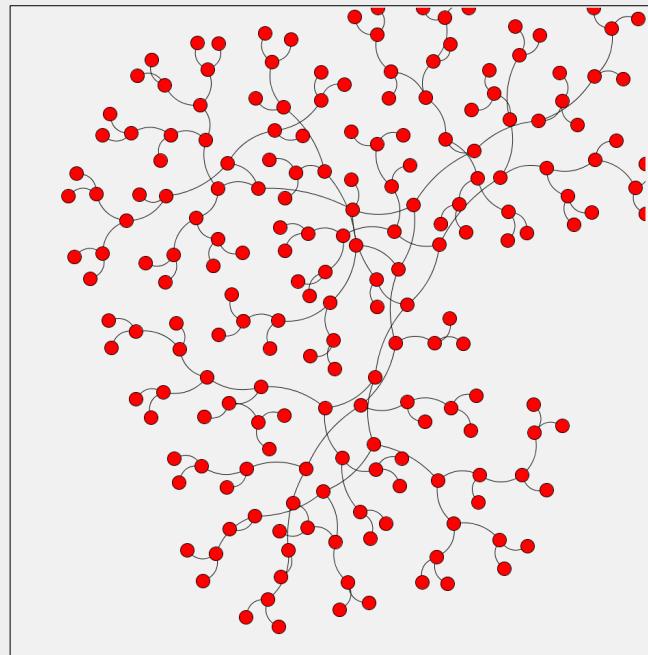


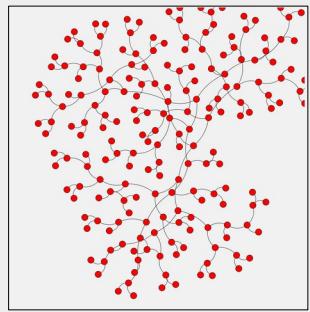
Datasets and slides:
<https://github.com/doktor-nick/intro-to-network-viz>

Introduction to Network Visualisation and Cytoscape



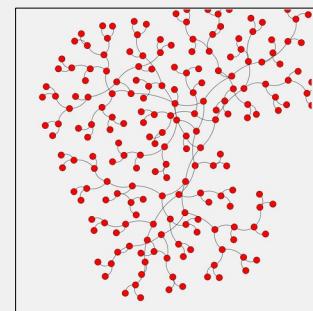
Nick Hamilton
n.hamilton@imb.uq.edu.au
IMB, RCC & QCIF - UQ

**Power corrupts.
PowerPoint corrupts absolutely.**
- Edward Tufte

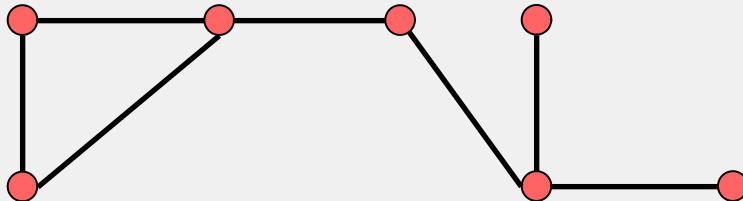


Fundamental Ideas of Networks / Graphs

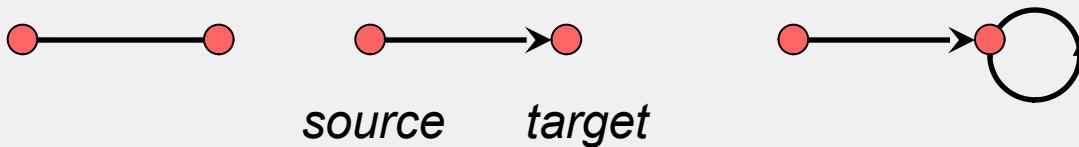
Core Definitions



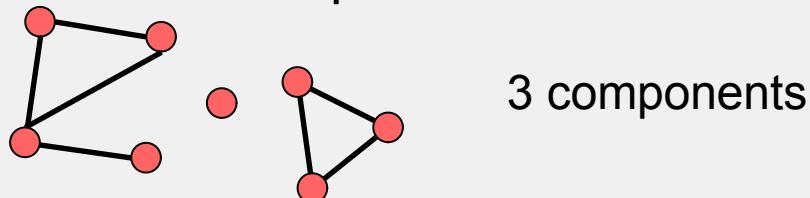
A network or graph is a collection of ***nodes*** or ***vertices*** and a set of **edges** that connect pairs of nodes.



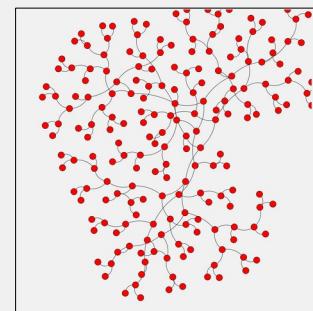
Edges may be ***undirected*** or ***directed*** or have ***loops***



A graph might have multiple disconnected ***components***

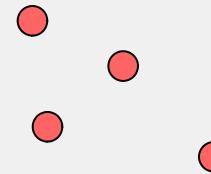
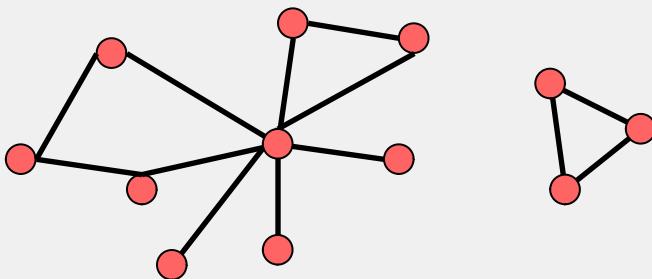


A simple example



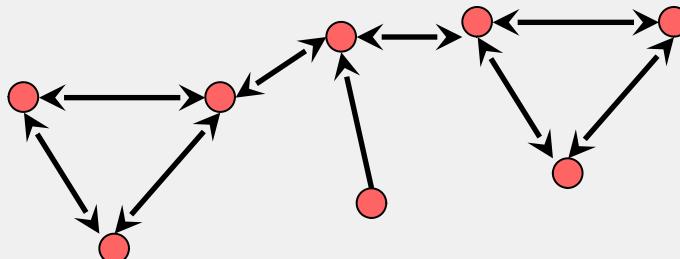
Nodes: people in this Zoom

Edges: “are friends”

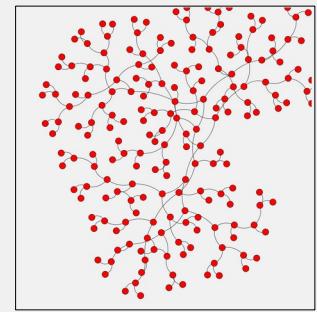


Nodes: people in this Zoom

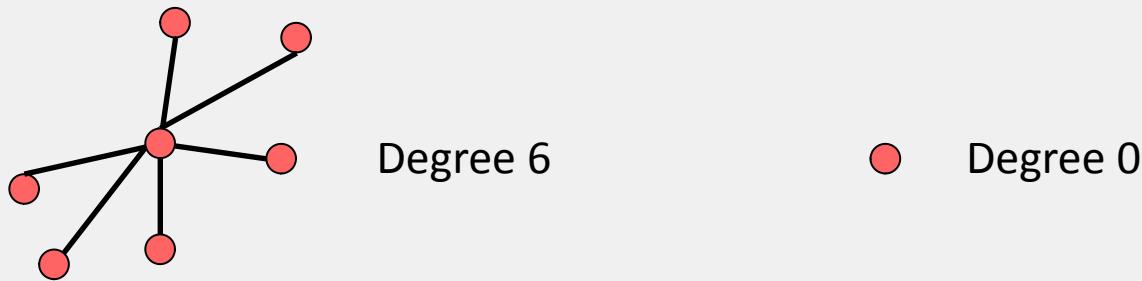
Edges: “likes”



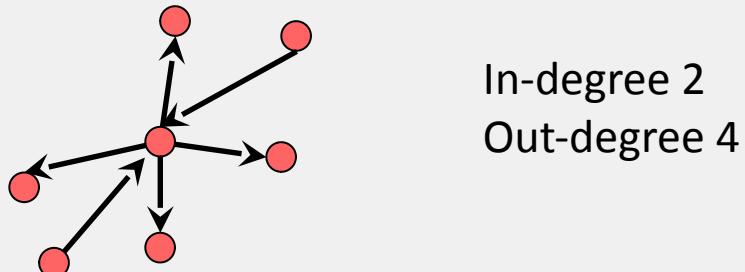
Which graph bit is the most important?



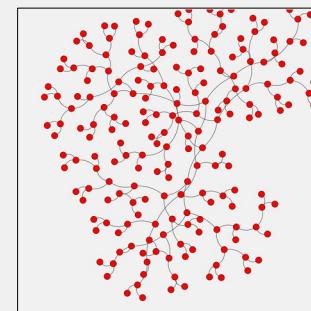
For an undirected graph, the ***degree*** of a node is the number of edges connected to a node



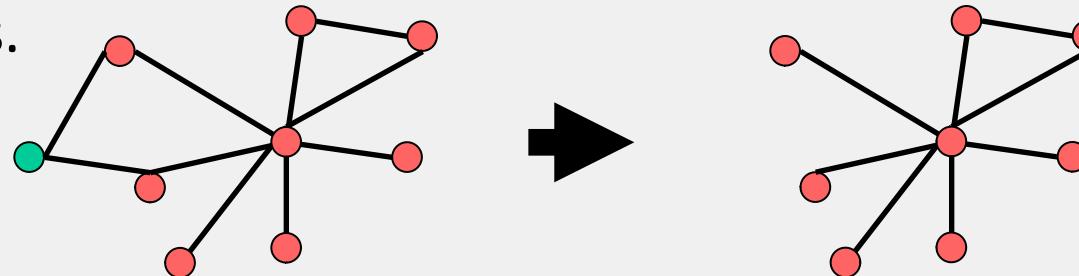
If the graph is **directed**, define ***in-degree*** and ***out-degree*** defined similarly



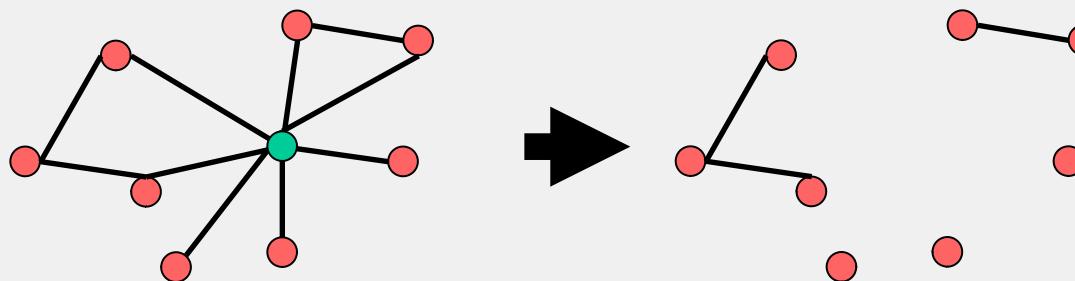
Robustness: What happens if I break it?



Node Deletion. Take the graph and delete a node and all its edges.



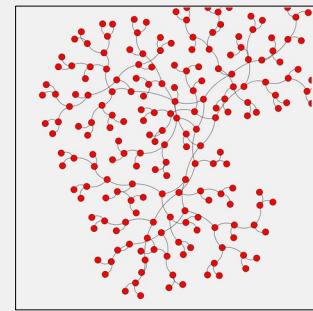
Node separation set: a subset of nodes whose deletion causes the number of components in the graph to increase



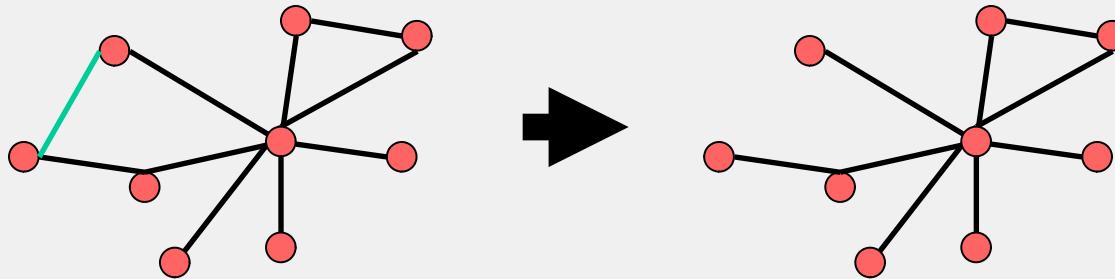
Mutations reducing activity in the p53 gene are present in over 50% of human tumours!

