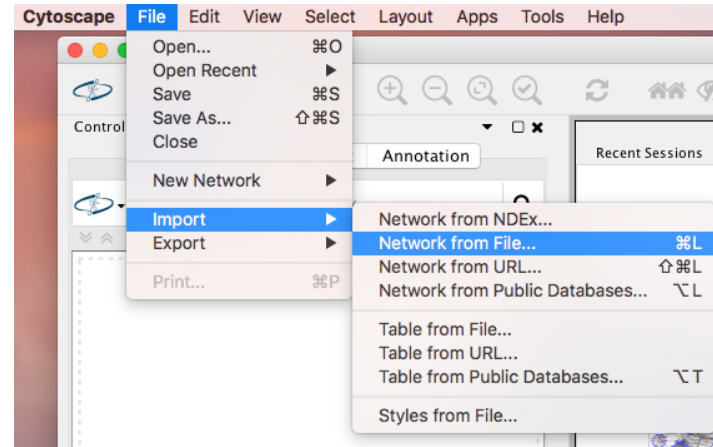
Loading Networks

- 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

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ENSDARG00000070656	geneExprCor	ENSDARG00000019339
ENSDARG00000070656	geneExprCor	ENSDARG00000095743

Loading Networks

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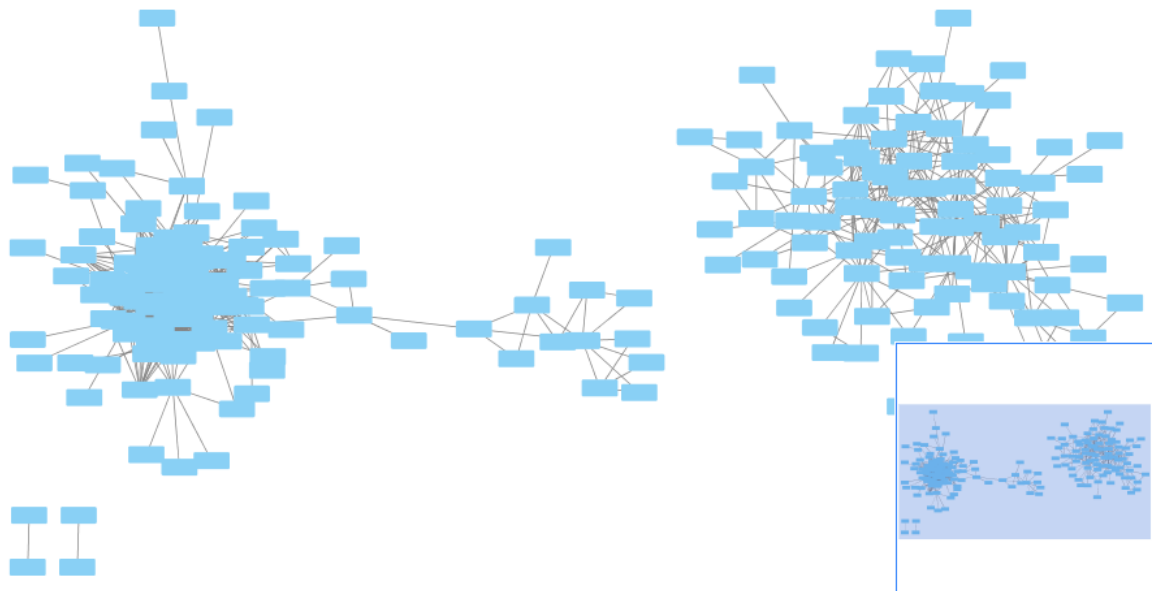
Network Style Select Annotation

Enter search terms for NDEx...

1 of 1 Network selected

3dpf_uninf_hom_vs_3dpf_uninf_sib.sif 1

3dpf_uninf_hom_vs_3dpf_uninf_sib.sif 205 1154



3dpf_uninf_hom_vs_3dpf_uninf_sib.sif

Table Panel

shared name	name
ENSDARG00000099...	ENSDARG...
ENSDARG00000012...	ENSDARG...
ENSDARG00000095...	ENSDARG...
ENSDARG00000086...	ENSDARG...
ENSDARG00000104...	ENSDARG...
ENSDARG00000070...	ENSDARG...
ENSDARG00000038...	ENSDARG...

Node Table Edge Table Network Table

Memory

Loading Networks

Session: New Session

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3dpf_uninf_hom_vs_3dpf_uninf_sib.sif 1

3dpf_uninf_hom_vs_3dpf_uninf_sib.sif 205 1154

ENSDARG00000105586

ENSDARG00000095046

ENSDARG00000096607

ENSDARG00000012261

ENSDARG00000035559

ENSDARG00000099966

ENSDARG00000070930

ENSDARG00000040440

ENSDARG00000086425

ENSDARG00000104644

ENSDARG00000058328

ENSDARG00000055838

ENSDARG00000033440

ENSDARG00000024277

ENSDARG00000000000

ENSDARG00000000000

ENSDARG00000000000

3dpf_uninf_hom_vs_3dpf_uninf_sib.sif

Table Panel

shared name	name
ENSDARG00000099...	ENSDARG...
ENSDARG00000012...	ENSDARG...
ENSDARG00000095...	ENSDARG...
ENSDARG00000086...	ENSDARG...
ENSDARG00000104...	ENSDARG...
ENSDARG00000070...	ENSDARG...
ENSDARG00000038...	ENSDARG...

Node Table Edge Table Network Table

Memory

Add extra node/edge information

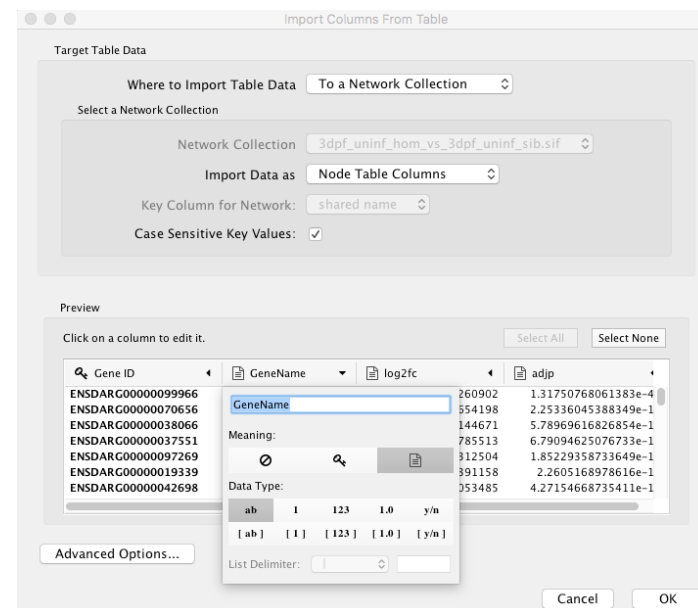
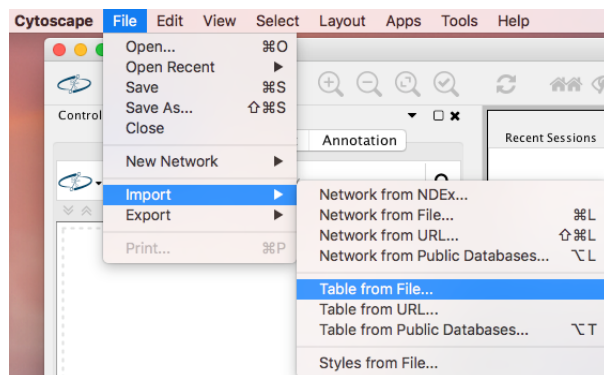
- Extra node information can be imported from a file containing a column that matches the node names

