

# BGGN 213

## Biological Network Analysis

Lecture 17

Barry Grant  
UC San Diego

<http://thegrantlab.org/bggn213>

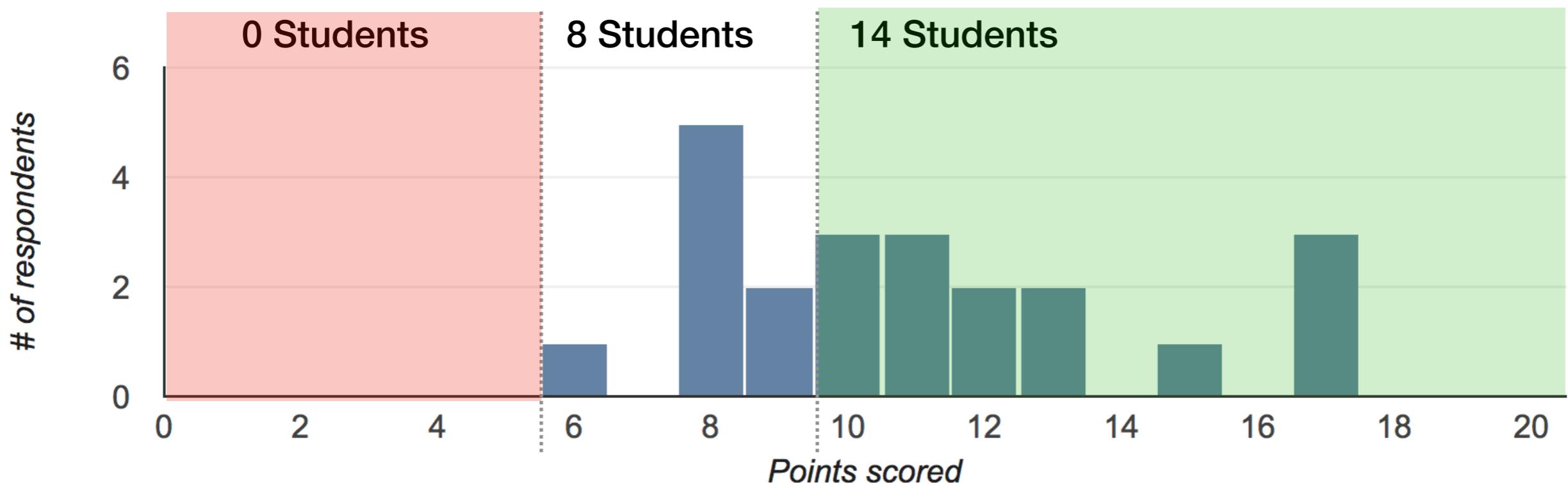
# R 'Knowledge Check' Quiz Results

Average  
11.05 / 20 points

Median  
10 / 20 points

Range  
6 - 17 points

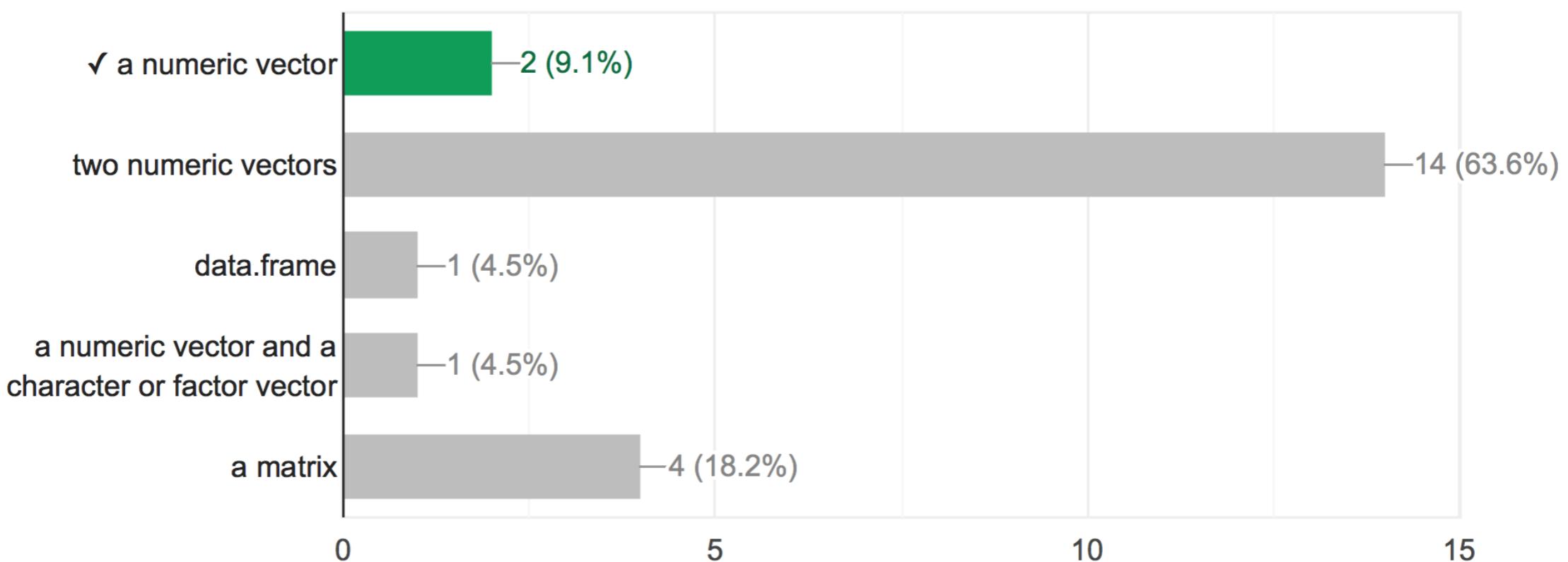
22 Total Students  
Total points distribution