(Haupt et al. 2003)

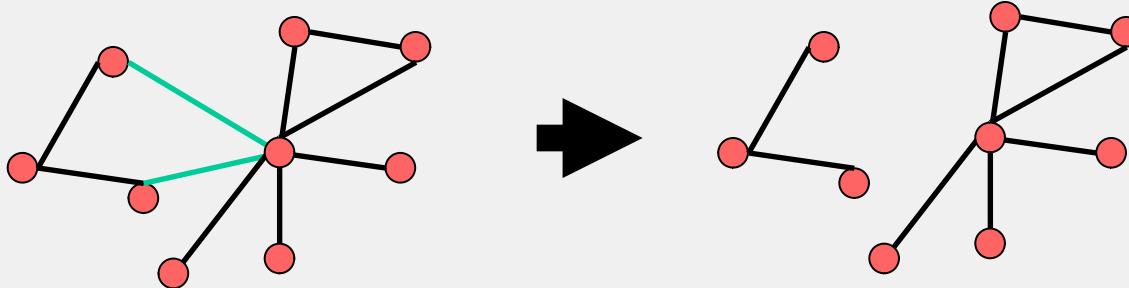
Robustness: What happens if I break it?



Edge Deletion. Delete an edge (but not the nodes it joins)



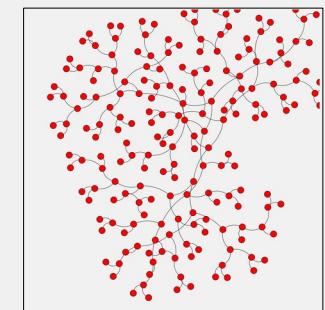
Cut set: as for node separation set, but deleting edges



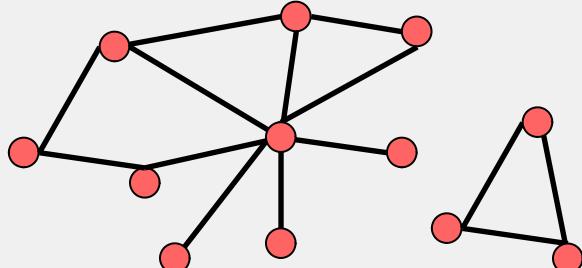
Network Robustness: how hard is it to break the network?

Delete a random node or edge: it is still connected?

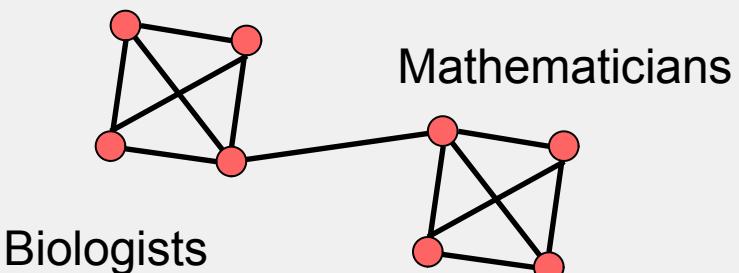
What are the (functional) modules?



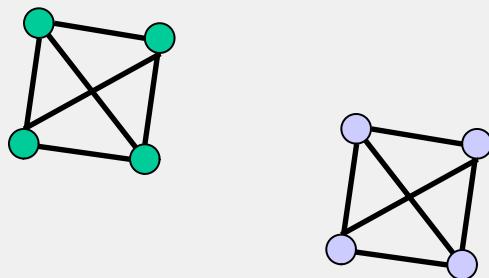
Components



But what about:

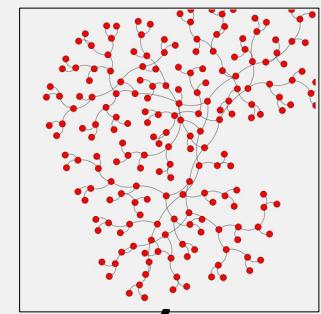


Clique. A subset of nodes, each pair joined by an edge

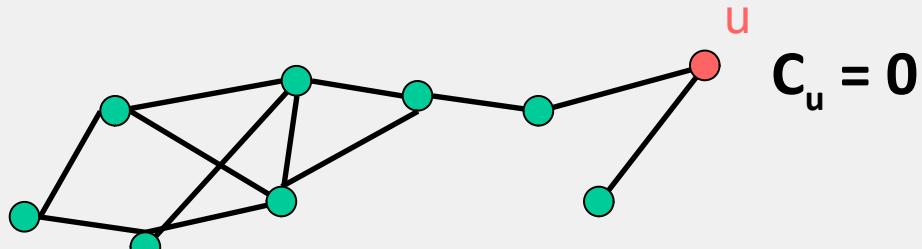


A **maximal clique** is contained in no larger clique

Clustering Coefficient

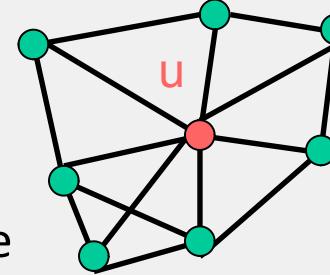


How do we tell if a **node u** is in a cluster?



Why? - Lots of **triangles** on the node

- i.e. mutual connection



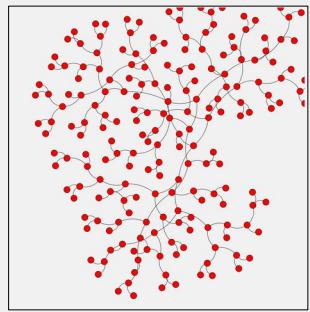
For a **node u** of **degree k**, where there are **e** **edges** between neighbours of u, define the **cluster coefficient** C_u as:

$$C_u = e / [k(k-1)/2]$$

triangles on u

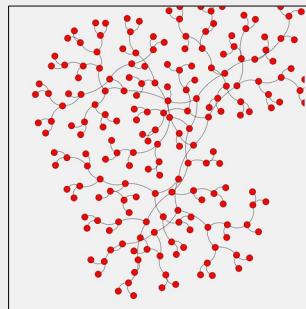
Maximum possible # triangles on u

For a graph, then define the **average cluster coefficient**



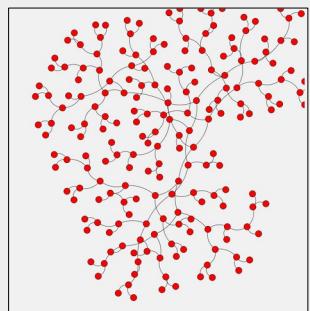
Introduction to Cytoscape for Creating and Visualising Networks

What we will cover in this introduction



- Basic interactive graph creation and interaction
- Simple formats for creating networks in Excel
- Network Analyser for basic network statistics
- Styles in Cytoscape
- Apps in Cytoscape
- Network layout
- Network filtering and selection
- Getting more help

Overview of the Cytoscape Interface



Session: New Session

File Edit View Select Layout Apps Tools Help

Control Panel

Network Style Select Annotation

Enter search terms for NDEX...

1 of 1 Network selected

Network Network

Table Panel

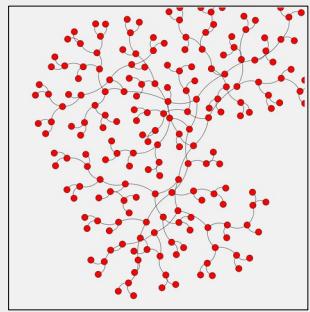
Network

shared name name

Node 1 A
Node 2 B
Node 3 C

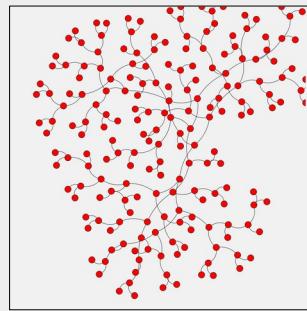
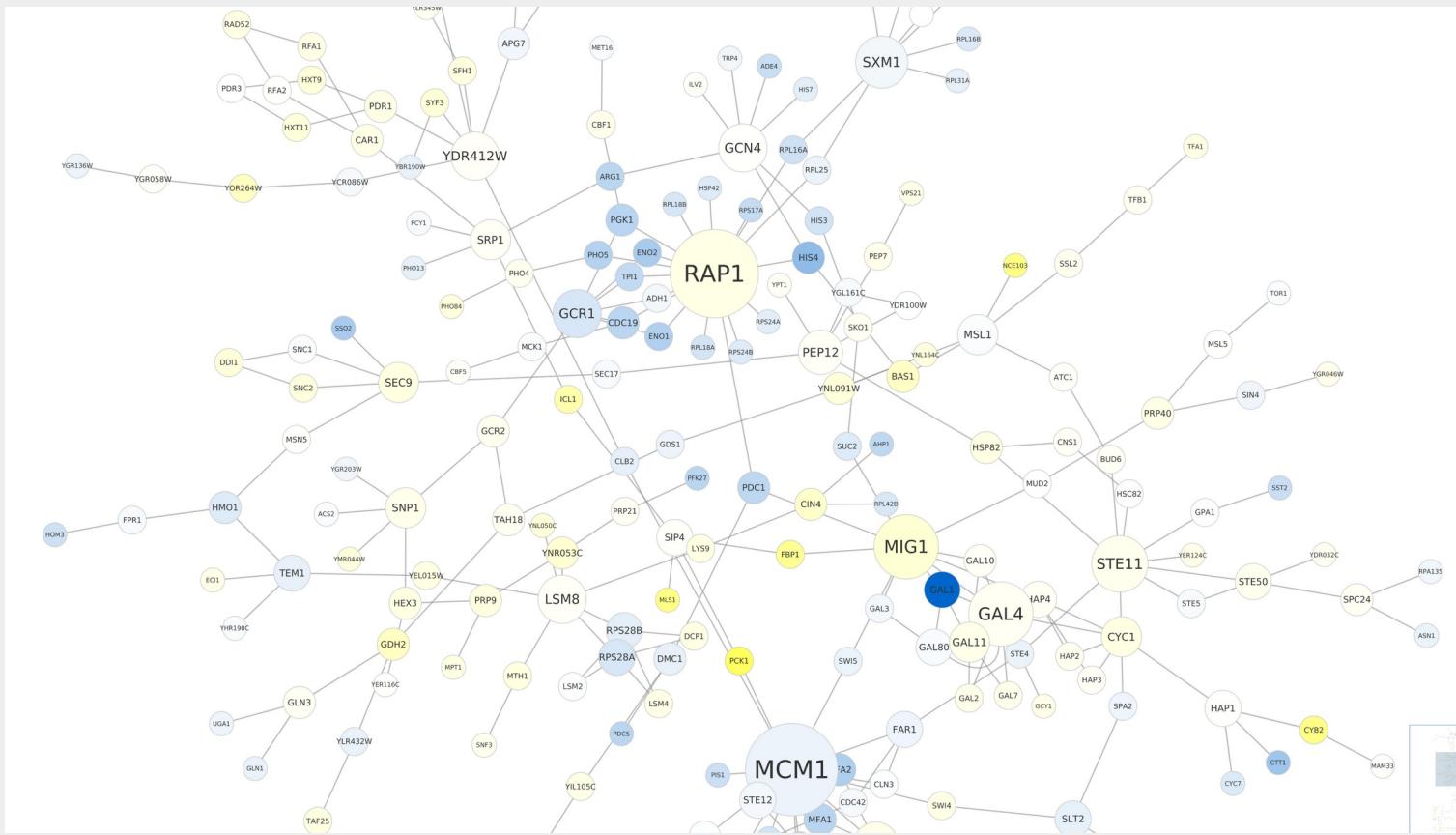
Memory

The screenshot shows the Cytoscape interface with a network graph containing three nodes labeled A, B, and C. Node A is at the top left, B is at the bottom left, and C is at the top right. There are two edges: one from A to B, and another from B to C. The interface includes a Control Panel on the left with tabs for Network, Style, Select, and Annotation, and a Table Panel at the bottom with columns for shared name and name, listing Node 1 (A), Node 2 (B), and Node 3 (C). The Table Panel also has tabs for Node Table, Edge Table, and Network Table.