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

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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

Session: New Session

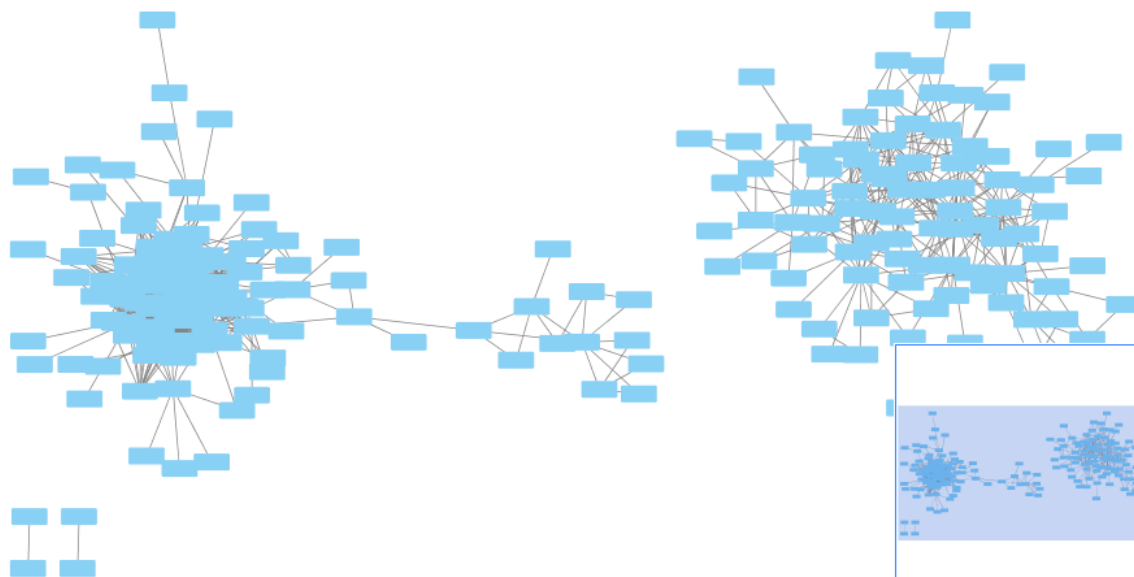
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3dpf_uninf_hom_vs_3dpf_uninf_sib.sif 205 1154



3dpf_uninf_hom_vs_3dpf_uninf_sib.sif

Table Panel

$f(x)$

shared name	name	GeneNan	log2fc	adjp
ENSDARG000000099...	ENSDARG...	polr2a	0.77350...	1.31750...
ENSDARG000000012...	ENSDARG...	eftud2	0.43041...	7.06488...
ENSDARG000000095...	ENSDARG...	prpf31	0.47628...	4.21870...
ENSDARG000000086...	ENSDARG...	prpf3	0.46136...	4.21870...
ENSDARG000000104...	ENSDARG...	CR9318...	2.66209...	0.00525...
ENSDARG000000070...	ENSDARG...	siich211...	-0.5837...	2.25336...
ENSDARG000000038...	ENSDARG...	kpna2	-0.5206...	5.78969...

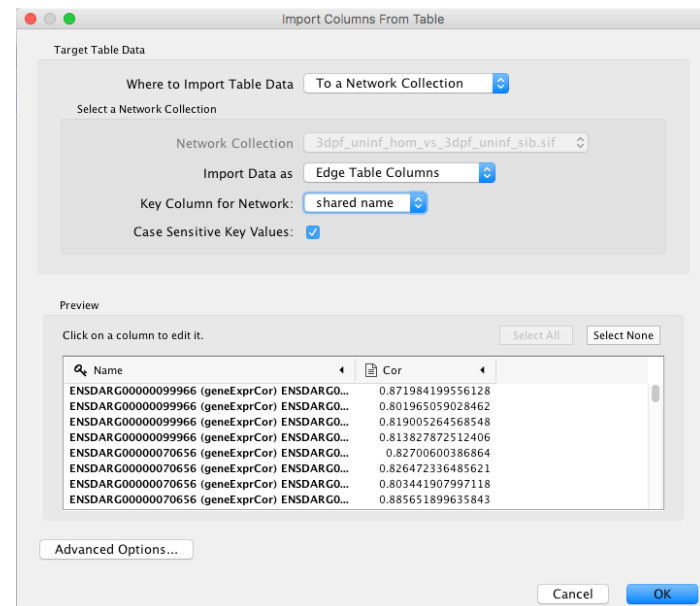
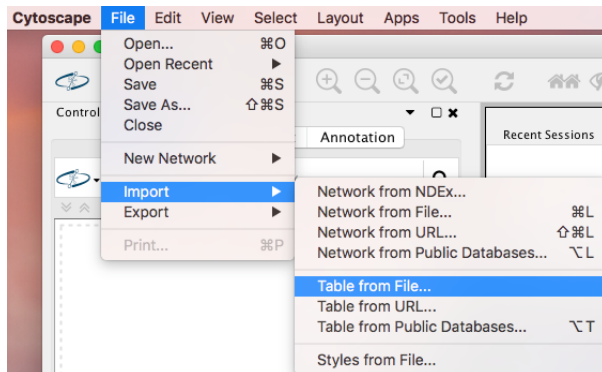
Node Table Edge Table Network Table