# Frequently Missed Questions

What is the minimum input required to produce a single-layer scatter plot

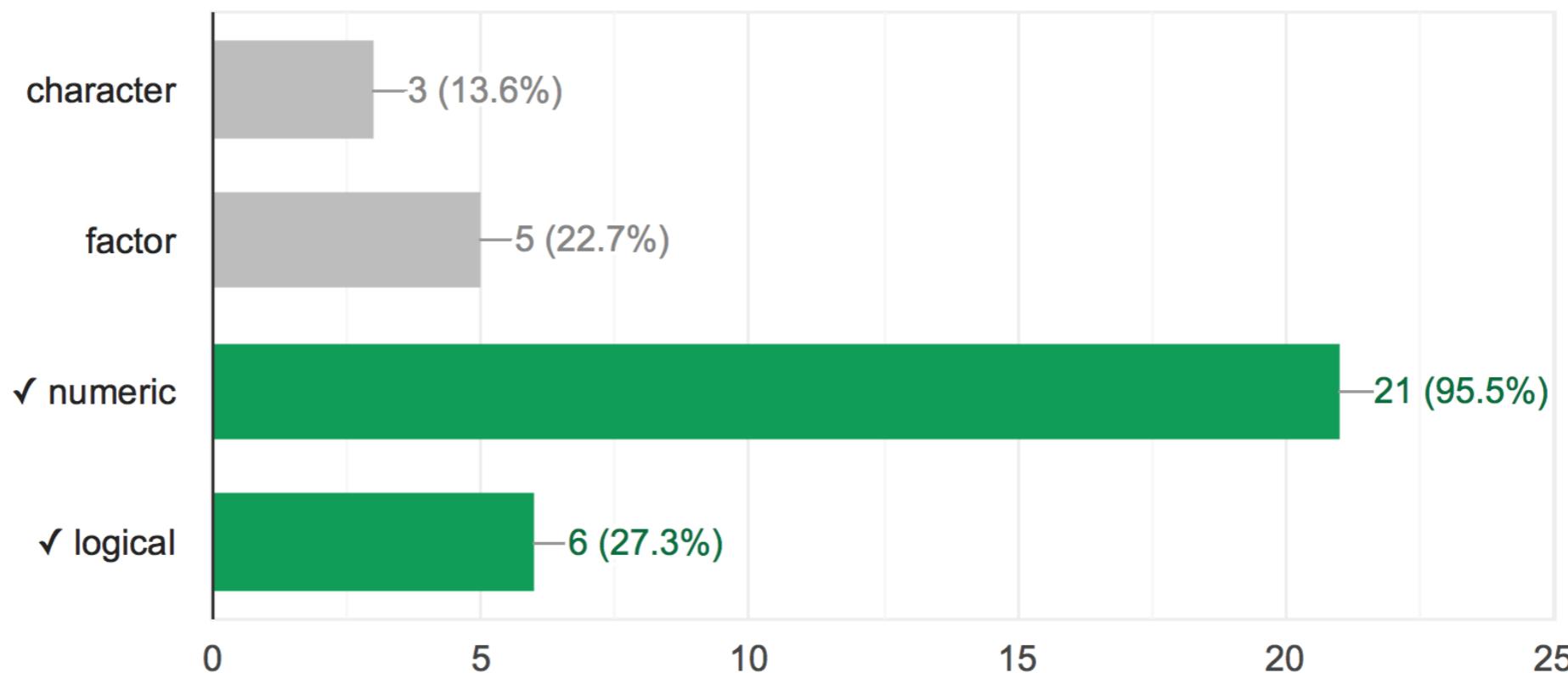
2 / 22 correct responses



# Frequently Missed Questions

jal <- function(x) {y=x^2; return(y)} #If I want to execute jal(hmk), what kind of data type can hmk be without r...n error message? Check all that apply

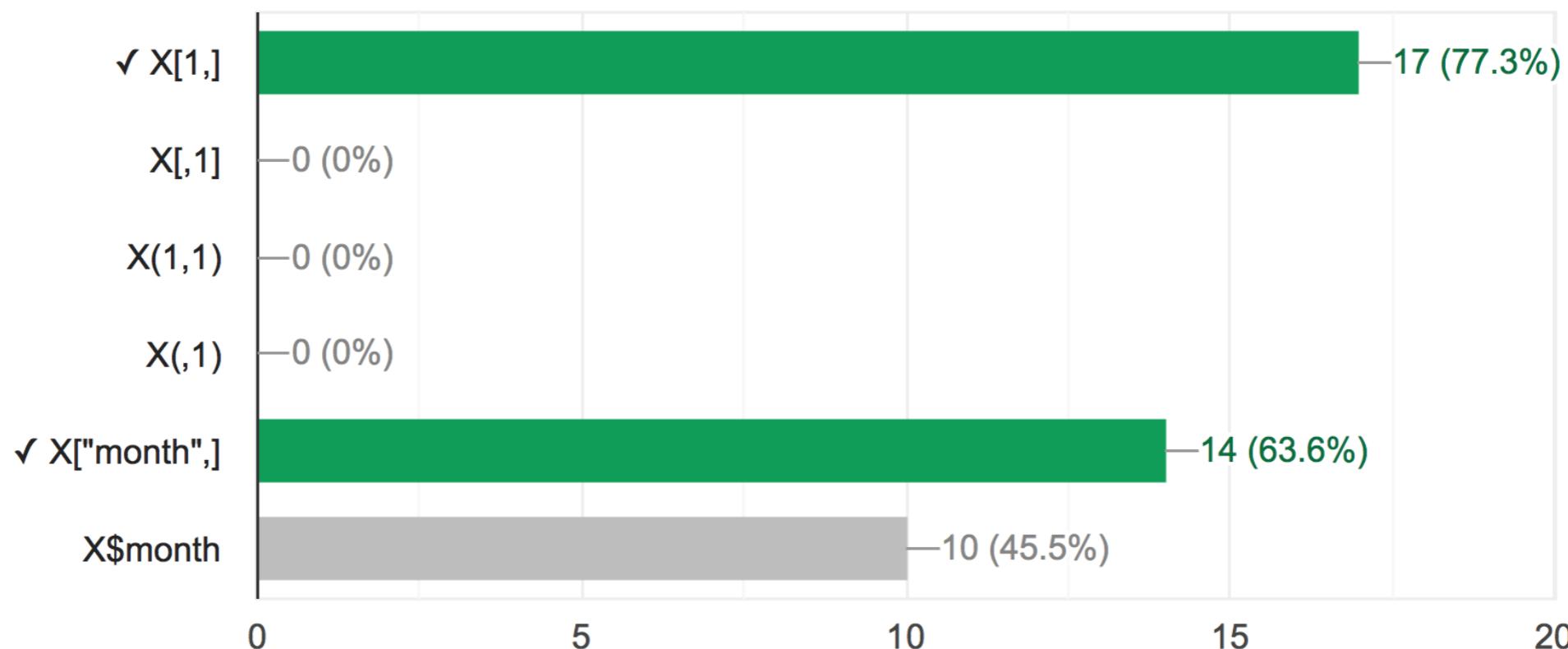
5 / 22 correct responses



# Frequently Missed Questions

Select the correct way(s) to extract a vector from a row in the data frame X.  
The name of the first row is month.