Some Example Networks in Cytoscape

Examples: Yeast Perturbation Network

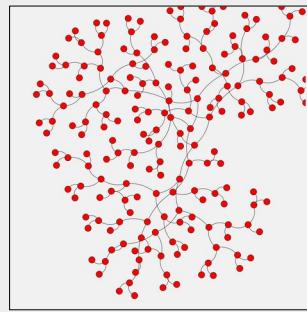
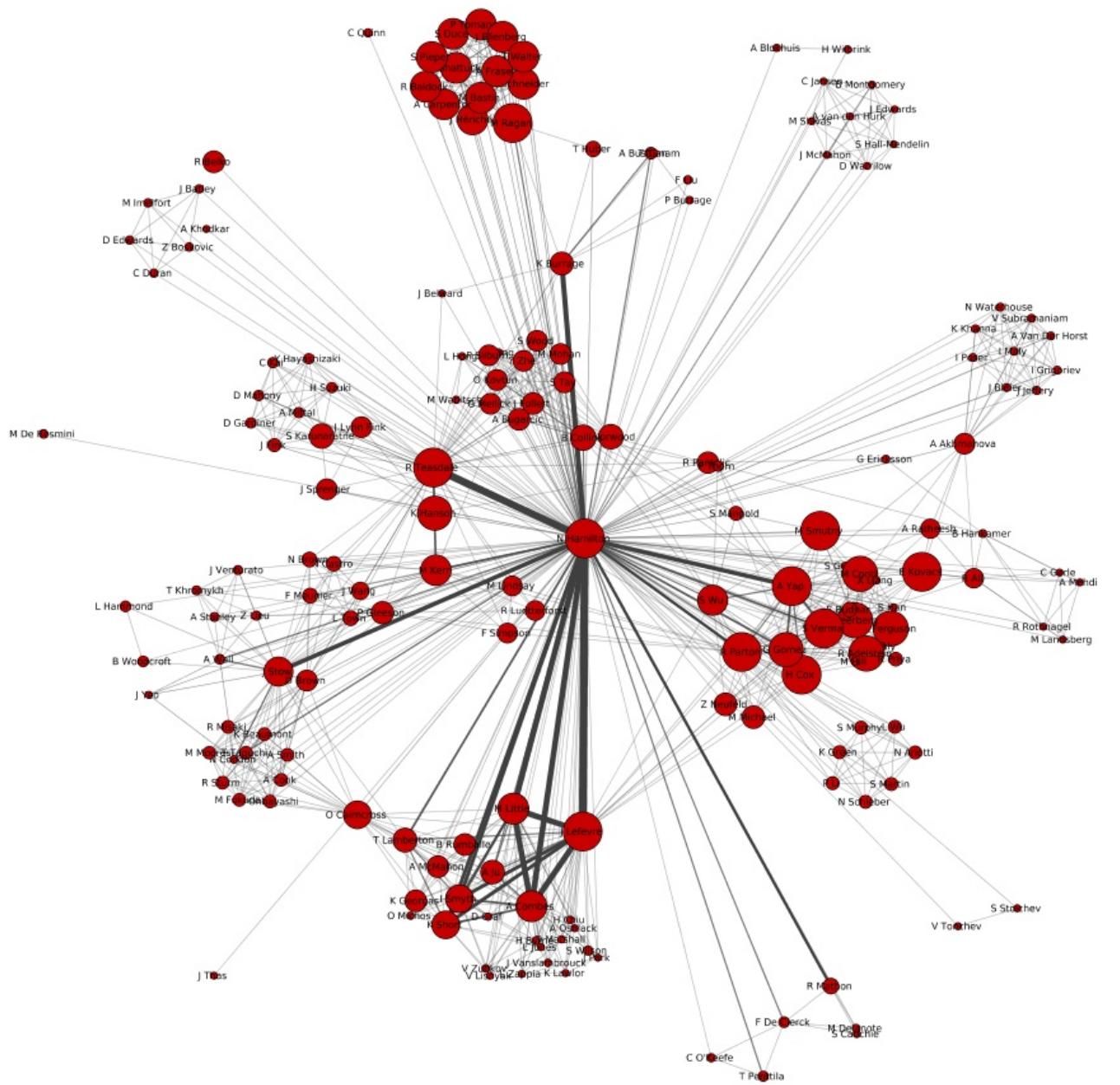


Nodes are proteins. **GAL1**, **GAL4**, **GAL80** are transcription factors which have been perturbed. Size represents number of interactions. Colour represents expression level when **GAL1** is perturbed.

Tutorial on protein expression data in Cytoscape:

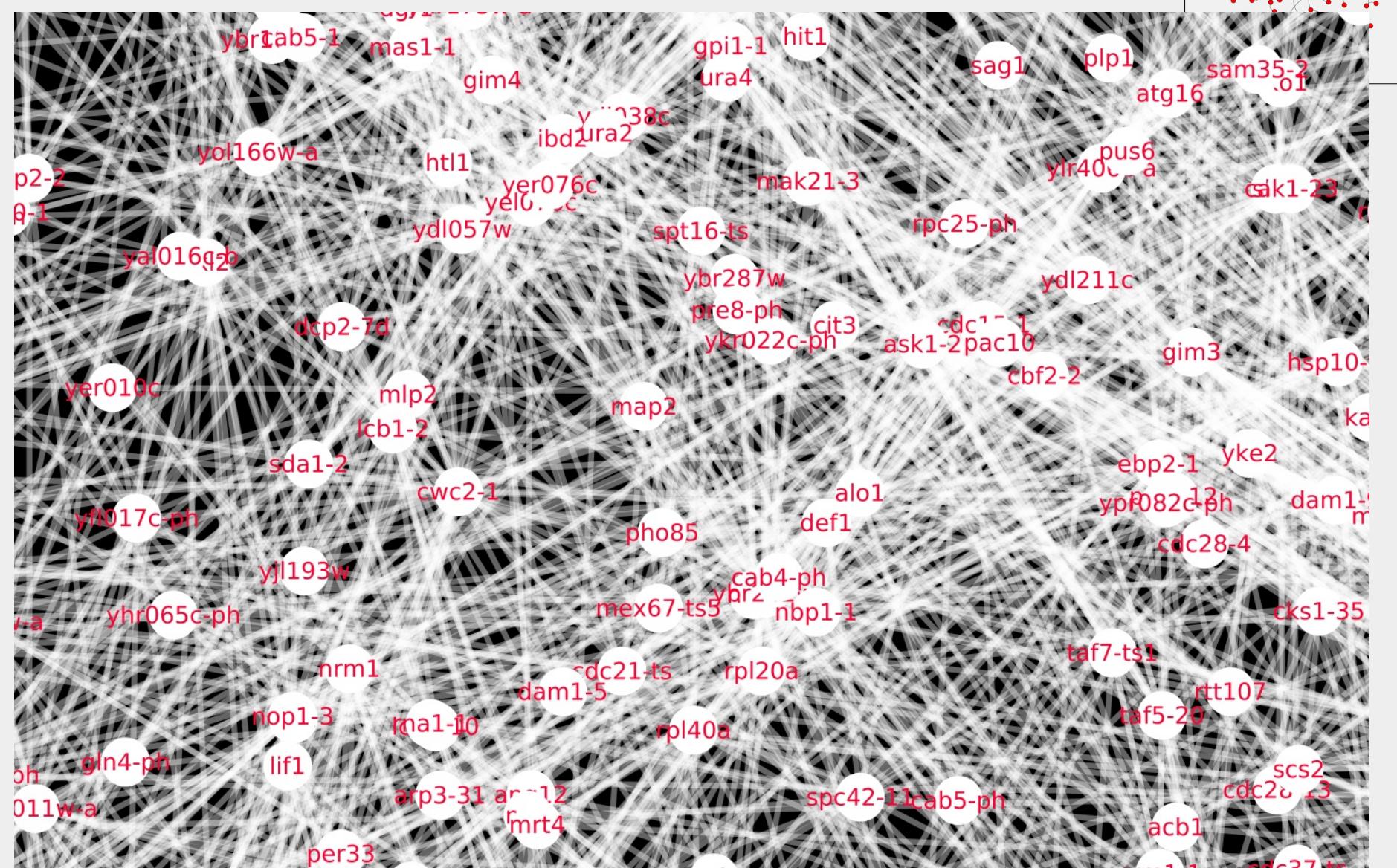
<https://cytoscape.org/cytoscape-tutorials/protocols/basic-data-visualization/#/>

Example: Co-publication Network

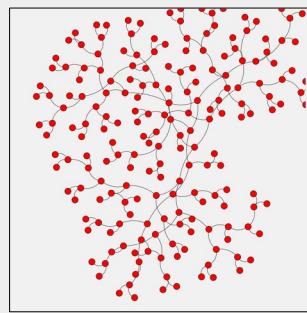


Who has published
with Dr Nick?

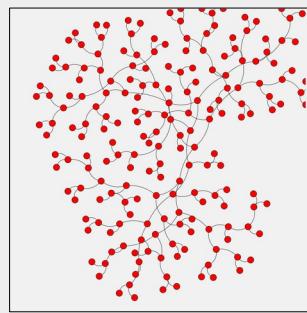
Examples: Yeast Gene Interactions



Bundling edges



Exercise: Create a simple graph interactively



- **Create a new empty network**

Select: File → New Network → Empty

Give it a name, e.g. “My Network”, and click OK.

- **Add 3 nodes**

Right click on the canvas and select: Add → Node 3 times

- **Rename the nodes in the Table Panel**

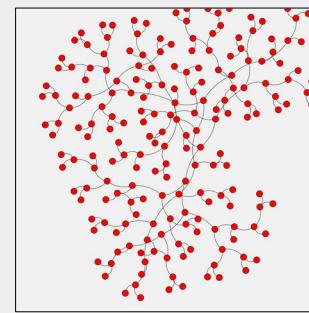
Change the “name” column to “A”, “B” and “C”

- **Add some edges**

Right click on a node and select: Add → Edge

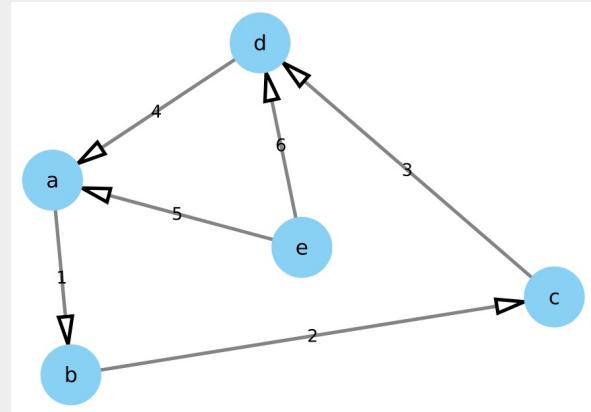
Left click on a node to connect to the selected node

Describing a network in a (Excel) File



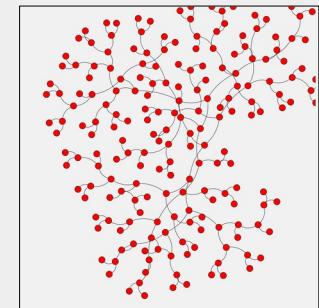
- An simple format in Excel can describe edges

	A	B	C	D
1	source	target	edge_property	src_node_property
2	a	b		1 Control
3	b	c		2 Control
4	c	d		3 Test
5	d	a		4 Control
6	e	a		5 Test
7	e	d		6 Test



- Each **row** corresponds to an edge, e.g. **a → b**
- A **column** can be labelled in any way you like, but each column will typically correspond to a **property** of:
 - source nodes, target nodes, edges

Exercise: Importing a Network from a (Excel) File



- File → Import → Network From File
- Select file **example_edges.csv**
- You need to tell the importer
 - Which column is the source nodes **source**
 - Which column are the target nodes **target**
 - Whether other columns are properties of source/target/edge

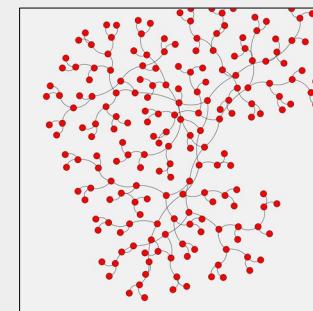
source

target

edge_property

src_node_property

Exercise: Create a simple Excel edge graph



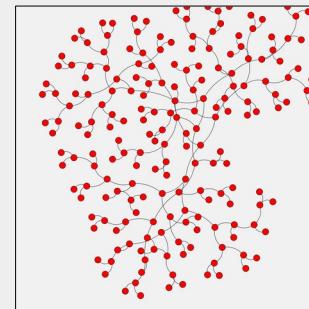
Create an Excel file that describes a network that -

- Has **nodes** Alice, Bob and Charlie
- Represents that
 - Alice likes Bob
 - Bob dislikes Charlie
 - Charlie likes Alice
 - Alice is a Scientist
 - Bob is a Historian
 - Charlie is an Engineer

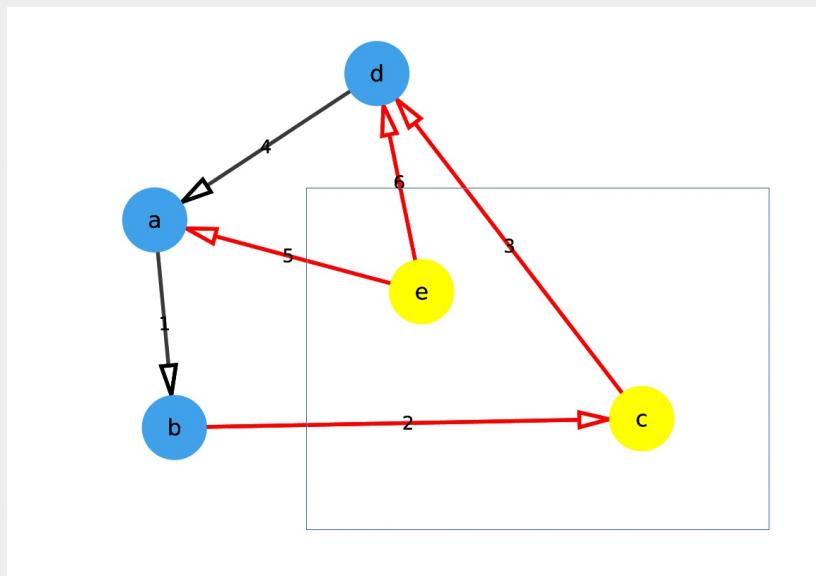
You will need columns for **source (person)**, **target (person)**,
relationship (like/dislike), **job**

Import this into Cytoscape (if you get stuck, have a look at file ABC.csv)