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

Session: New Session

Control Panel

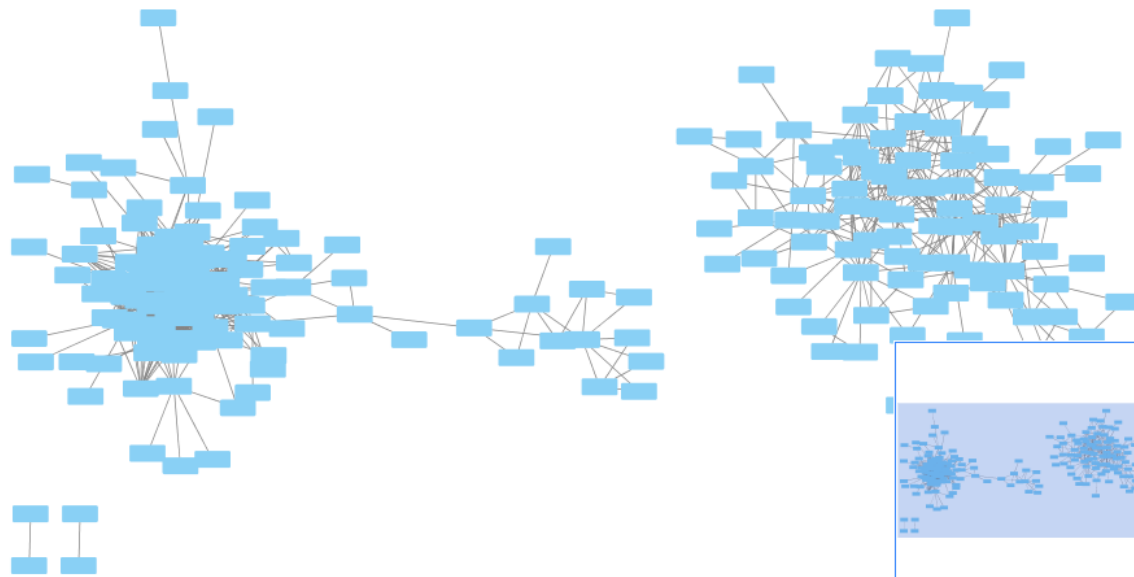
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Enter search terms for NDEx...

1 of 1 Network selected

3dpf_uninf_hom_vs_3dpf_uninf_sib.sif 1

3dpf_uninf_hom_vs_3dpf_uninf_sib.sif 205 1154



3dpf_uninf_hom_vs_3dpf_uninf_sib.sif

Table Panel

shared name	shared interaction	name	interaction	Cor
ENSDARG00000099...	geneExprCor	ENSDARG...	geneExprCor	0.87198...
ENSDARG00000099...	geneExprCor	ENSDARG...	geneExprCor	0.80196...
ENSDARG00000099...	geneExprCor	ENSDARG...	geneExprCor	0.81900...
ENSDARG00000099...	geneExprCor	ENSDARG...	geneExprCor	0.81382...
ENSDARG00000070...	geneExprCor	ENSDARG...	geneExprCor	0.82700...
ENSDARG00000070...	geneExprCor	ENSDARG...	geneExprCor	0.82647...
ENSDARG00000070...	geneExprCor	ENSDARG...	geneExprCor	0.80344...

Node Table Edge Table Network Table

Memory

Add styles to nodes

Session: New Session

Control Panel

Network Style Select Annotation

default

Properties

Def. Map. Byp.

Border Paint

0.0 Border Width

Fill Color

Column log2fc

Mapping Type Continuous Mapping

Current Mapping

35.0 Height

Image/Chart 1

Label

Label Color

12 Label Font Size

Shape

Size

255 Transparency

75.0 Width

Node Edge Network

3dpf_uninf_hom_vs_3dpf_uninf_sib.sif

Table Panel

shared name	name	GeneNan	log2fc	adjp
ENSDARG000000099...	ENSDARG...	polr2a	0.77350...	1.31750...
ENSDARG000000012...	ENSDARG...	eftud2	0.43041...	7.06488...
ENSDARG000000095...	ENSDARG...	prpf31	0.47628...	4.21870...
ENSDARG000000086...	ENSDARG...	prpf3	0.46136...	4.21870...
ENSDARG000000104...	ENSDARG...	CR9318...	2.66209...	0.00525...
ENSDARG000000070...	ENSDARG...	sich211...	-0.5837...	2.25336...
ENSDARG000000038...	ENSDARG...	kpna2	-0.5206...	5.78969...

Node Table Edge Table Network Table

Memory

Add styles to nodes

Session: New Session

Control Panel

Network Style Select Annotation

default

Properties

Def.	Map.	Byp.	
☐	☐	☐	Border Paint
0.0	☐	☐	Border Width
☐	☐	☐	Fill Color
35.0	☐	☐	Height
☐	☐	☐	Image/Chart 1
☐	☐	☐	Label
Column			GeneName
Mapping Type			Passthrough Mapping
☐	☐	☐	Label Color
12	☐	☐	Label Font Size
☐	☐	☐	Shape
☐	☐	☐	Size
255	☐	☐	Transparency
75.0	☐	☐	Width
☐ Lock node width and height			

Node Edge Network

3dpf_uninf_hom_vs_3dpf_uninf_sib.sif

Table Panel

shared name	name	GeneName	log2fc	adjp
ENSDARG000000099...	ENSDARG...	polr2a	0.77350...	1.31750...
ENSDARG000000012...	ENSDARG...	eftud2	0.43041...	7.06488...
ENSDARG000000095...	ENSDARG...	prpf31	0.47628...	4.21870...
ENSDARG000000086...	ENSDARG...	prpf3	0.46136...	4.21870...
ENSDARG000000104...	ENSDARG...	CR9318...	2.66209...	0.00525...
ENSDARG000000070...	ENSDARG...	si:ch211...	-0.5837...	2.25336...
ENSDARG000000038...	ENSDARG...	kpna2	-0.5206...	5.78969...

Node Table Edge Table Network Table

Memory

Add styles to nodes

Session: New Session

Control Panel

Network Style Select Annotation

default

Properties

Def. Map. Byp.

Border Paint

0.0 Border Width

Fill Color

35.0 Height

Image/Chart 1

Label

Column GeneName

Mapping Type Passthrough Mapping

Label Color

12 Label Font Size

Shape

Size

255 Transparency

75.0 Width

☐ Lock node width and height

Node Edge Network

3dpf_uninf_hom_vs_3dpf_uninf_sib.sif

Table Panel

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

Node Table Edge Table Network Table

Memory

Add styles to nodes

Session: New Session

Control Panel

Network Style Select Annotation

default

Properties

Def. Map. Byp.