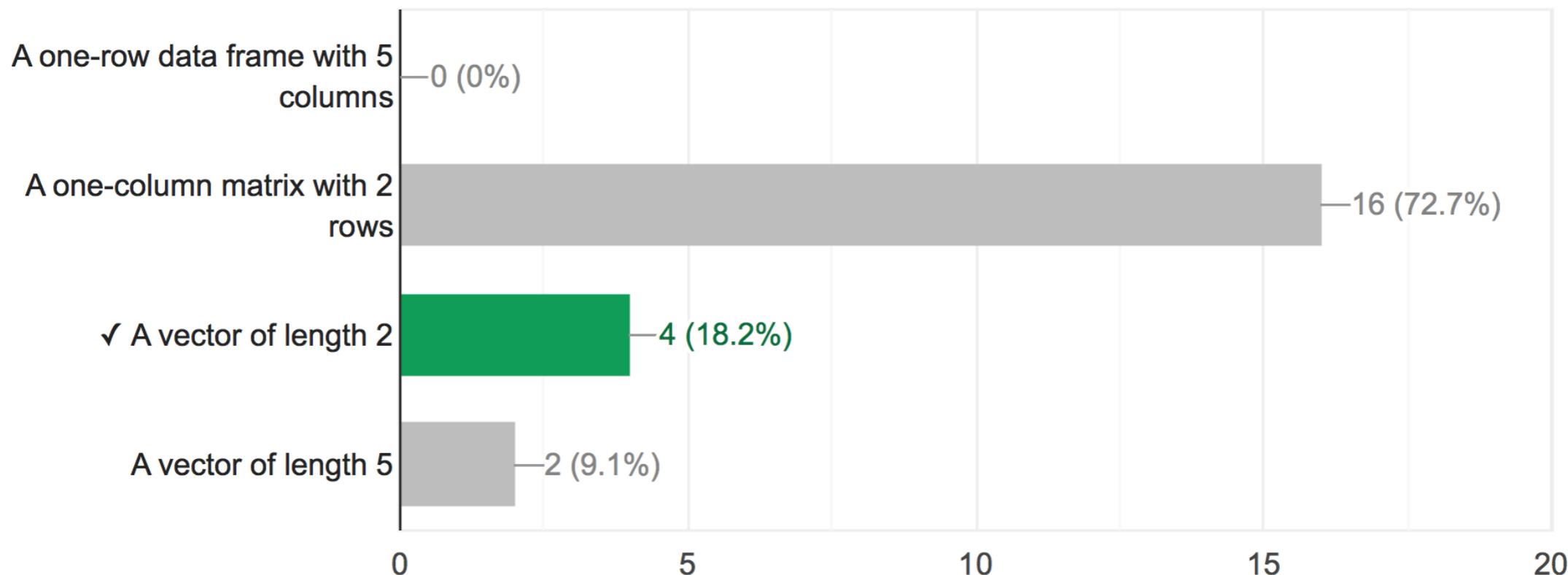
9 / 22 correct responses



# Frequently Missed Questions

If I have a data frame "df" with 2 rows and 5 columns, what will `df[,1]` return?