Moving and selecting node and edges manually



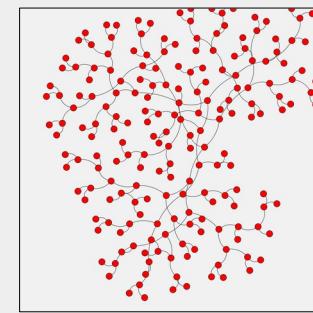
- Select individual nodes or edges: **Left mouse click**
- Add to selection: **Ctl + left mouse click**
- Select multiple nodes and edges: **Shift + left mouse drag**
- Move a node: **Mouse left click drag**



Shift dragging to select

Network Analyser

Cytoscape has a built in function that generates many of the commonly used network statistics or measures



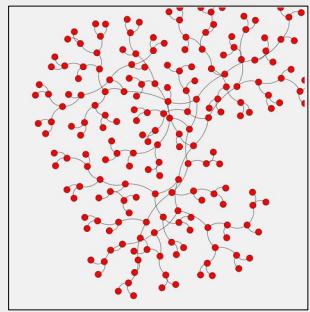
Tools → Analyse Network

The results can then be seen in **Table Panel**

By clicking on the table headings, results are sorted, so that the large degree nodes can be easily found, for instance

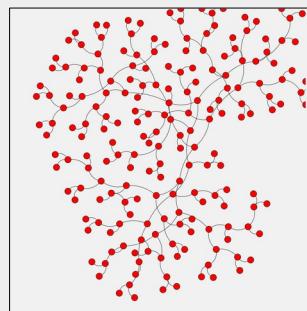
Try running Network Analyser on the networks you have made

Table Panel													
shared	name	AverageShortestPathLength	ClusteringCoefficient	ClosenessCentrality	IsSi	P	SelfLo	Eccer	Stress	Degree	BetweennessCentrality	NeighborhoodConnectivity	
Node 29	Node 29	3.4137931	1.0	0.29292929	<input type="checkbox"/>	0	0	6	0	2	0.0	4.5	
Node 28	Node 28	3.0	0.0	0.33333333	<input type="checkbox"/>	0	0	5	108	2	0.09244663	4.0	
Node 27	Node 27	2.75862069	0.16666667	0.3625	<input type="checkbox"/>	0	0	6	122	4	0.0833216	3.75	
Node 26	Node 26	3.75862069	0.0	0.26605505	<input type="checkbox"/>	0	0	7	36	2	0.02315271	2.5	
Node 25	Node 25	2.34482759	0.0	0.42647059	<input type="checkbox"/>	0	0	4	376	5	0.33657635	3.2	
Node 24	Node 24	2.79310345	0.0	0.35802469	<input type="checkbox"/>	0	0	5	92	3	0.06468449	4.66666667	
Node 23	Node 23	3.48275862	0.0	0.28712871	<input type="checkbox"/>	0	0	6	0	1	0.0	5.0	
Node 22	Node 22	3.31034483	0.0	0.30208333	<input type="checkbox"/>	0	0	6	170	3	0.15106732	2.33333333	



Styles in Cytoscape

Styles in Cytoscape



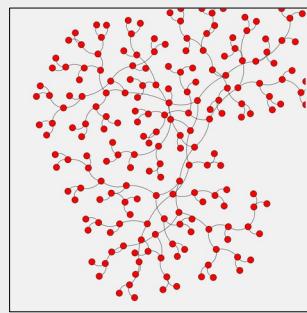
- Cytoscape has a number of **built in styles** that define the colours, shapes and line types of the network visualisation
- These can be found in the **Style tab** of the **Control Panel**
- Once selected a **Style may be modified** to change the colours or shapes of nodes or edges, or add images or annotations
- Style properties can also be **mapped using node/edge Table properties**
 - E.g. the colour and/or size of a node could correspond to the degree (number of edges) of a node
 - Mappings can be continuous, discrete or “pass through”

The Style tab

Default property column

Mapping column

Current Style Select



Control Panel

Network Style Select Annotation Social Network Input Panel AutoAnnotate

BioPAX_SIF

Properties ▾

Def. Map. Byp.

Border Paint
Border Width
Fill Color
Height
Image/Chart 1
Label
Label Color
Label Font Size
Shape
Size
Transparency
Width
 Lock node width and height

Node Edge Network

Diagram View

ErdosRenyi_1565667709504_690

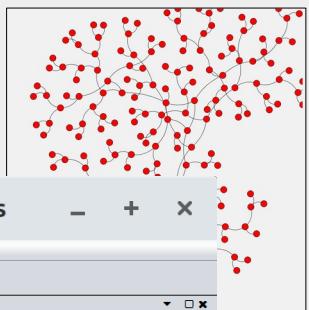
Table Panel

shared name name

Node 29	Node 29
Node 28	Node 28
Node 27	Node 27
Node 26	Node 26

Node Table Edge Table Network Table

Built in Styles in Cytoscape



Session: /home/nick/Cytoscape/Workshop/CytoscapeWorkshopSlidesData/WorkshopData/random_network.cys

File Edit View Select Layout Apps Tools Help

Control Panel Network Style Select Annotation Social Network Input Panel AutoAnnotate BioPAX Properties

Jrce Target Big Labels Curved Directed Minimal Sample1 size_rank Universe

Source Target Source Target default black default Gradient1 Marquee Nested Network Style Ripple Sample2 Sample3 size_rank_0 Solid

BioPAX

The main workspace displays a network graph with 30 nodes labeled Node 0 through Node 29. The graph is a sparse Erdős-Rényi random graph. The node sizes are proportional to their degree. The network has a diameter of 8 and a radius of 4.

Results Panel

Network Statistics of ErdosRenyi_1565667709504_690 (undirected)

Closeness Centrality	Stress Centralit
Neighborhood Connectivity Distribution	Bet
Topological Coefficients	Shortest Path Length Distribution
Simple Parameters	Node Degree Distribution
Clustering coefficient : 0.101	Number of nodes : 30
Connected components : 1	Network heterogeneity : 0.116
Network diameter : 8	Shortest paths : 870 (100%)
Network radius : 4	Characteristic path length : 3.257
Network centralization : 0.116	Avg. number of neighbors : 2.867
Number of isolates : 0	Number of s : 0
Number of multi-edge nodes : 0	Multi-edge no. : 0
Analysis time : 0.000000	Analysis time : 0.000000

Table Panel

Node Table Edge Table Network Table

Save Statistics Visualize Parameters

Node 5 Node 5 2.55172... 0.06666... 0.39189... 0 0 5 318 6 0.23527... 3.0 0 6 0.80603... 0.2333:▲

Node 25 Node 25 2.34482... 0.0 0.42647... 0 0 4 376 5 0.33657... 3.2 0 5 0.83189... 0.2363:▲

Node 20 Node 20 2.51724... 0.1 0.39726... 0 0 5 216 5 0.19891... 3.2 0 5 0.81034... 0.2363:▲

Node 14 Node 14 2.68965... 0.2 0.37179... 0 0 5 216 5 0.15959... 3.8 0 5 0.78879... 0.2833:▲

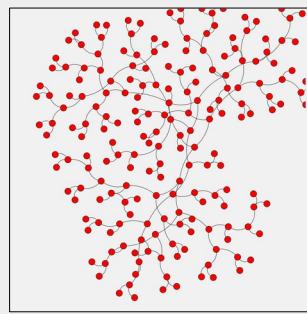
Node 27 Node 27 2.75862... 0.16666... 0.3625 0 0 6 122 4 0.08332... 3.75 0 4 0.78017... 0.2954:▲

Node 17 Node 17 2.72413... 0.16666... 0.36708... 0 0 6 208 4 0.14906... 4.0 0 4 0.78448... 0.3181:▲

Node 6 Node 6 2.82758... 0.33333... 0.35365... 0 0 6 74 4 0.04612... 3.75 0 4 0.77155... 0.2715:▲

Memory

Changing Style Properties



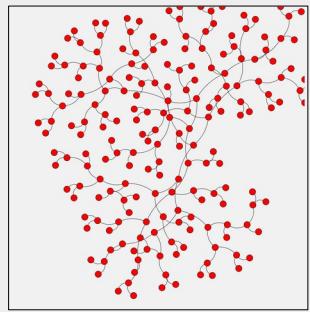
To change the **Default** color/shape etc of **nodes**

- Select the Style tab and select the Node subtab
- Click on the Default (**Def.**) column of the property to change
- Select the new Default colour/shape etc

To **Map** a node property to depend on a **column in the node table**

- Select the Style tab and select the Node subtab
- Click on the **Map** column of the property, e.g. size or colour, to change
Column/Mapping type selection sub-menus will appear
- Select the Node table **Column** to use for the mapping
- Select whether to use a continuous, discrete, or pass through mapping
- Continuous mapping will give a default colour scheme, for instance, a discrete mapping may need further selections, e.g. different colours for each value

Similarly for edges



Types of mapping for node & edge table data

Discrete Mapping

- There are a small number of different cases and you want a different colour/size/shape for each based on a column in your edge or node table

Continuous mapping

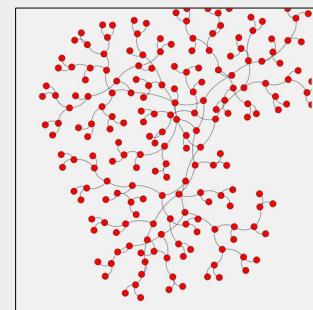
- Each node or edge has a continuous number associated with it, i.e. temperature or expressions level, so use this number as a size or colour on a spectrum for the node or edge

Passthrough Mapping

- Values in a network column are passed directly to the property. Typically used for node/edge labels.

Exercise: Visualising the Moreno Sociograms

- Who wants to sit next to whom?



In 1934 Moreno published a classic study in social networks on relationships between children in the classroom and how these change over time. In it each child was invited to pick two other children they would like to sit next to in the class. The results were visualised as networks. Here we will look at the grade 3 class.

File → Open the network **Sociogram3-boy-girl.cys**

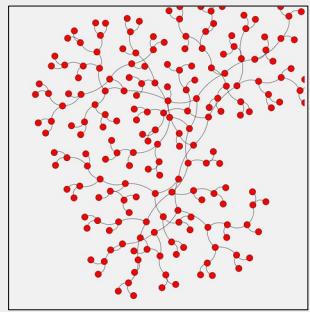
Run the **Network Analyser** to calculate network statistics (with ‘**treat as directed**’ selected)

1. Map the **Fill Colour** of nodes by a **discrete map** of the **Sex** property and choose different colours for Boys and Girls.
2. Map the Node **Size** to a **continuous mapping** of the **indegree**.

[Bonus: If you’re feeling tricky, see if you can put arrow heads on the edges]

Who is most popular? Who doesn't like anyone? What is noticeable about boys/girls?

Other things you can do with Styles

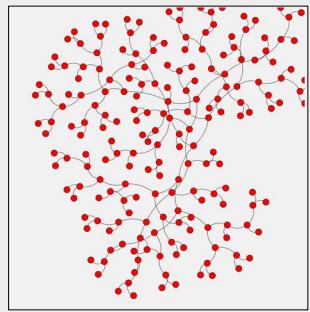


Create new styles

Add images/charts/graphics to nodes

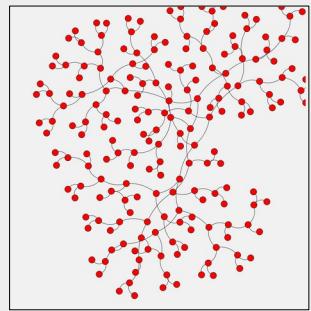
Fine tune label positions

For more: <http://manual.cytoscape.org/en/stable/Styles.html>



Apps in Cytoscape

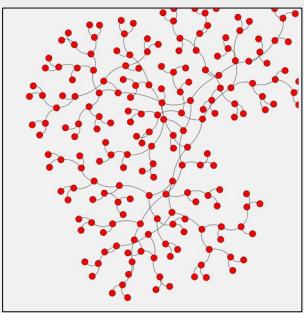
Apps in Cytoscape



Cytoscape has an App Store built in that can extend its functionality. For instance:

- DynNetwork: Visualise dynamic networks
- Mclique: find maximal cliques
- Yfiles: different layout algorithms
- ANIMO: dynamic modelling of biological networks
- Social Network: import publication graphs
- dot-app: Import/export of Graphviz files in Cytoscape

Each App has documentation and a tutorial



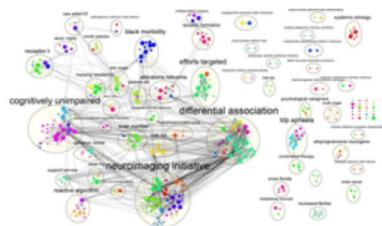
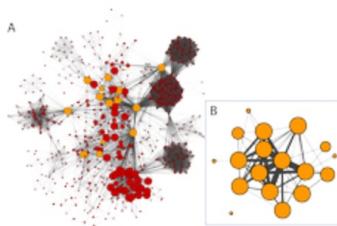
SocialNetwork

Summarizes how individuals are connected by building networks where nodes represent authors and edges represent publications.

★★★★★ (3) 5318 downloads | posts | citations 

[Details](#) [Release History](#)

Categories: data visualization, social network analysis



The Social Network Cytoscape app creates a visual summary of how individuals are connected. Biological networks can be visualized and analyzed using Cytoscape. Often researchers want to go beyond the network of proteins or genes and also look at the inter-connectedness between colleagues and institutions. Who tends to publish together? What institutions are most collaborative? Are there inter-disciplinary connections in my institution? The app addresses these questions by building co-publication networks where nodes represent authors, edges represent co-authorship and how frequently co-authors collaborate is indicated by the thickness of an edge.