Border Paint

0.0 Border Width

Fill Color

35.0 Height

Image/Chart 1

Label

Label Color

12 Label Font Size

Shape

Column log2fc

Mapping Type Continuous Mapping

Current Mapping

Size

255 Transparency

75.0 Width

Node Edge Network

3dpf_uninf_hom_vs_3dpf_uninf_sib.sif

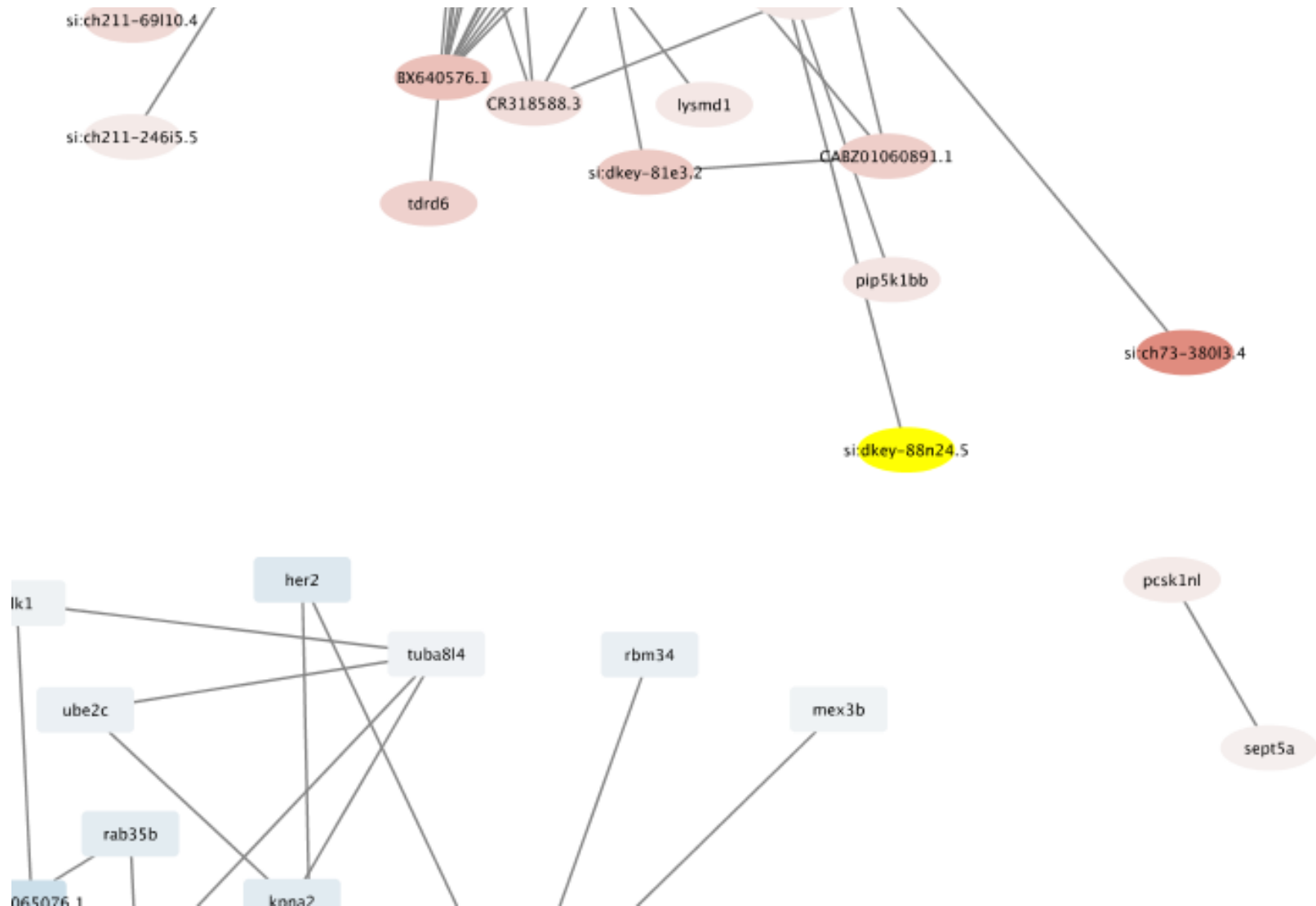
Table Panel

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

Node Table Edge Table Network Table

Memory

Add styles to nodes



Add styles to edges

Session: New Session

Control Panel

Network Style Select Annotation

default

Properties

Def. Map. Byp.

Color (Unselected)

Column Cor

Mapping Type Continuous Mapping

Current Mapping

0.80 0.9

Label

Label Color

10 Label Font Size

Line Type

None Source Arrow Shape

Source Arrow Unselected Paint

Stroke Color (Unselected)

None Target Arrow Shape

Target Arrow Unselected Paint

255 Transparency

2.0 Width

Node Edge Network

3dpf_uninf_hom_vs_3dpf_uninf_sib.sif

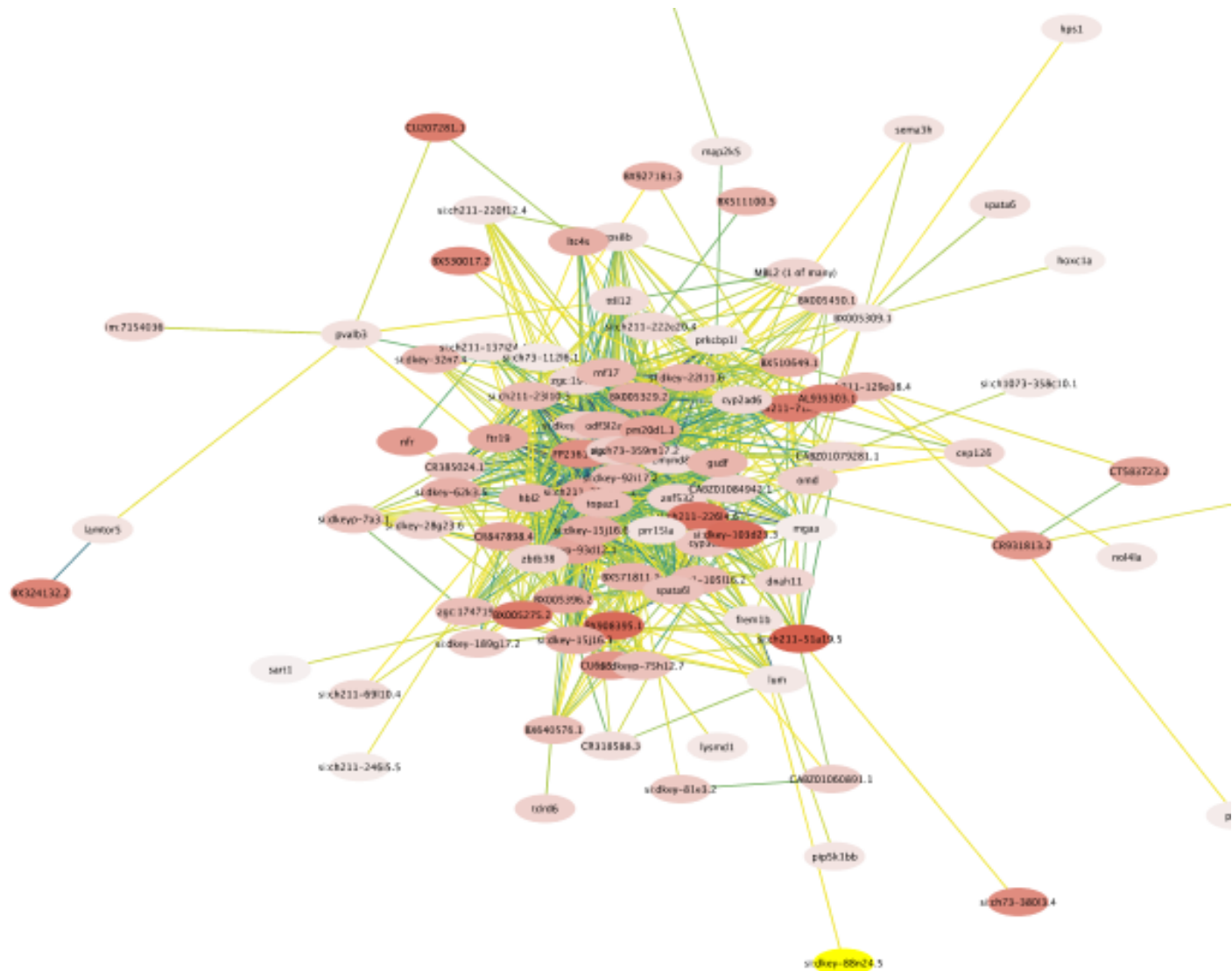
Table Panel

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ENSDARG00000113...	ENSDARG...	si:dkey-...	1.70419...	0.00681...