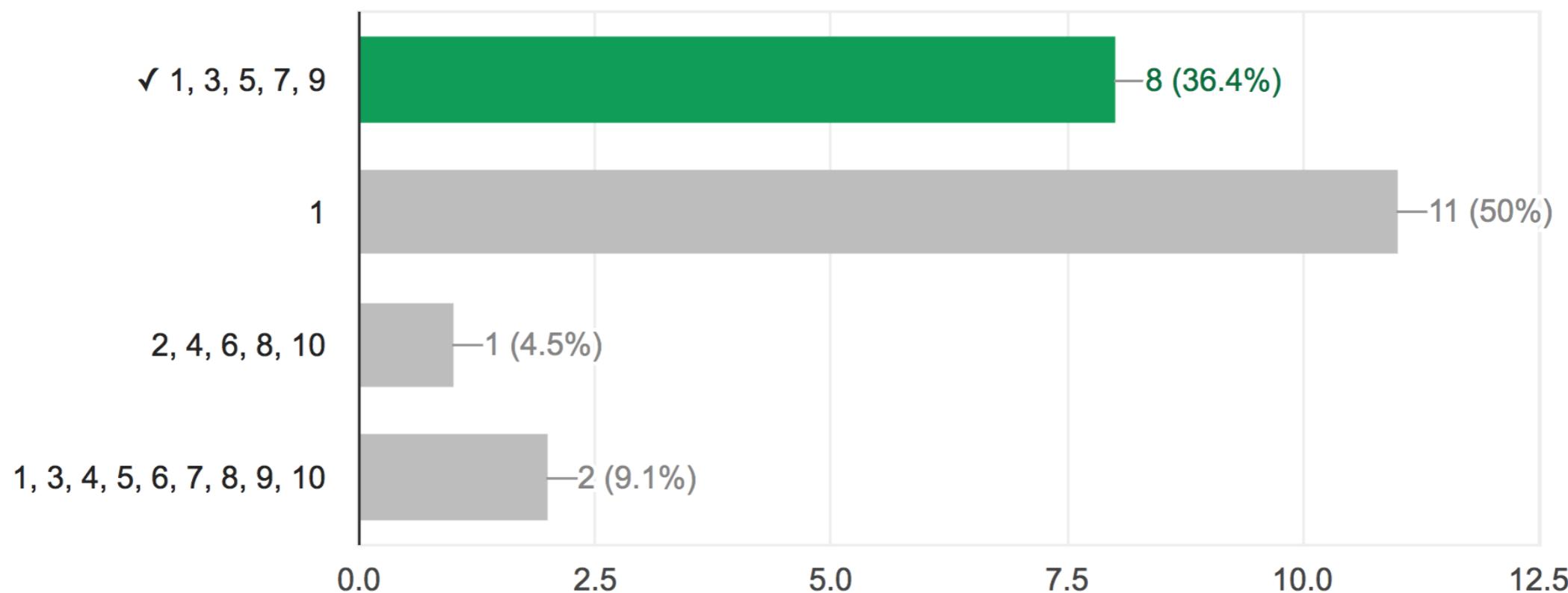
4 / 22 correct responses



# Frequently Missed Questions

If `x <- 1:10` Predict without using R the result of: `x[ c(TRUE, FALSE) ]`

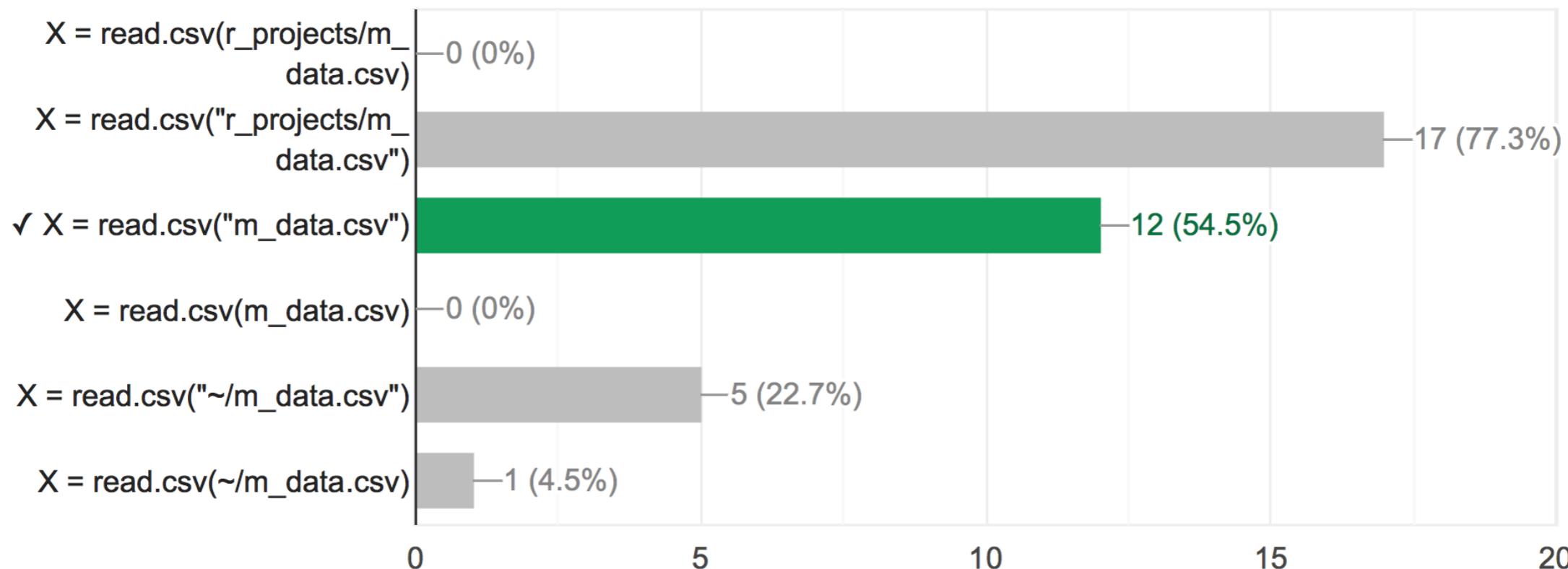
8 / 22 correct responses



# Frequently Missed Questions

The working directory is in the "r\_projects" folder, and it contains the file m\_data.csv. Select the correct way(s) to read m\_data into X.