Authors:

- Victor Kofia (University of Toronto)
- Gary Bader (University of Toronto)
- Ruth Isserlin (University of Toronto)

CYTOSCAPE 3

 [Install](#)

Version 1.3.0

Released 5 Dec 2016

Works with Cytoscape 3.2

Download Stats [Click here](#)

RESOURCES

 [Ask a question](#)

 [Search posts](#)

 [Website](#)

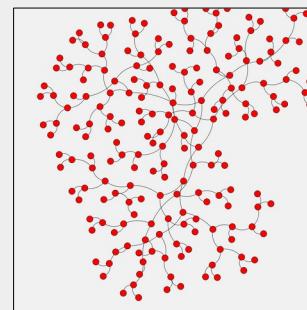
 [Tutorial](#)

 [Cite this App](#)

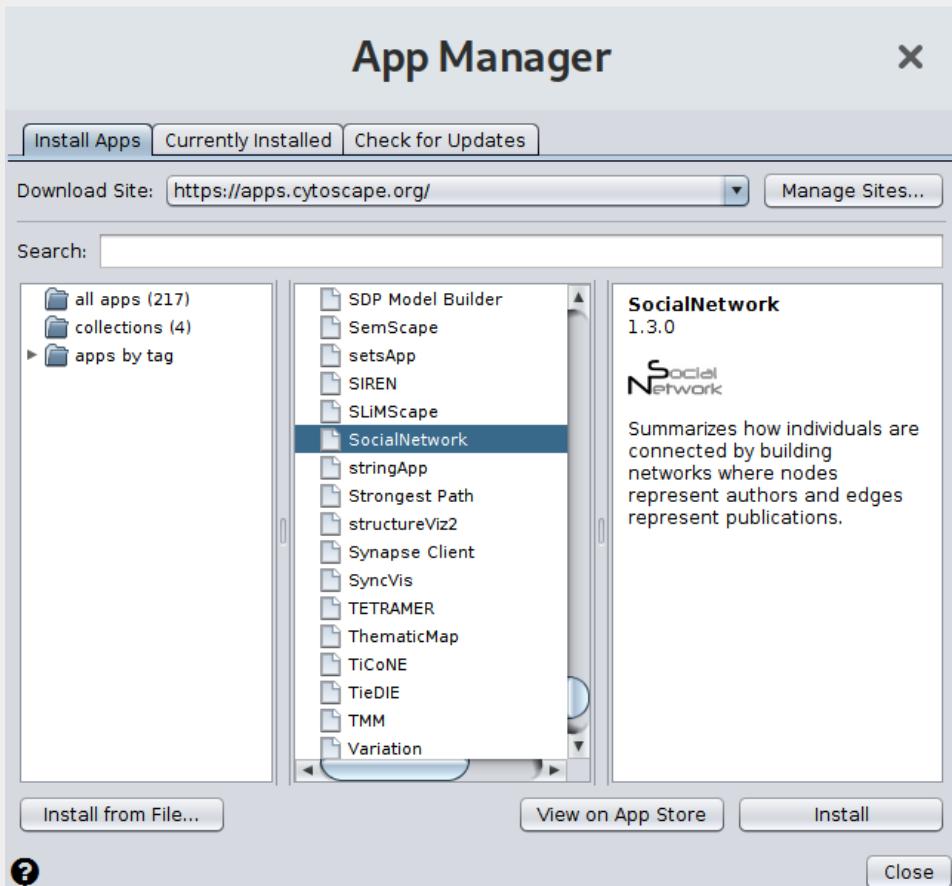
 [Code Repository](#)

 [E-mail](#)

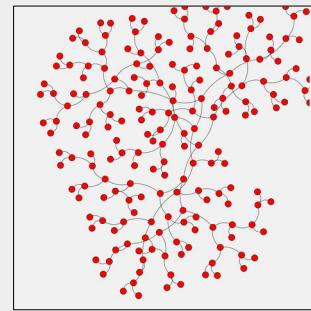
Exercise: Install the Social Network App and the dot-app App



- Click Apps → App Manager to start the manager
- Scroll down and select **SocialNetwork**
- To see documentation click [View on App Store](#)
- Click **Install**
- Similarly for **dot-app**



Extension Exercise: Downloading your SCOPUS publications



- For UQ researchers search for **SCOPUS** in the library catalogue

<http://library.uq.edu.au/screens/opacmenu.html>

and select the

Database/ Available online result

PAGE 1 49,580,901 Results Personalise

1 JOURNAL
Scopus.
Check holdings at Warehouse Journal (BP04667) >
Available online >

2 DATABASE
Scopus.
Available online >

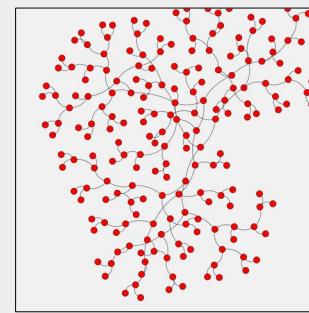
3 ARTICLE / multiple sources exist. see all
Scopus.(info.sciverse.com/scopus)(Website overview)
Swoger, Bonnie J. M.
Library Journal, March 1, 2013, Vol.138(4), p.97(3)
than ISI's Web of Knowledge. Scopus is an excellent... Scopus Elsevier info.sciverse.com... /scopus Content Elsevier's multidisciplinary >
Available online >

- Monash go directly to

<https://go.openathens.net/redirector/www.monash.edu?url=https://www.scopus.com>

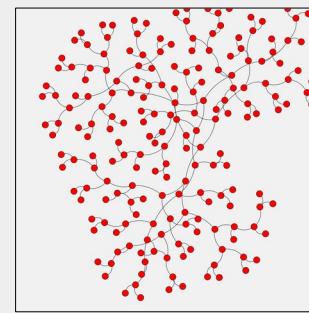
- Login using your UQ/Monash credentials when requested

Extension Exercise: Downloading your SCOPUS publications



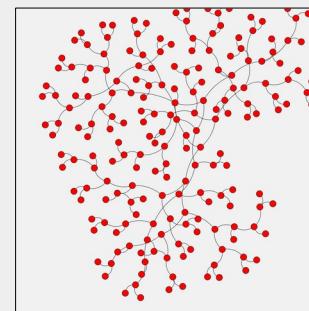
- In SCOPUS select **Authors search** and put in you name or ORCID
 - Select the author that is you, and click “**Show Documents**”
 - Check select “**All**” then click “**Export**”
 - Select “**CSV**” as the method of export
 - Click the “**Export**” button
-
- Note: the “Author Id” column needs to be deleted once downloaded as SCOPUS have recently changed format
Open the downloaded file in Excel, delete the column, and save.

Extension Exercise: Downloading your SCOPUS publications

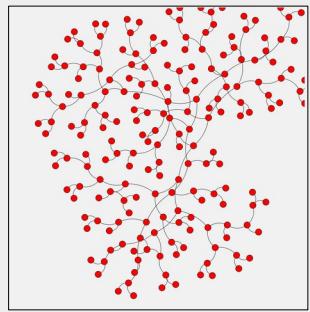


- In SCOPUS select **Authors search** and put in you name or ORCID
 - Select the author that is you, and click “**Show Documents**”
 - Check select “**All**” then click “**Export**”
 - Select “**CSV**” as the method of export
 - Click the “**Export**” button
-
- Note: the “Author Id” column needs to be deleted once downloaded as SCOPUS have recently changed format
Open the downloaded file in Excel, delete the column, and save.

Exercise: Importing a SCOPUS network into Cytoscape

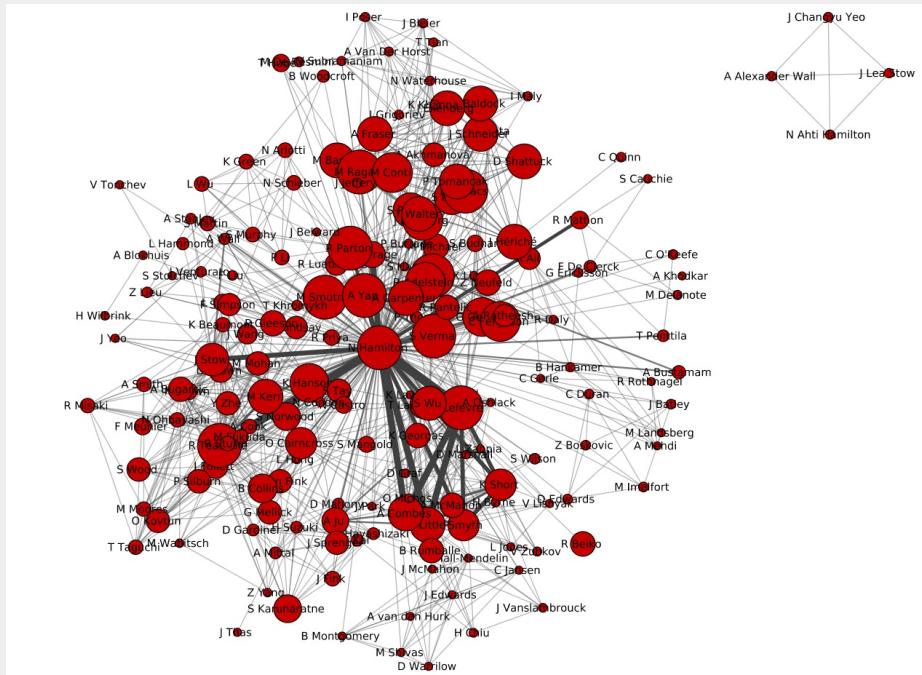
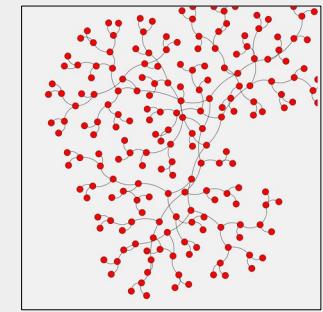


- Start the Social Network App
 - Apps → Social Network → Show Social Network
- A **Social Network** tab should appear on the **Control Panel**
- Select that tab and then select **File Input** as **SCOPUS**
- Click “...” to select the **nhamilton_scopus.csv** file containing SCOPUS network
- Click **Create Network** and a (possibly messy) network should be visualised
- Observe the horrible mess



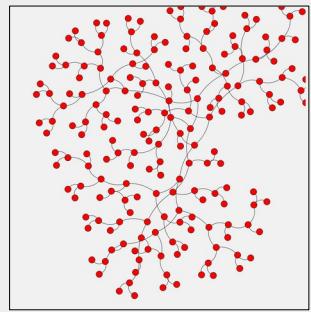
Network Layout in Cytoscape

Different approaches to layout of networks



- Different networks will suit different methods of layout
No one algorithm is best for all
- What is a good/bad layout?
 - avoid edge/node crossing
 - allows you to find structure and see relationships

Layout algorithms in Cytoscape

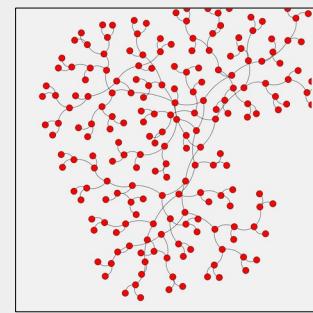
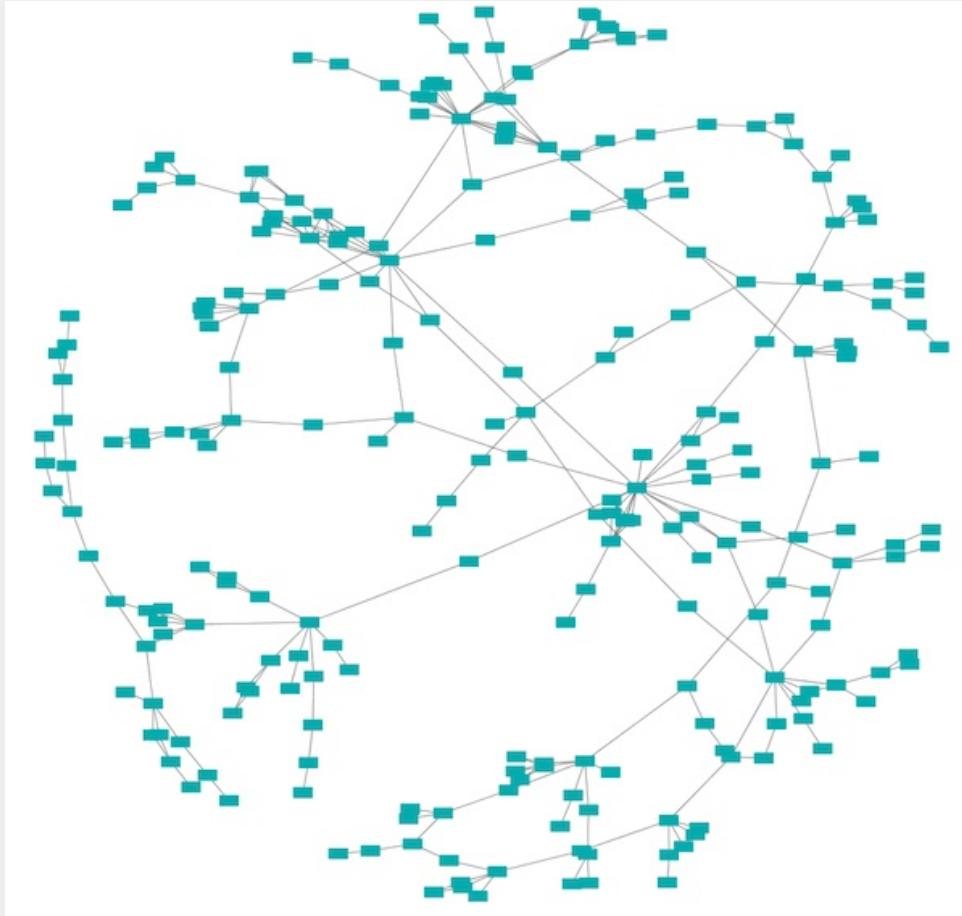