Node Table Edge Table Network Table

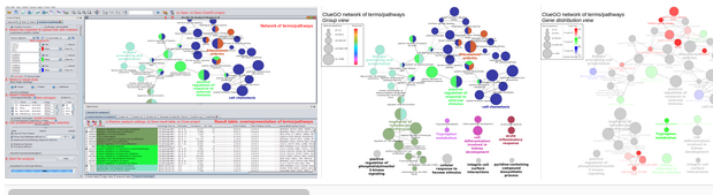
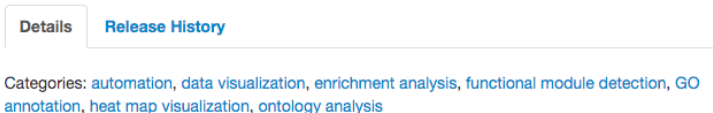
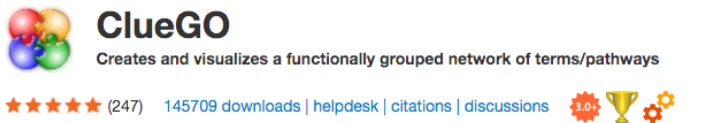
Memory

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



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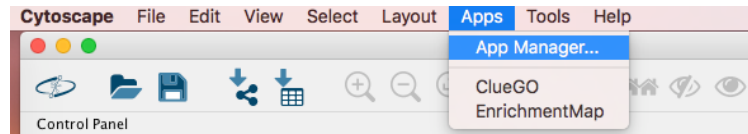
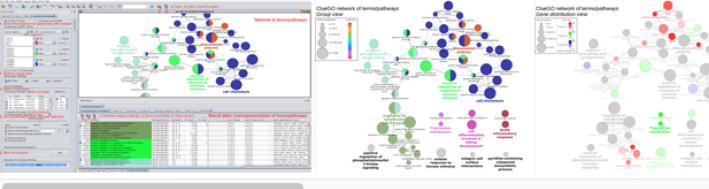


ClueGO
Creates and visualizes a functionally grouped network of terms/pathways

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

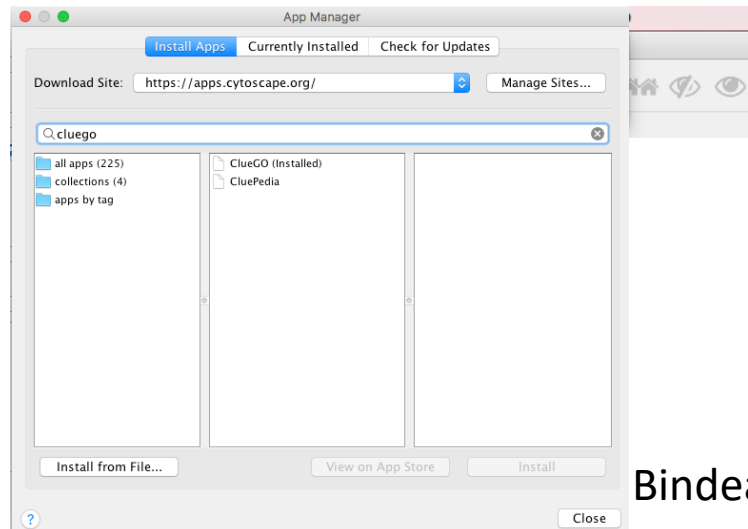
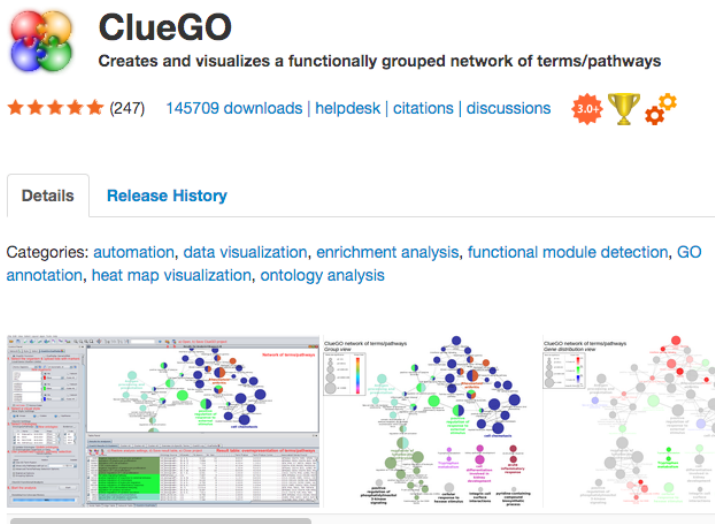
Details **Release History**

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



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ClueGO

Cytoscape File Edit View Select Layout Apps Tools Help

App Manager...
ClueGO
EnrichmentMap

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
☐	C... Huma...	5...	04.09...	
☐	C... CORU...	3...	04.09...	
☐	C... Chrom...	2...	27.02...	
☒	GO Biolog...	1...	27.02...	
☐	GO Cellul...	2...	27.02...	
☐	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

Session: New Session

Welcome to Cytoscape

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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 ndexbio.org Ivacaftor Coauthor Styles Demo TCGA Colorectal Can... Yeast Gene Interactio... Yeast Perturbation

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Table Panel

Drag table files here

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ClueGO

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Analysis Mode ClueGO v2.5.5

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CluePedia: ☐ Genes/miRNAs

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Load Marker List(s)

Danio rerio [7955]

Automatic

File Network

Visual Style

☒ Groups ☐ Significance

ClueGO Settings

Ontologies/Pathways

T...	Name	#	Date	Shape
☐	Chr...Chromosom...2...	27.03.2019	El...	
☒	GO BiologicalPr...	27.03.2019	El...	
☒	GO CellularCo...	27.03.2019	El...	
☒	GO ImmuneSyst...	27.03.2019	El...	
☒	GO MolecularF...	27.03.2019	El...	
☒	KEGGKEGG	1...	27.03.2019	El...

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- ☐ IBA (Inferred from Biological Aspect of Ancestor)
- ☐ IBD (Inferred from Biological Aspect of Descende...)