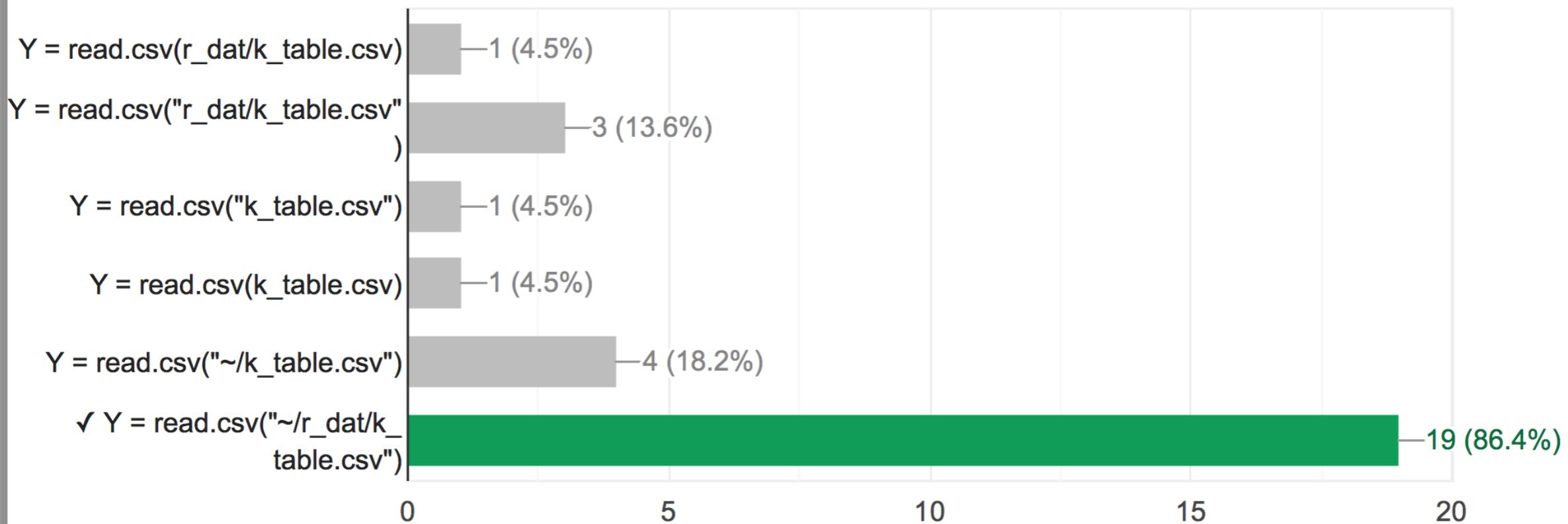
4 / 22 correct responses



# Frequently Missed Questions

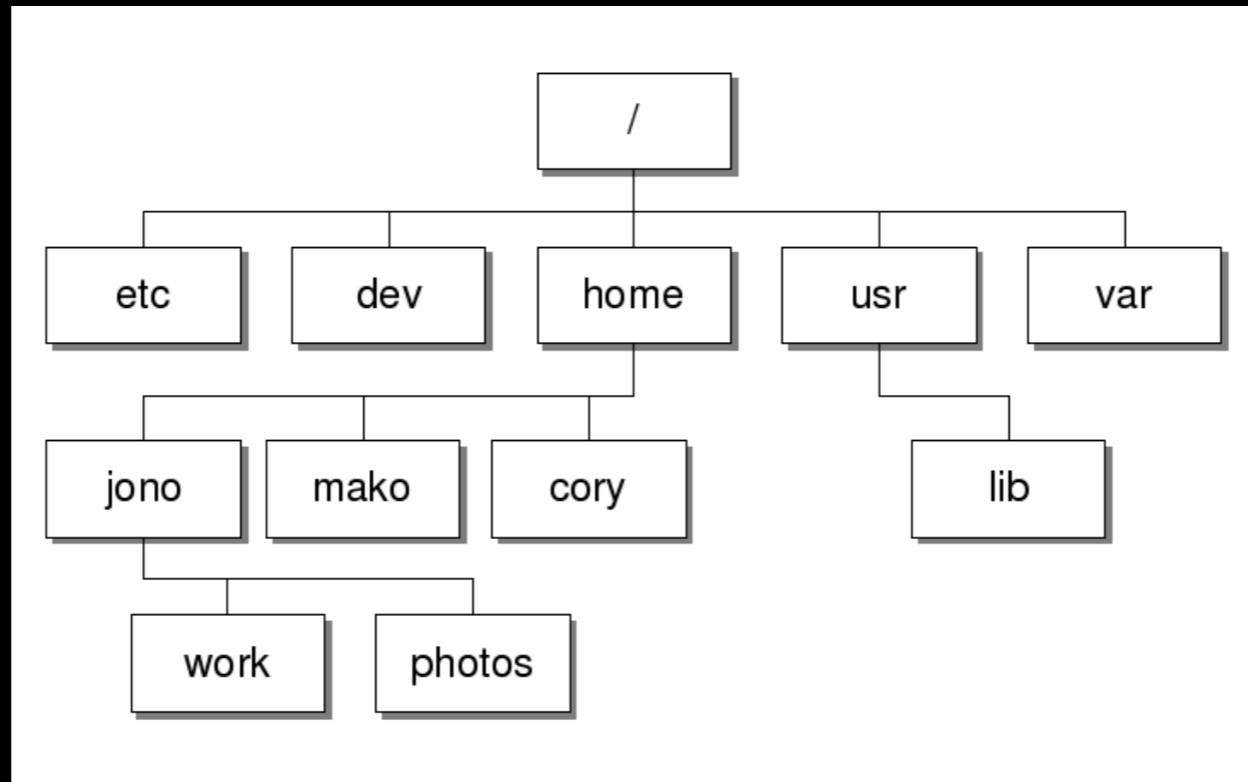
The "r\_dat" folder is not in your working directory but it is in your home directory. It contains the file k\_table.csv. What is the correct way(s) to read k\_table.csv into Y.

15 / 22 correct responses



# File System Structure

- Information in the file system is stored in files, which are stored in directories (folders). Directories can also store other directories, which forms a directory tree.



- The forward slash character '**/**' is used to represent the root directory of the whole file system, and is also used to separate directory names. E.g. **/home/jono/work/bggn213\_notes.txt**

# UNIX Basics: Using the filesystem

<b>ls</b>	List files and directories
<b>cd</b>	Change directory (i.e. move to a different 'folder')
<b>pwd</b>	Print working directory (which folder are you in)
<b>mkdir</b>	<u>M</u> a <u>K</u> e a new <u>D</u> I <u>R</u> ectories
<b>cp</b>	<u>C</u> o <u>P</u> y a file or directory to somewhere else
<b>mv</b>	<u>M</u> o <u>V</u> e a file or directory (basically rename)
<b>rm</b>	<u>R</u> e <u>M</u> ove a file or directory

# Side Note: File Paths

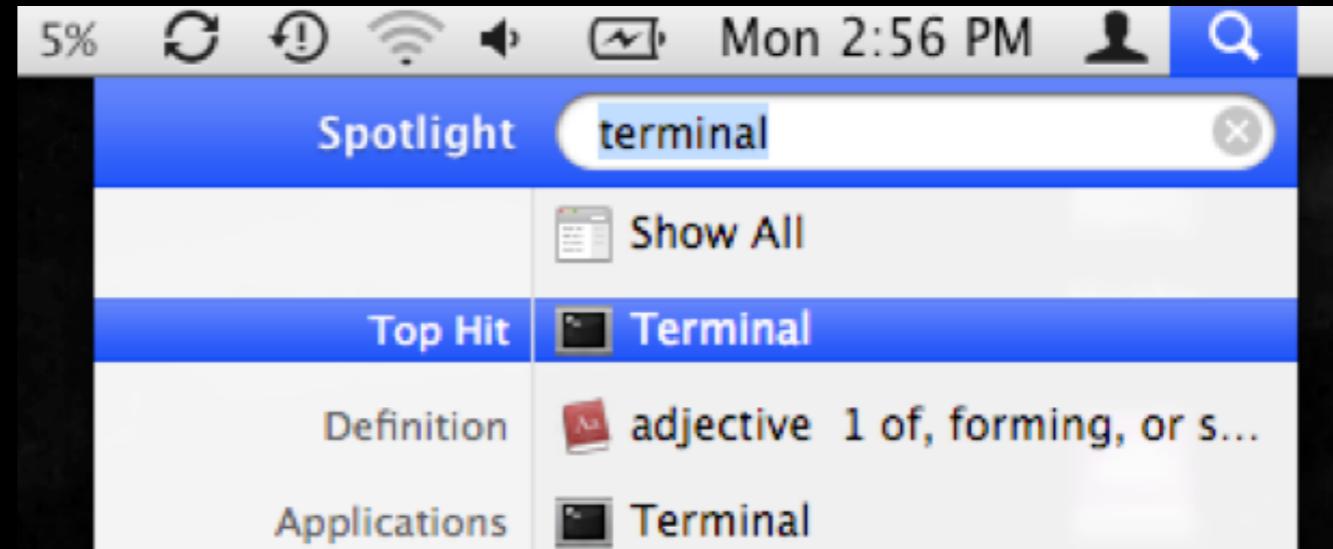
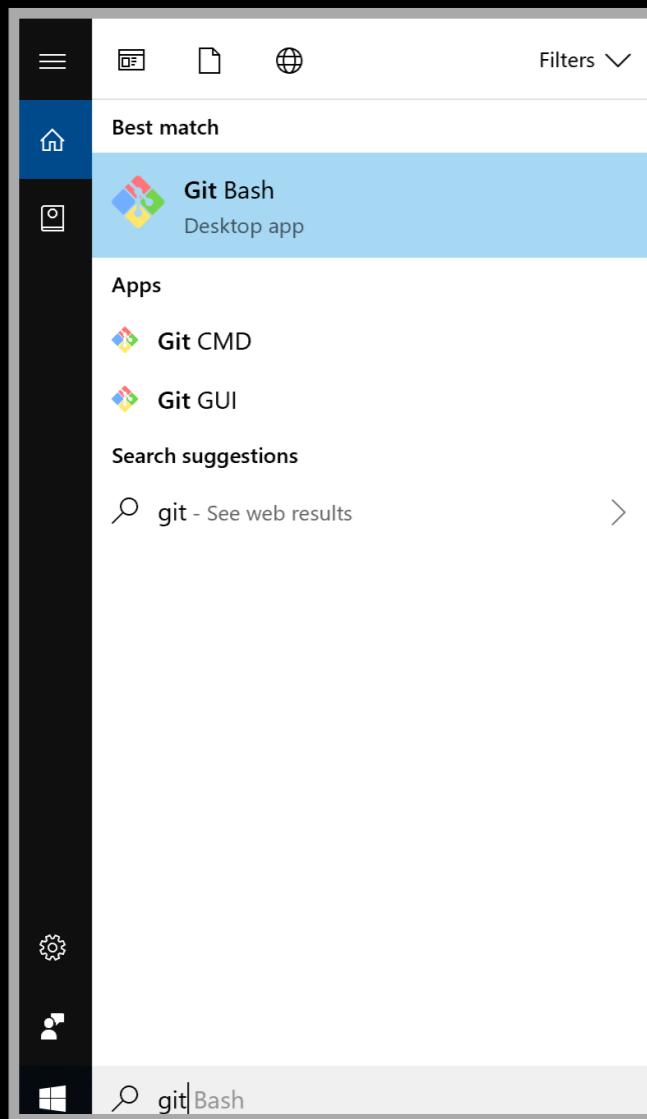
- An **absolute path** specifies a location from the root of the file system. E.g. **/home/jono/work/bggn213\_notes.txt**
- A **relative path** specifies a location starting from the current location. E.g. **../bggn213\_notes.txt**