Cytoscape has several built in methods of laying out graphs to make them pretty or to help you find information in them

The following slides outline some of these, and borrow heavily images from the Cytoscape documentation at

http://manual.cytoscape.org/en/stable/Navigation_and_Layout.html

Spring Layout

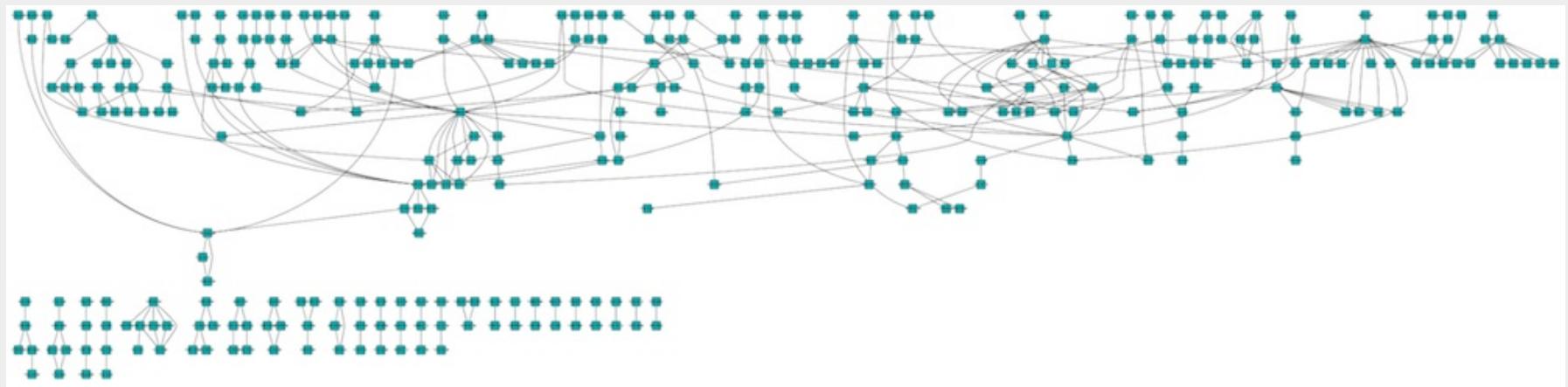
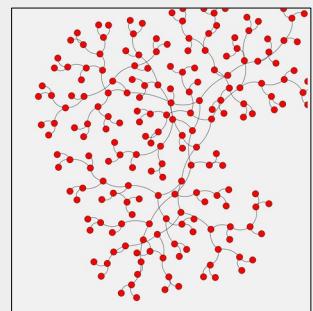


Each edge is a “spring”, each node “repels” all the others

Force of the spring can be proportional to an edge weight

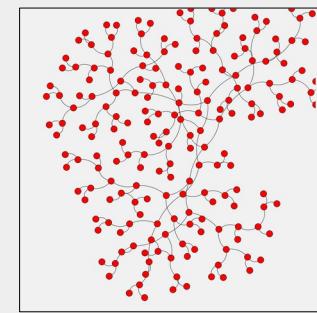
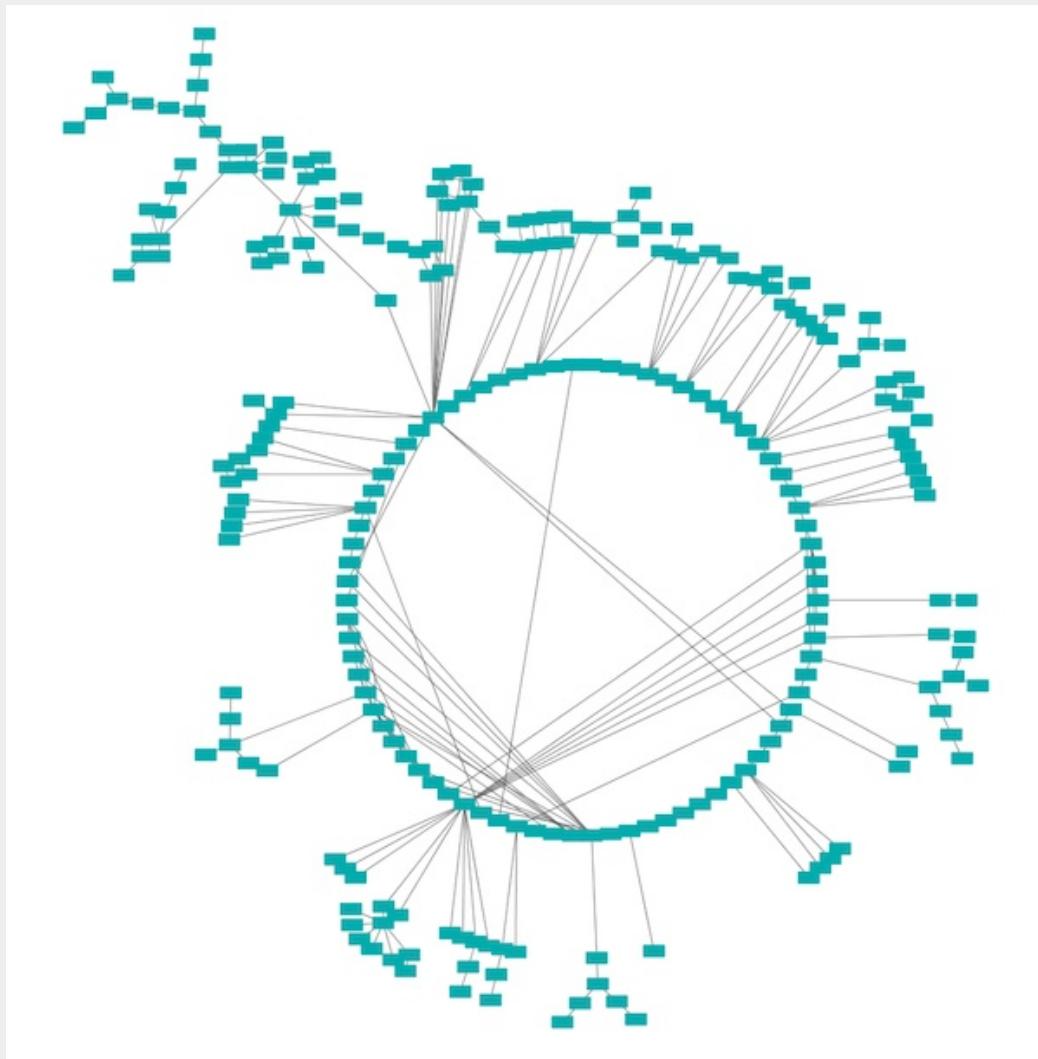
A good generic algorithm to try first

Hierarchical Layout



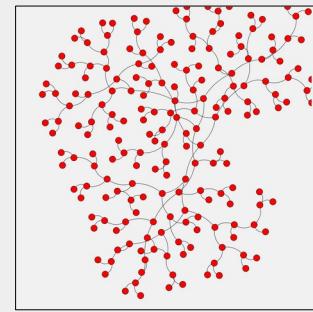
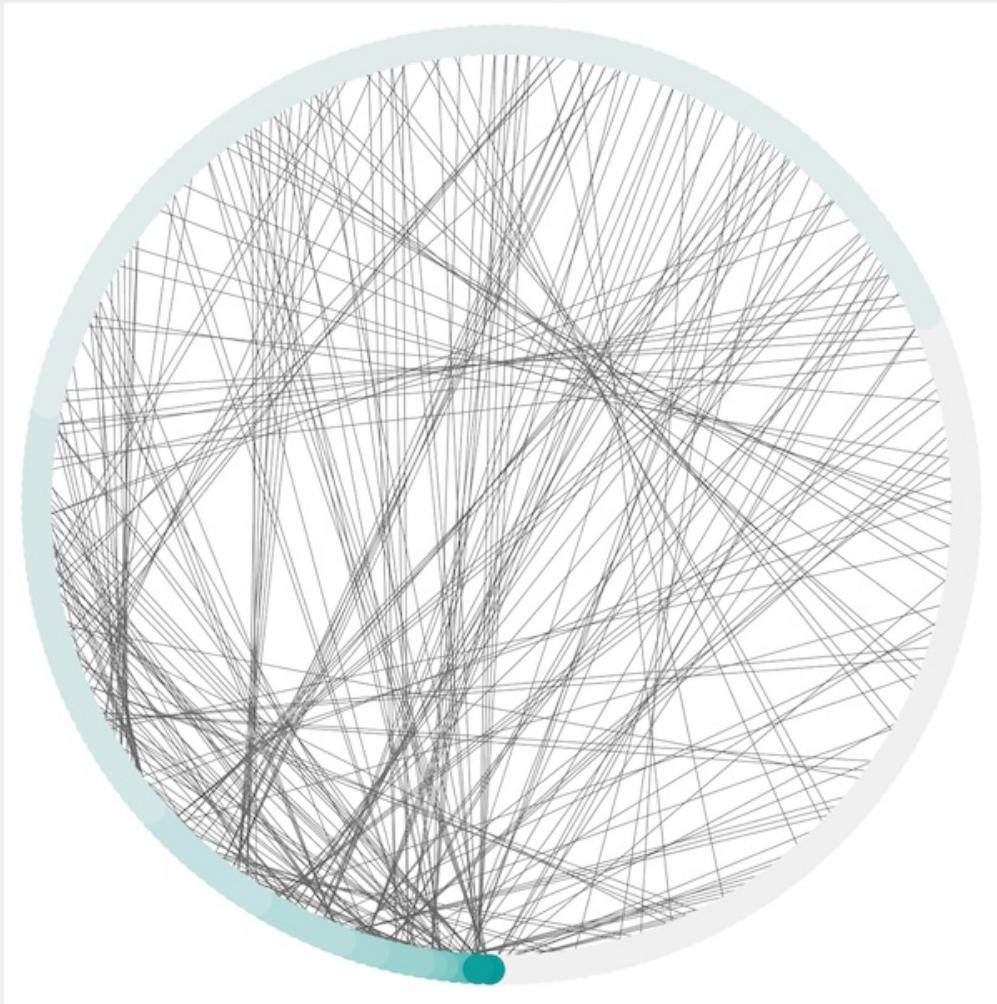
For when there are layers or flow in your network