Network Specificity

Global Medium Detailed

☐ Use GO Term Fusion

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Affinity Purification Import & Save Ivacaftor Coauthor Styles Demo

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

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☒ Groups ☐ Significance

ClueGO Settings

Ontologies/Pathways

T...	Name	#	Date	Shape
☐	Chr...Chromosom...2...	27.03.2019	El...	
☒	GO BiologicalPr...	27.03.2019	El...	
☒	GO CellularCo...	27.03.2019	El...	
☒	GO ImmuneSyst...	27.03.2019	El...	
☒	GO MolecularF...	27.03.2019	El...	
☒	KEGGKEGG	27.03.2019	El...	

Evidence

Code

- ☒ All
- ☐ All_Experimental (EXP,IDA,IMI,IMP,IGI,IEP)
- ☐ 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

Cytoscape File Edit View Select Layout Apps Tools Help

Session: New Session

Control Panel

Network Style Select Annotation **ClueGO**

Global Medium Detailed

☐ Use GO Term Fusion ?

☒ Show only Pathways with pV ≤ 0.05000

☒ Advanced Term/Pathway Selection Options

GO Tree Interval

3 Min Level 8 Max Level ?

GO Term/Pathway Selection (#/% Genes)

Cluster #1

3 Min #Genes 4.000 %Genes

GO Term/Pathway Network Connectivity (Kappa Score)

Low Medium High Score: 0.4 ?

☒ Statistical Options

Advanced Statistical Options

Enrichment (Right-sided hypergeometric test) ?

Bonferroni step down pV Correction

☐ mid-P-values ☐ Doubling ?

Reference Set Options

☒ Selected Ontologies Reference Set ?

☐ Predefined IDs Reference Set

☐ Custom Reference Set

☒ Grouping Options

Preferred Layout

Select Layout: Prefuse Force Directed Layout Apply

ClueGO Functional Analysis

Start

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Bonferroni

☒ Bonferroni step down

Benjamini-Hochberg

None

pV Correction ?

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Control Panel

Network Style Select Annotation ClueGO

Analysis Mode

ClueGO: ☒ Functional Analysis ☐ Preselected Functions

CluePedia: ☐ Genes/m

Check out CluePedia as well!

To visualize Genes along with Pathways -> App Stc

Load Marker List(s)

Danio rerio [7955] # Automatic #

File Ne

Visual Style

☒ Groups ☐ Significance

ClueGO Settings

Ontologies/Pathways

...	Name	#	Date	Shape
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☒	GO Biologic...1...	27.03.2...		
☒	GO Cellular...1...	27.03.2...		
☒	GO Immun... 5...	27.03.2...		
☒	GO Molecul...3...	27.03.2...		
☒	KE...KEGG	1...	27.03.2...	

Evidence

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☒ All
☐ All_Experimental
☐ All_without_IEA
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Results for Analysis0

Table Panel

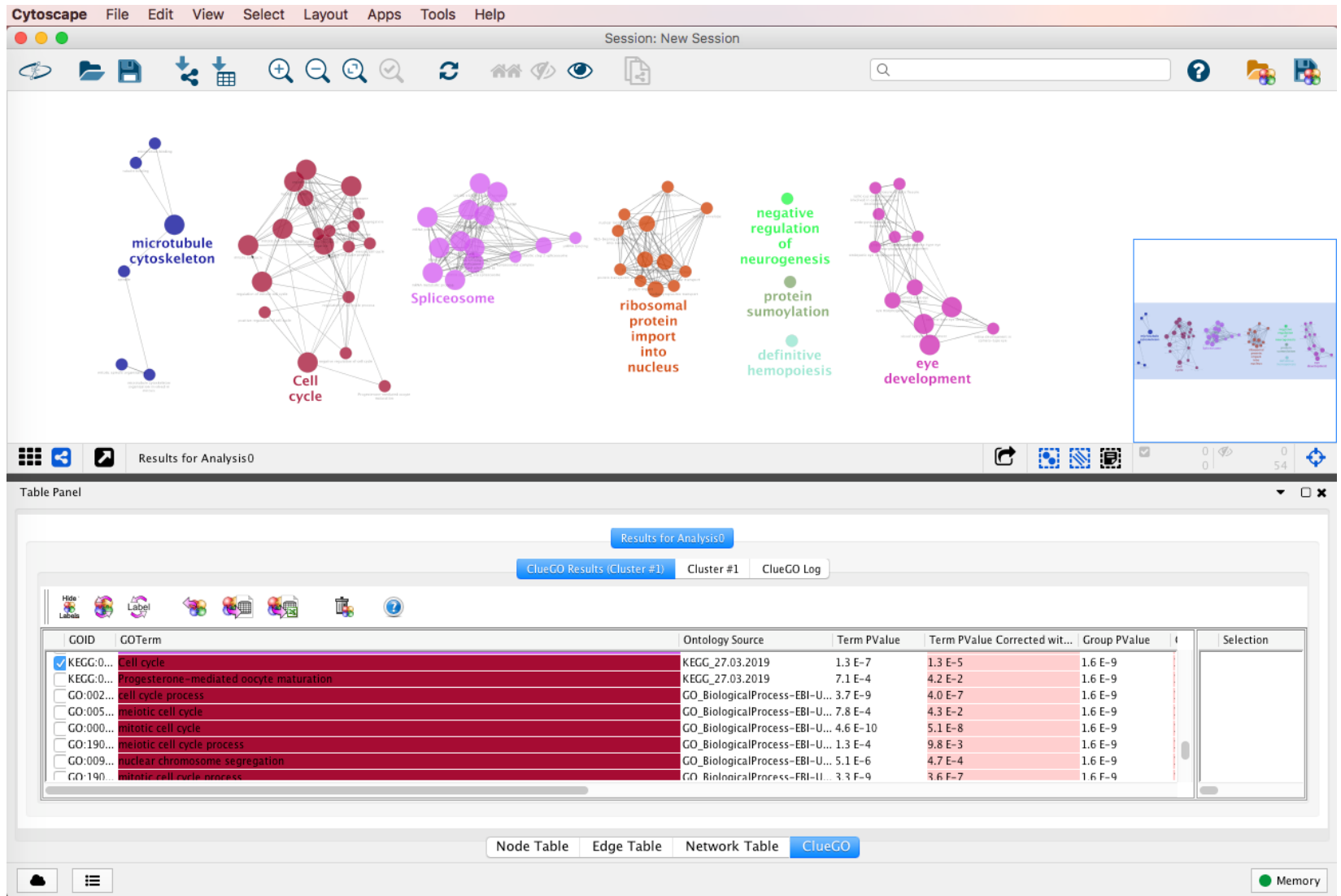
Results for Analysis0

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

Node Table Edge Table Network Table ClueGO

Memory

ClueGO



Enrichment Map

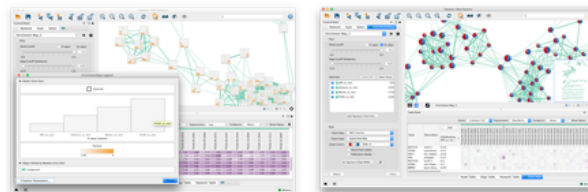
- <https://enrichmentmap.readthedocs.io/en/latest>
- Inputs:
 - GSEA
 - DAVID/BINGO/Great
 - Generic