.	Single dot ‘.’ (for current directory)
..	Double dot ‘..’ (for parent directory)
~	Tilda ‘~’ (for your home directory)
<b>[Tab]</b>	Pressing the tab key can autocomplete names

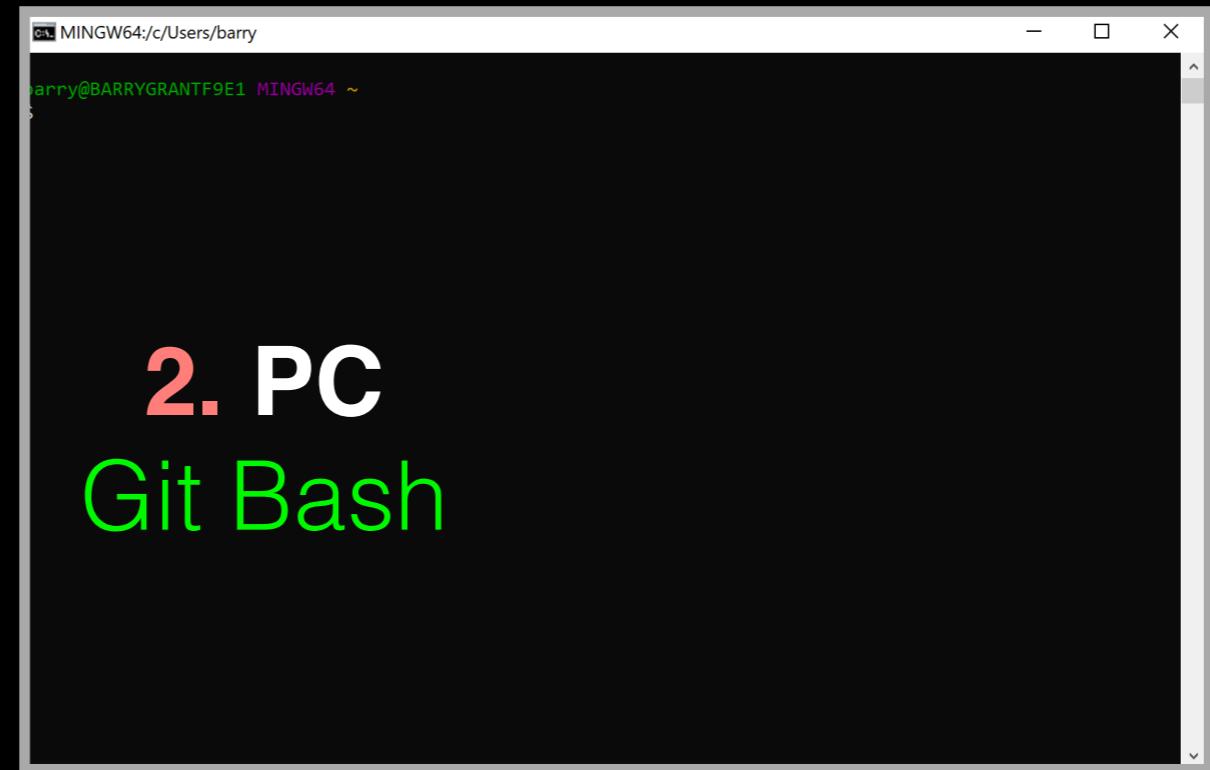
Do it Yourself!

# Lets get started....

## 1. Mac Terminal



## 2. PC Git Bash



## 3. OR: RStudio Terminal

In RStudio: Tools > Terminal > New Terminal

The screenshot shows a terminal window in RStudio with the title bar "2. class-material (bash)". The window contains the following text:

```
# Print Working Directory: a.k.a. where the hell am I? This is a comment line
> pwd This is our first UNIX command :-
Don't type the ">" bit it is the "shell prompt"!

# List out the files and directories where you are
> ls
```

A red arrow points to the first line starting with ">". A green box highlights the text "This is our first UNIX command :)" and the text "Don't type the ">" bit it is the "shell prompt"!" is enclosed in a red box.

- Q.** What do you see after each command?
- Q.** Does it make sense if you compare to your Mac: *Finder* or Windows: *File Explorer*?