Circle Layout



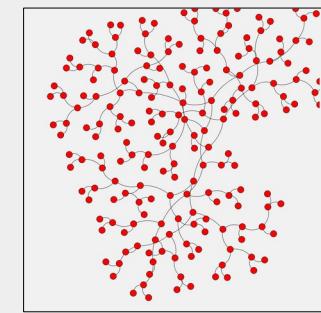
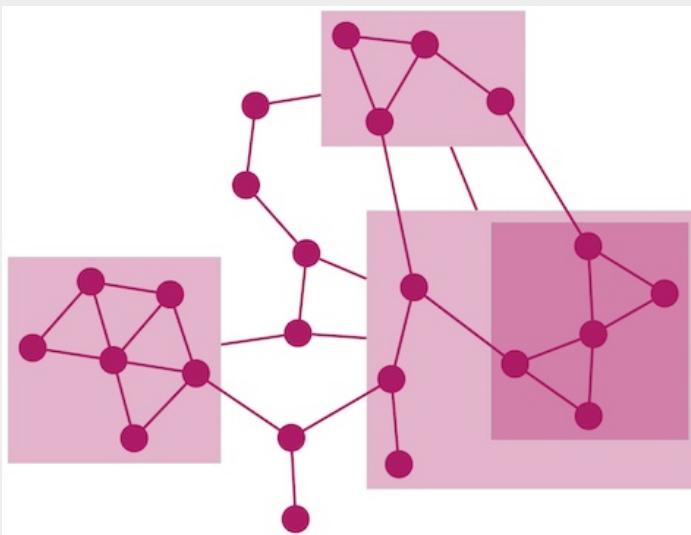
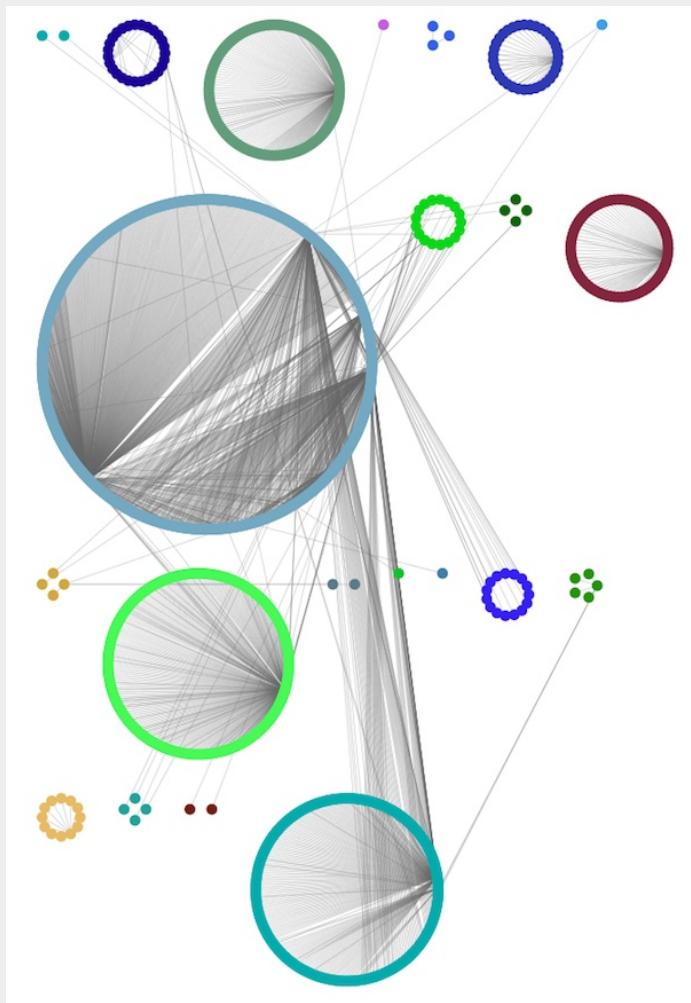
Attempts to arrange nodes in circular layers

Attribute Circle Layout



Nodes are on a circle, but are grouped according to a property you select in the Node Table

Also ...

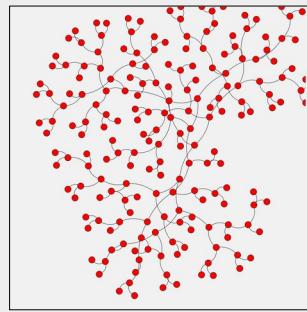


YDR140C	YDR111C	YDR054B	YDR103C	YDR205W	YBR239W	YDR362C	YDR222W	YDR149W	YME044C	YDR019C	YIL126N	YDR023C	YDR215W	YML122C	
YHR071W	YHR014C	YML015W	YDR008W	YIL111W	YIL033C	YBR024W	YLS113C	YDR103W	YIL165W	YCA069C	YMR118H	YFR014C	YAL046C	YMR332C	
YDR311B	YOR179C	YER113W	YBR072W	YGL079W	YBR121C	YIL111B	YBR024W	YIL113W	YDR103W	YDR062W	YLR119C	YFR014C	YAL046C	YML094C	
YNL047W	YNL130C	YPR049W	YPL275W	YBR010C	YPR048C	YIL029W	YER005C	YLR173C	YDR103W	YLR110C	YPR029W	YIL029C	YLR110W	YCL033W	
YDR174W	YLD028W	YKL101W	YOL156B	YLS219W	YIL021W	YOL136C	YLS205W	YNR005C	YIL024W	YPR015W	YLR145W	YLR137C	YER054C	YLR023C	YOR166W
YBL050W	YBL166W	YKL109W	YHR171B	YBR127W	YIL028W	YOL311B	YLS149W	YLG237C	YIL022C	YBL014W	YLR153C	YLR137C	YER054C	YLR023C	YIL159W
YKL097W	YME044W	YOL155W	YBR059W	YBR045C	YKL279C	YCA058C	YLS149W	YLR154W	YME054C	YPR014W	YPR048C	YER054C	YLR023C	YOR166W	YOL279W
YIL143C	YDR134C	YNG012W	YNL236B	YCR111W	YOL226C	YML0312	YIL312W	YLS162C	YLR116W	YER051CA	YNL086C	YOR264W	YKL011W	YER023C	YIL139C
YBL020W	YCL015C	YPL248C	YLR081B	YBR099W	YBR099W	YBL006C	YIL113W	YML100C	YIL109C	YSL277C	YHR141C	YOL149W	YLR137C	YOR166W	YCL033W
YDR032C	YBR040W	YOL127W	YBL155W	YML116W	YOL029C	YOL070C	YDR046W	YLR153C	YBL248C	YIL010W	YNC154C	YER070C	YML108W	YOR257W	
YER127W	YLR117C	YDR135W	YPR119B	YDR053C	CAG038W	YOR161C	YMK019C	YPL113W	YIL134W	YIL105C	YOR127C	YER141W	YAL024W	YOL286C	
YGL012C	YCR086W	YDR412W	YPR028B	YBR093C	YOL171W	YBR221B	YIL005C	YPR038W	YNL302C	YML114C	YML117C	YOM014C	YPR010C	YOL127W	
YGL026C	YDR074W	YPR052C	YBR120W	YIL113C	YKL52C	YBR274W	YLA044C	YML215W	YBR084W	YOL120C	YNC307C	YAL011W	YER012W	YNC210W	
YDR129W	YER012W	YKL248W	YIL149W	YLR248W	YMK033C	YBR238B	YIL115C	YGL134W	YHR051C	YOL113W	YR222W	YHR051C	YPR053C	YNC231C	
YGR050W	YER032C	YFL118W	YER041W	YIL177C	YBR029W	YBR010W	YER021W	YLR171W	YER016Z	YOL230W	YOL222W	YER016Z	YPR010C	YOL121C	
YGL049C	YOL122W	YOR120W	YER041C	YIL177C	YLR248C	YIL113C	YER021W	YLR171W	YER017C	YCA021C	YOL221C	YER017C	YPR010C	YOL121C	YER011W

See the documentation for more

http://manual.cytoscape.org/en/stable/Navigation_and_Layout.html

Additional methods: yFiles layout algorithms

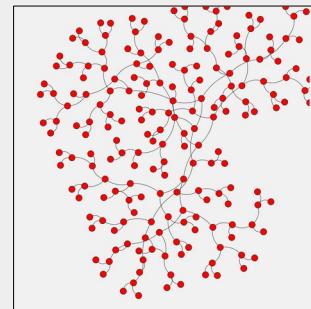
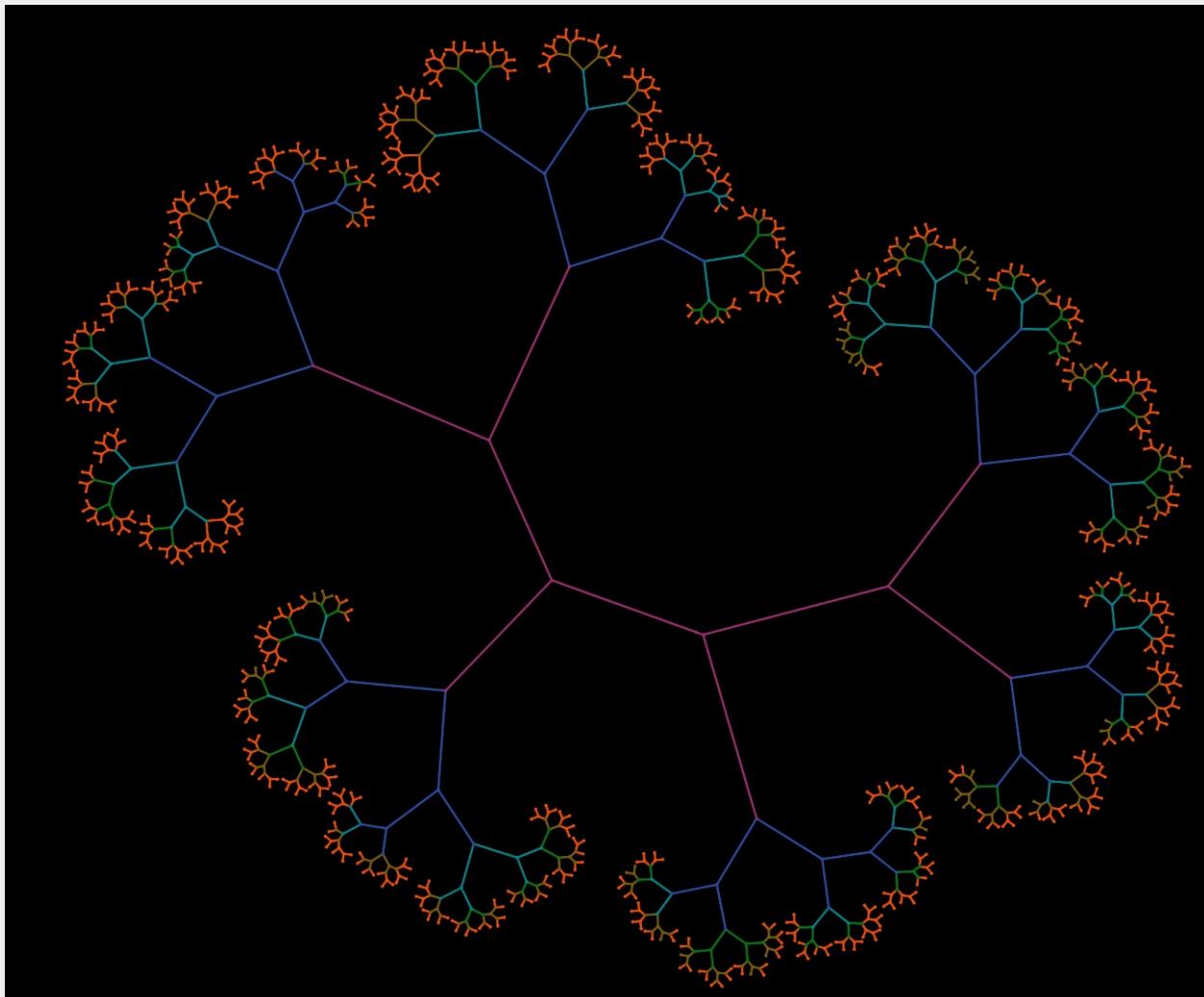


- Circular Layout
- Hierarchic Layout
- Hierarchic Layout Selected Nodes
- Organic Layout
- Orthogonal Layout
- Radial Layout
- Tree Layout
- Orthogonal Edge Router
- Organic Edge Router

Documentation and Examples

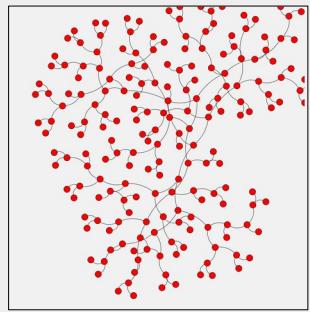
<https://www.yworks.com/products/yfiles-layout-algorithms-for-cytoscape>

Yfiles Layout



Yfiles layouts seem to be “better” than the in-built methods

The “Organic” method can be a good method to try first



Exercise: Installing yFiles layout

To install the yFiles layout methods

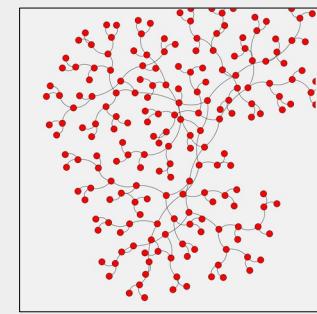
Layout → Install yFiles

The yFiles methods are then available under the Layout menu

More information on yFiles

<https://www.yworks.com/products/yfiles-layout-algorithms-for-cytoscape>

Exercise: Trying different layout algorithms



Try out some of the built in and yFiles layout

algorithms on your own (if you have it) or Dr Nick's SCOPUS publication network

Which look good/bad? Why?

Are there clusters of authors? What properties cluster them?

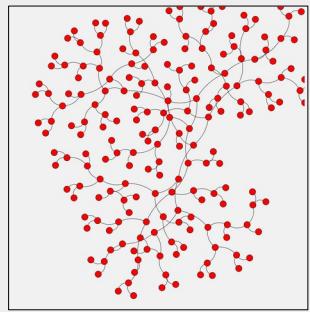
Do you notice anything unusual?

Are there any errors in the data?