 **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	nuclear division	3.62E-07	3.65E-05	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	nuclear division	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: 1-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

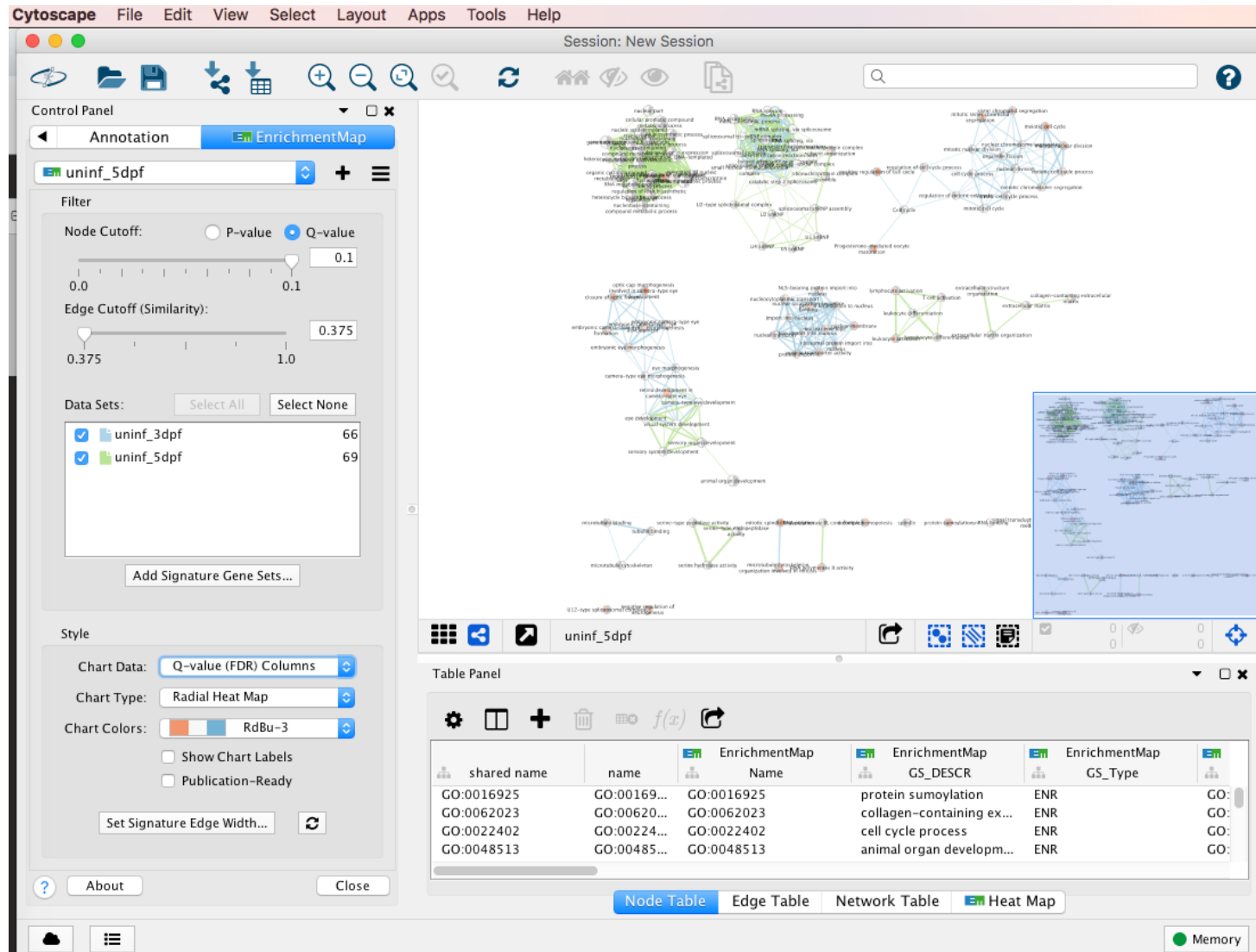
Metric: Jaccard

☐ Scientific Notation ☒ Show Advanced Options

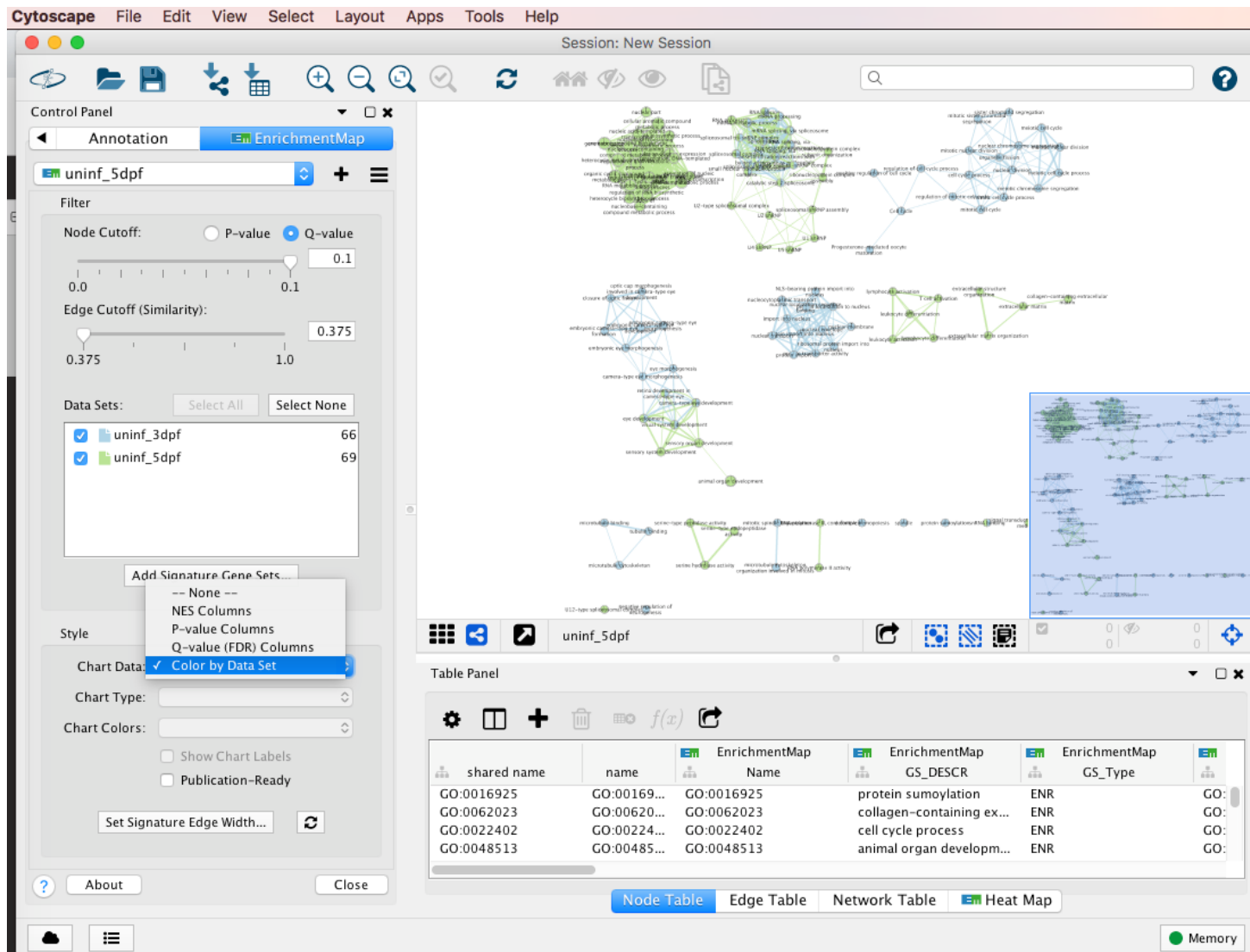
Reset Cancel Build

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

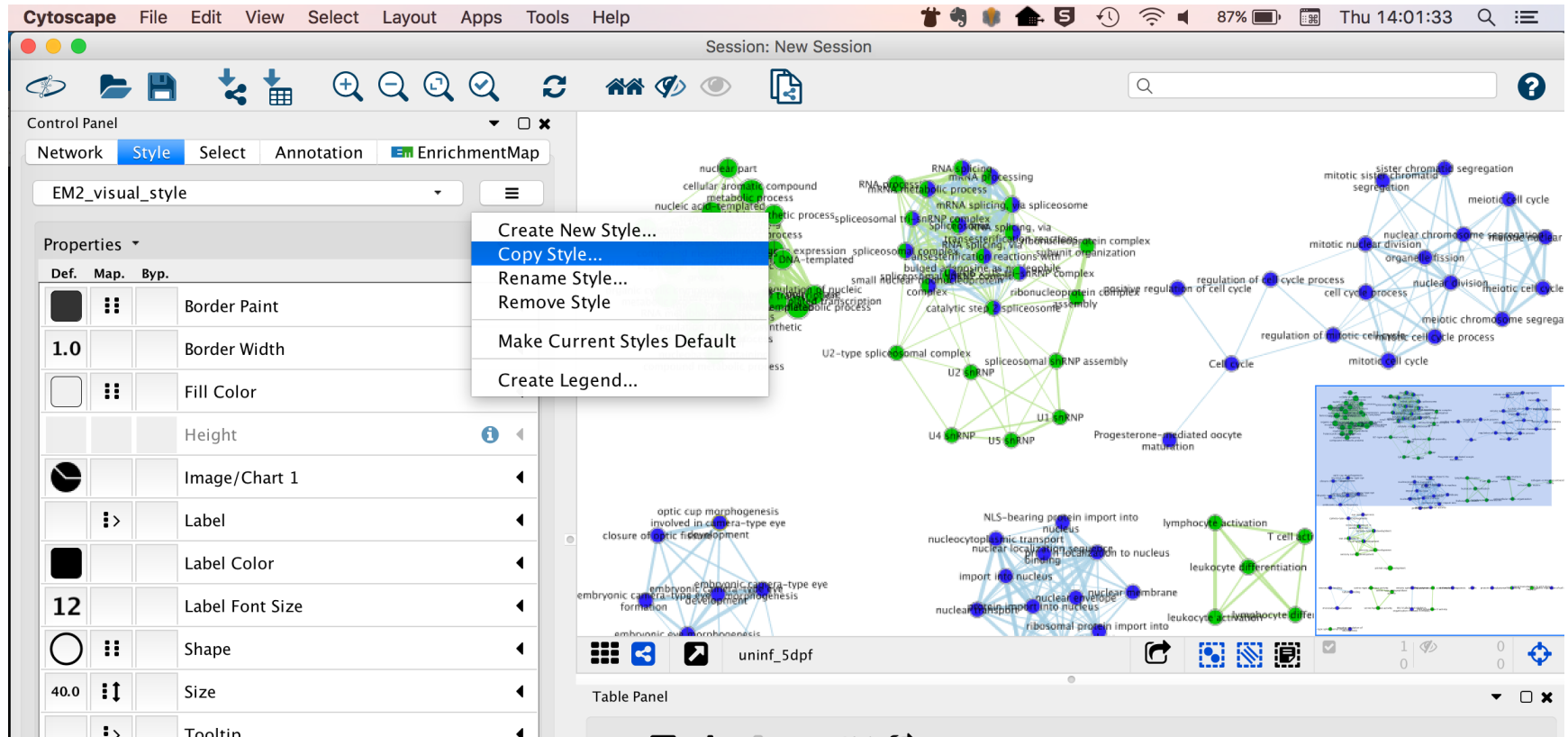
Enrichment Map



Enrichment Map

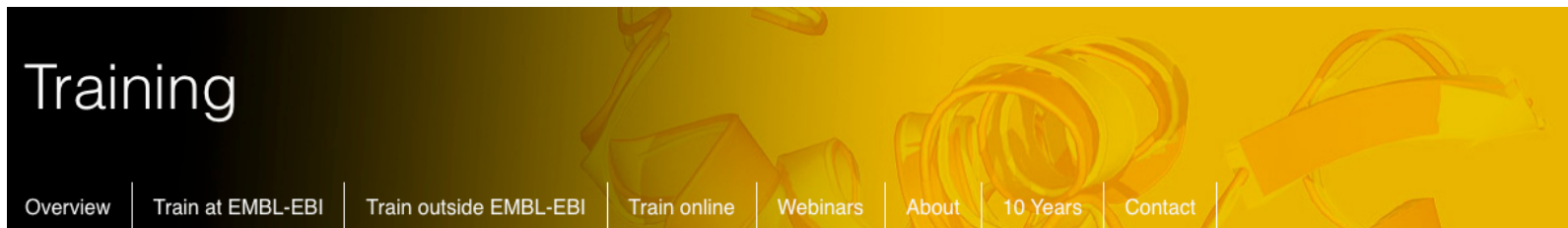


Enrichment Map



Learning Cytoscape

- CytoScape training
 - <https://www.ebi.ac.uk/training/events/2020/advanced-network-analysis-and-visualisation-cytoscape>



Advanced Network Analysis and Visualisation in Cytoscape

Date: Thursday 23 - Friday 24 April 2020

Venue: European Bioinformatics Institute (EMBL-EBI) - Wellcome Genome Campus, Hinxton, Cambridge, CB10 1SD, United Kingdom

Application opens: Monday 14 October 2019

Application deadline: Friday 03 January 2020

Participation: Open application with selection

Contact: [Rebecca Nicholl](#)

Registration fee: £130

[Apply now »](#)