# Change to your Desktop directory

> cd ~/Desktop

> pwd

# Download an online file to your current directory

> curl -O [https://bioboot.github.io/bggn213\\_W19/class-material/bggn213\\_01\\_unix.zip](https://bioboot.github.io/bggn213_W19/class-material/bggn213_01_unix.zip)

Q. Does what you see at each step make sense if you compare to your Mac: *Finder* or Windows: *File Explorer*?



```
# Download any file to your current directory/folder  
> curl -O https://bioboot.github.io/bggn213\_S18/class-material/bggn213\_01\_unix.zip
```

```
# List out the files and directories where you are (NB: Use TAB for auto-complete)  
> ls  
> ls bggn213_01_unix.zip
```

```
# Un-zip your downloaded file  
> unzip bggn213_01_unix.zip  
> ls
```

```
# Change directory (i.e. move to the folder named bggn213_01_unix)  
> cd bggn213_01_unix  
> ls  
> pwd
```

**Q.** Does what you see at each step make sense if you compare to your Mac: *Finder* or Windows: *File Explorer*?



```
# Practice moving around the file system...  
> cd projects  
> ls  
> pwd  
> cd ..
```

# Basics: Using the filesystem

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<b>rm</b>	<u>R</u> e <u>M</u> ove a file or directory

Basics	File Control	Viewing & Editing Files	Misc. useful	Power commands	Process related
<code>ls</code>	<code>mv</code>	<code>less</code>	<code>curl</code>	<code>grep</code>	<code>top</code>
<code>cd</code>	<code>cp</code>	<code>head</code>	<code>chmod</code>	<code>find</code>	<code>ps</code>
<code>pwd</code>	<code>mkdir</code>	<code>tail</code>	<code>wc</code>	<code>sed</code>	<code>kill</code>
<code>man</code>	<code>rm</code>	<code>nano</code>	<code>echo</code>	<code>sudo</code>	<code>Ctrl-c</code>
<code>ssh</code>	<code> </code> (pipe)	<code>touch</code>	<code>source</code>	<code>git</code>	<code>Ctrl-z</code>
<code>scp</code>	<code>&gt;</code> (write to file)		<code>cat</code>	<code>R</code>	<code>bg</code>
	<code>&lt;</code> (read from file)		<code>tmux</code>	<code>python</code>	<code>fg</code>

# Inspecting text files

- **less** - visualize a text file:
  - use arrow keys
  - page down/page up with “space”/“b” keys
  - search by typing “/”
  - quit by typing “q”
- Also see: **head**, **tail**, **cat**, **more**

# Creating text files

Creating files can be done in a few ways:

- With a **text editor** (such as **nano**, **emacs**, or **vi**)
- With the **touch** command (`> touch a_file`)
- From the command line with **cat** or **echo** and **redirection** (more on this later)
- **nano** is a simple text editor that is recommended for first-time users. Other text editors have more powerful features but also steep learning curves

# Creating and editing text files with **nano**

In the terminal type:

> nano yourfilename.txt

^G	Get Help	^O	WriteOut	^R	Read File
^X	Exit	^J	Justify	^W	Where Is
^Y	Prev Page	^K	Cut Text	^C	Cur Pos
^V	Next Page	^U	UnCut Txt	^T	To Spell



^ - Press Control

- There are many other text file editors (e.g. vim, emacs and sublime text, etc.)

# Connecting to remote machines (with **ssh**)

**Most high-performance computing (HPC) resources can only be accessed by ssh (Secure SHell)**

> ssh [user@host.address]

**For example:**

> ssh barry@bio3d.ucsd.edu  
User    Host address

> ssh -i ~/bggn213\_private\_key tb170077@IP\_ADDRESS  
Optional key file    User    Host address

# Copying to and from remote machines (**scp**)

- The **scp** (Secure CoPy) command can be used to copy files and directories from one computer to another.

```
> scp [file] [user@host]:[destination]  
> scp localfile.txt barry@bigcomputer.net:/remotedir/.
```

Basics	File Control	Viewing & Editing Files	Misc. useful	Power commands	Process related
ls	mv	less	chmod	grep	top
cd	cp	head	echo	find	ps
pwd	mkdir	tail	wc	sed	kill
man	rm	nano	curl	sudo	Crl-c
ssh	 (pipe)	touch	source	git	Crl-z
scp	> (write to file)		cat	R	bg
	< (read from file)		tmux	python	fg

# **Process** refers to a running instance of a program

<b>top</b>	Provides a real-time view of all running processes
<b>ps</b>	Report a snapshot of the current processes
<b>kill</b>	Terminate a process (the “force quit” of the unix world)
<b>Crl-c</b>	Stop a job
<b>Crl-z</b>	Suspend a job
<b>bg</b>	Resume a suspended job in the background
<b>fg</b>	Resume a suspended job in the foreground
<b>&amp;</b>	Start a job in the background