Import (File → Import Network from File) the network

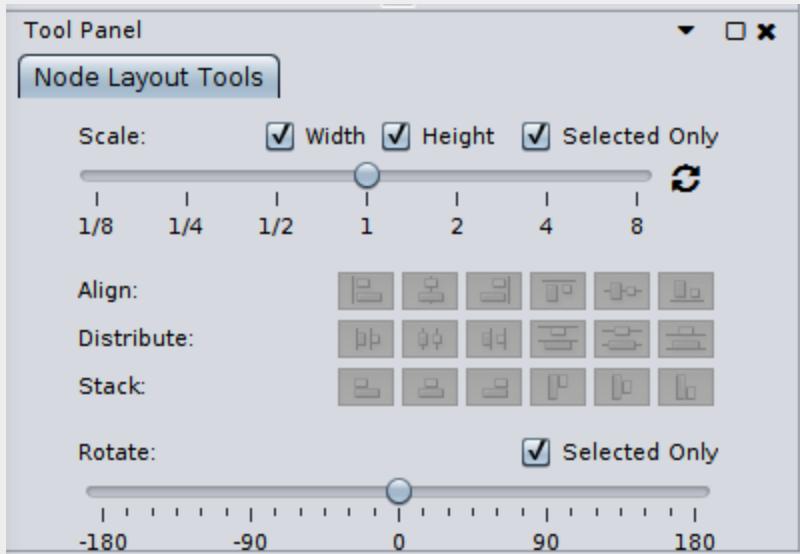
kidney_stages7-12.dot

and try some different layouts



Node Layout Tools for Scaling

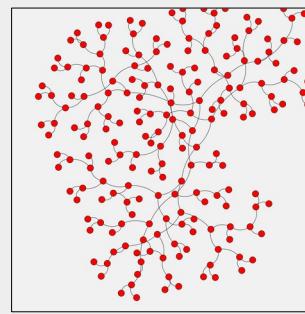
- Select Layout → Layout Tools and a panel will appear in the bottom left corner



- This can be used to scale the relative size of (selected) nodes to the edge length, or rotate (selected) parts

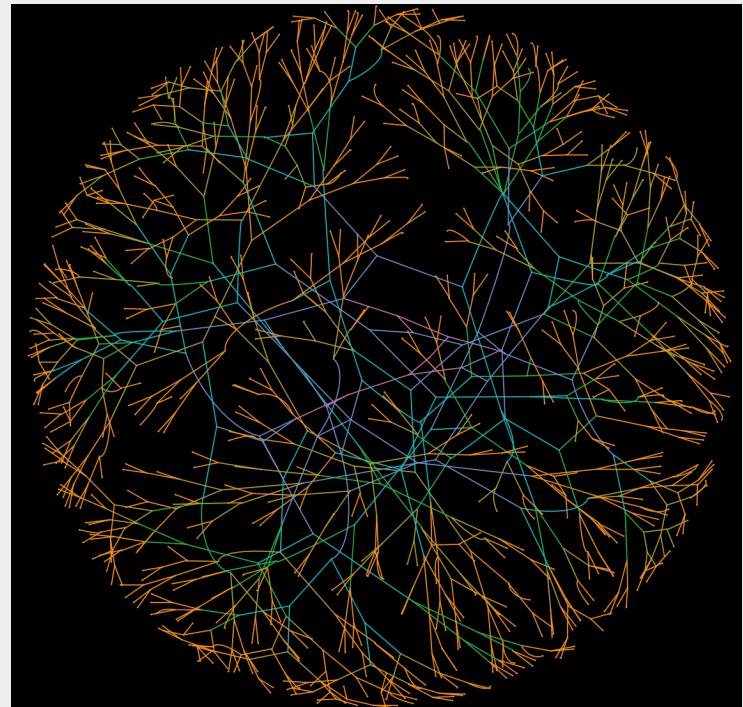
Dealing with edge overlaps

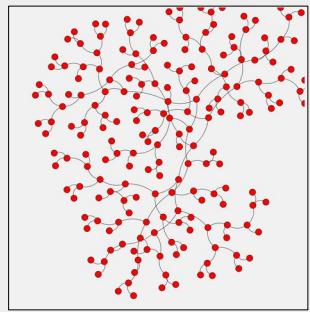
- Often edges will overlap, perhaps unnecessarily
- Dealing with this can be complicated
- The simplest approach is to try a different algorithm, or fix the “errors” by hand if there are only a small number of them
- Also, parameters to the layout algorithm can be tweaked



Layout → Settings

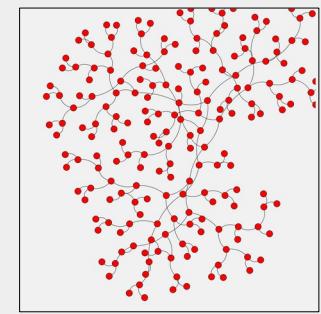
Try reducing gravity,
increasing repulsion



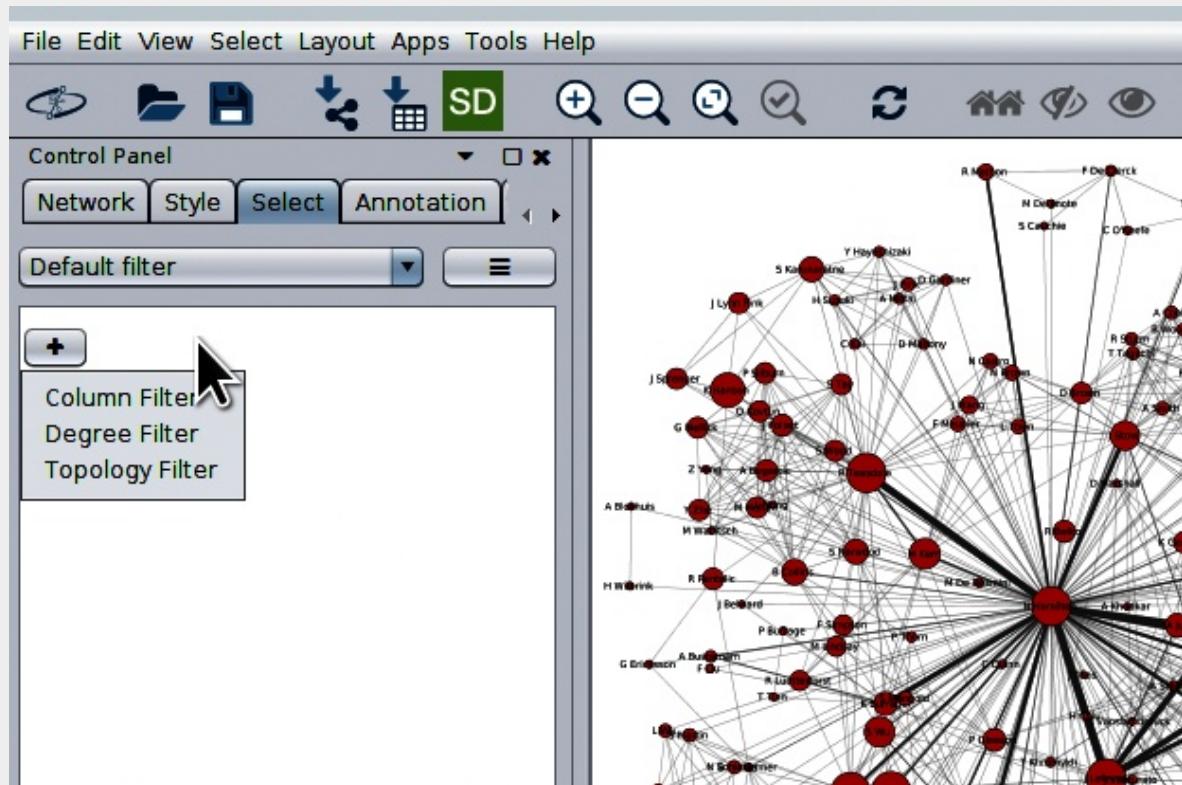


Network Filtering

Network Filtering

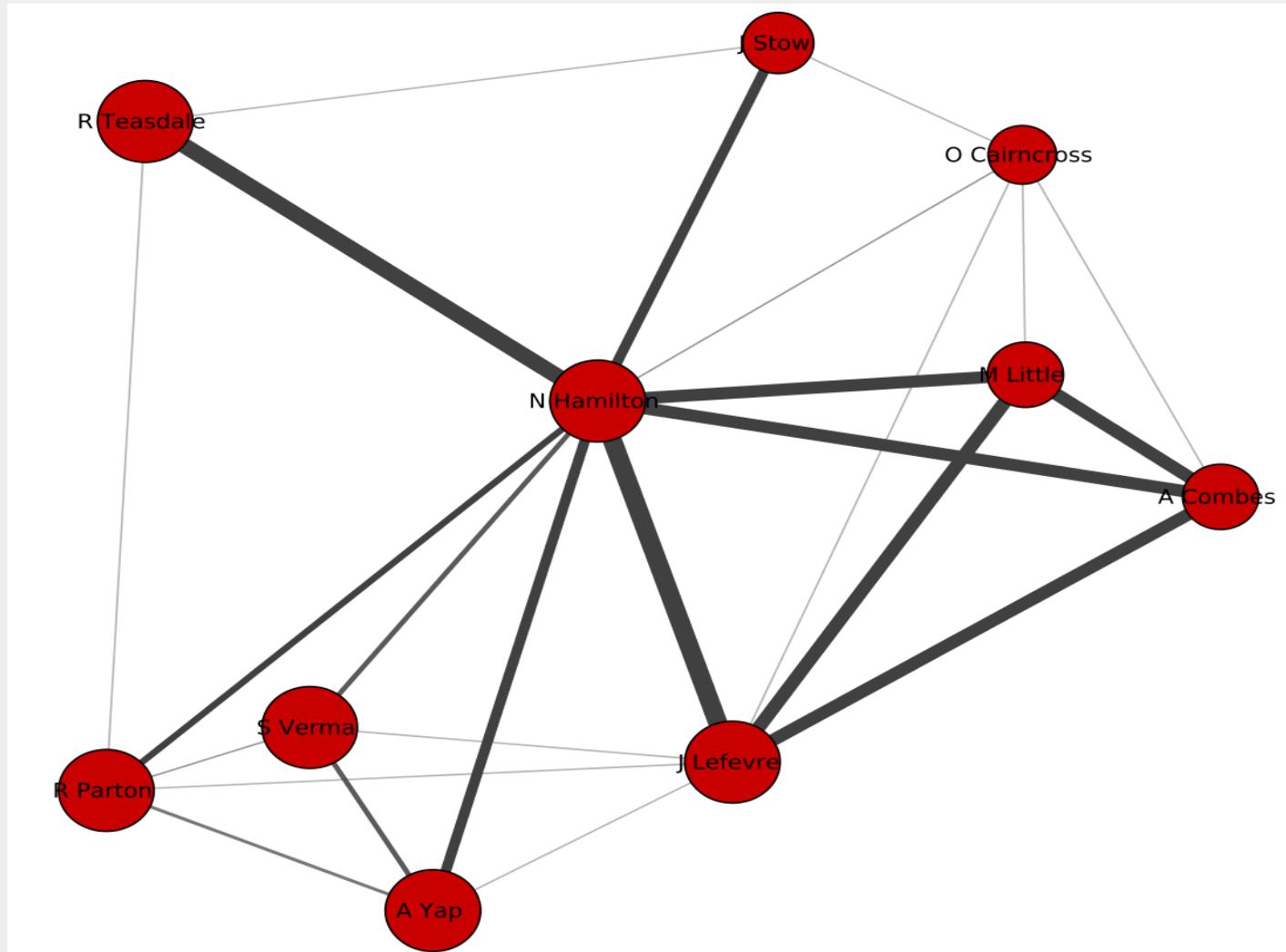
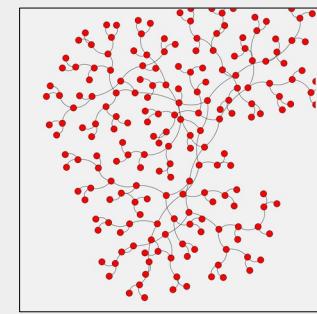


- Sometimes you may want to select nodes or edges in a network based on some property they have
 - Cytoscape has facilities for selecting based on column data in the **Table Panel**, the degree of nodes, or the topology

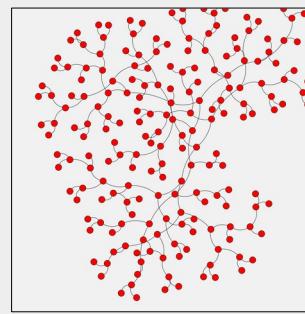


Network Filtering

Once a filter has created a selection a new graph is easily created from that selection



Other things you can do in Cytoscape

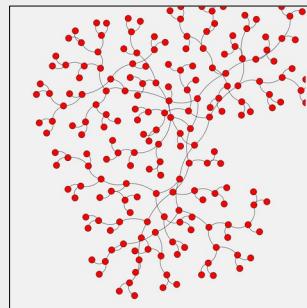


- Nested networks
- Edge bending and bundling
- Column data functions – a bit like functions in Excel
- Annotations with images/shapes/text/arrows
- Link out to web URLs
- Use cytoscape.js for javascript networks in web pages
- Control Cytoscape from R or other programming languages

And many more things ...

<http://manual.cytoscape.org/en/stable/>

Getting more help



A quick tour of Cytoscape

http://manual.cytoscape.org/en/stable/Quick_Tour_of_Cytoscape.html

The Cytoscape User manual

<http://manual.cytoscape.org/en/stable/>

Cytoscape Tutorials

<https://github.com/cytoscape/cytoscape-tutorials/wiki>

Online Help Groups

<https://groups.google.com/forum/?fromgroups#!forum/cytoscape-helpdesk>

Hacky Hour at UQ: every Tuesday 3-4pm online via Zoom



@HackyHourStLuc