*Do it Yourself!*

# Hands-on time

Sections 1 to 3 of software carpentry UNIX lesson

<https://swcarpentry.github.io/shell-novice/>

<https://explainshell.com>

~20 mins

# BIMM 143

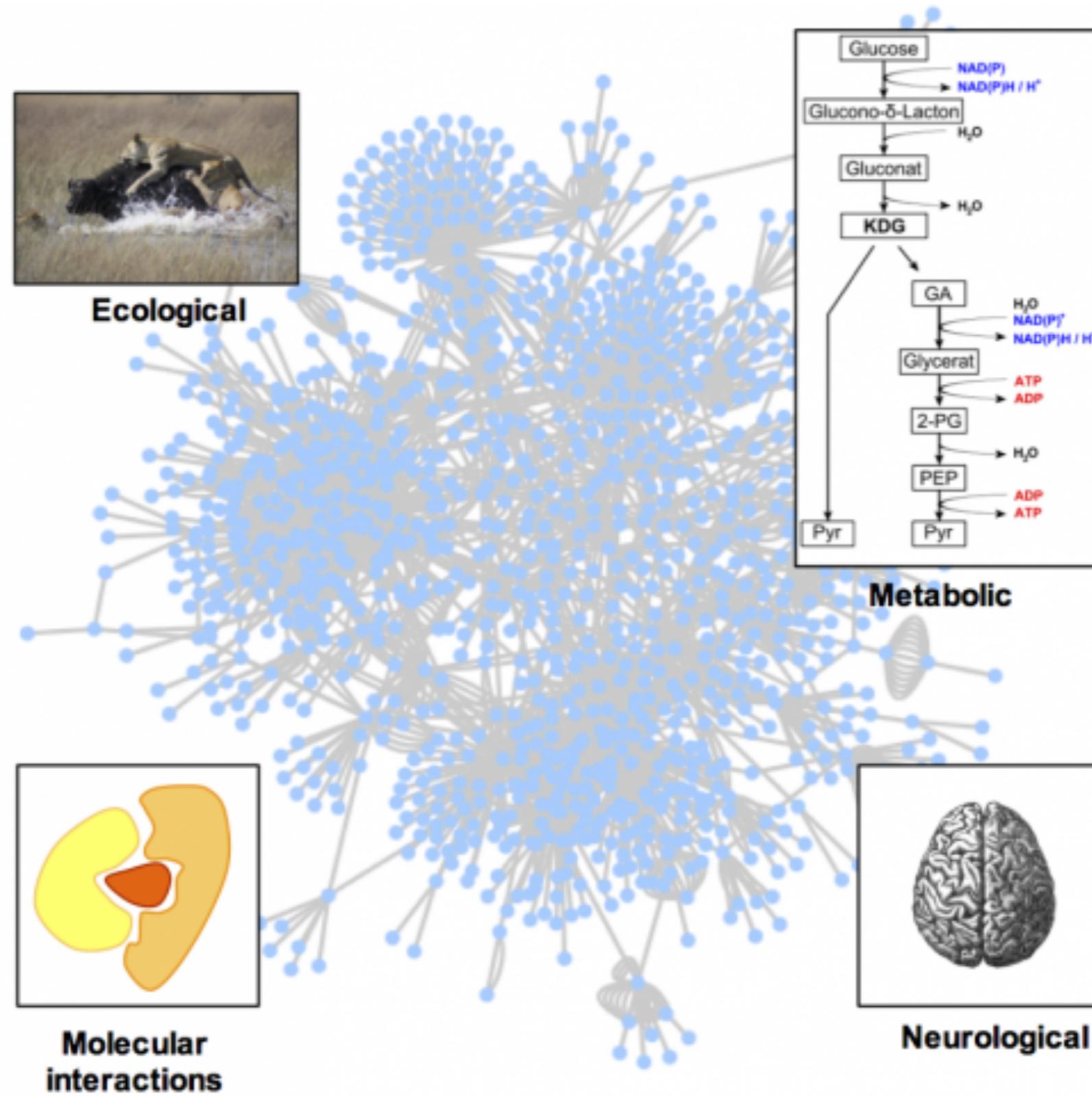
## Biological Network Analysis

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<http://thegrantlab.org/bimm143>

# Networks can be used to model many types of biological data



# **TODAYS MENU:**

- ▶ **Network introduction**
- ▶ **Network visualization**
- ▶ **Network analysis**
- ▶ **Hands-on:**  
Cytoscape and R (igraph) software tools  
for network visualization and analysis

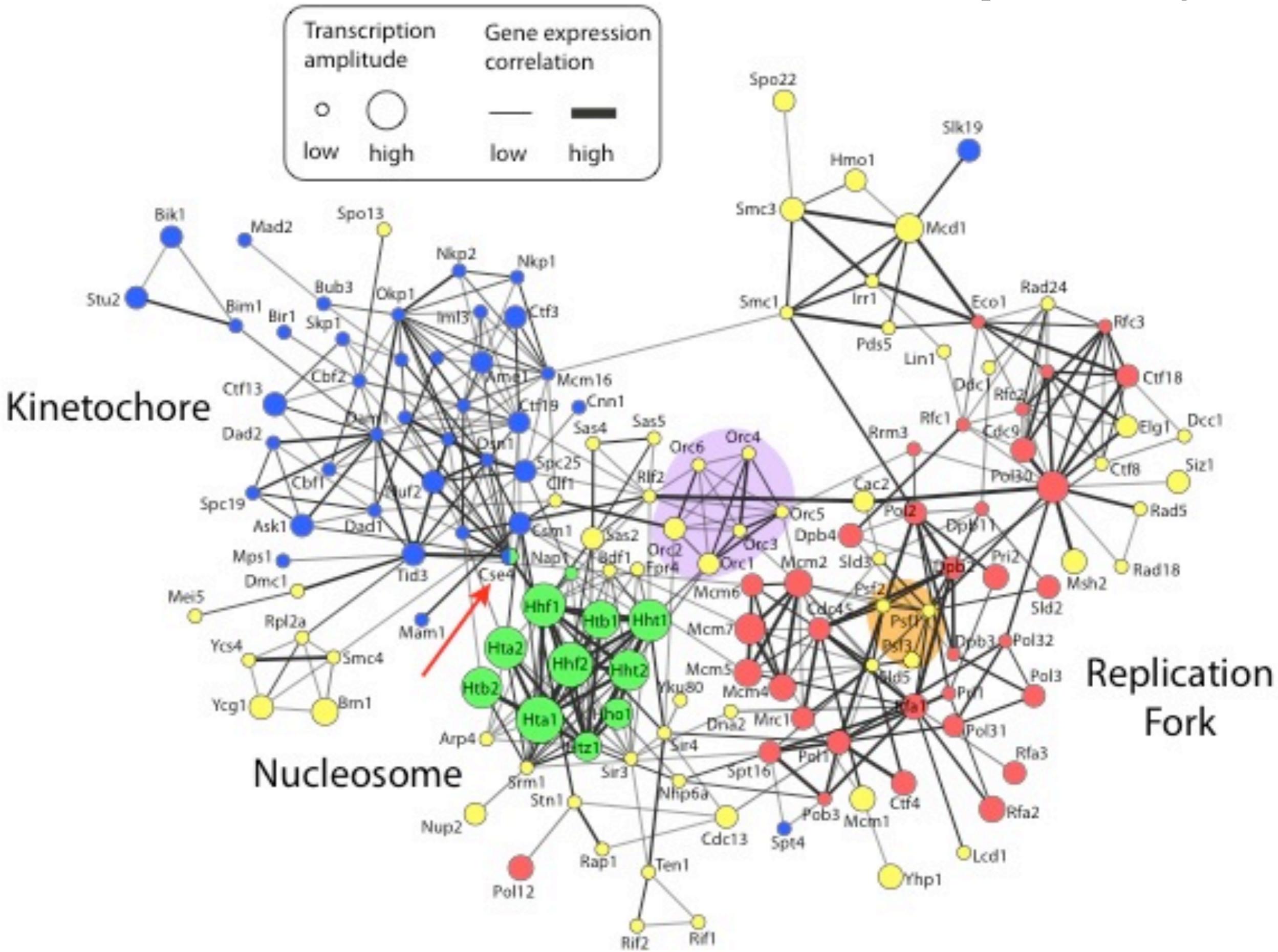
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# Biological Networks

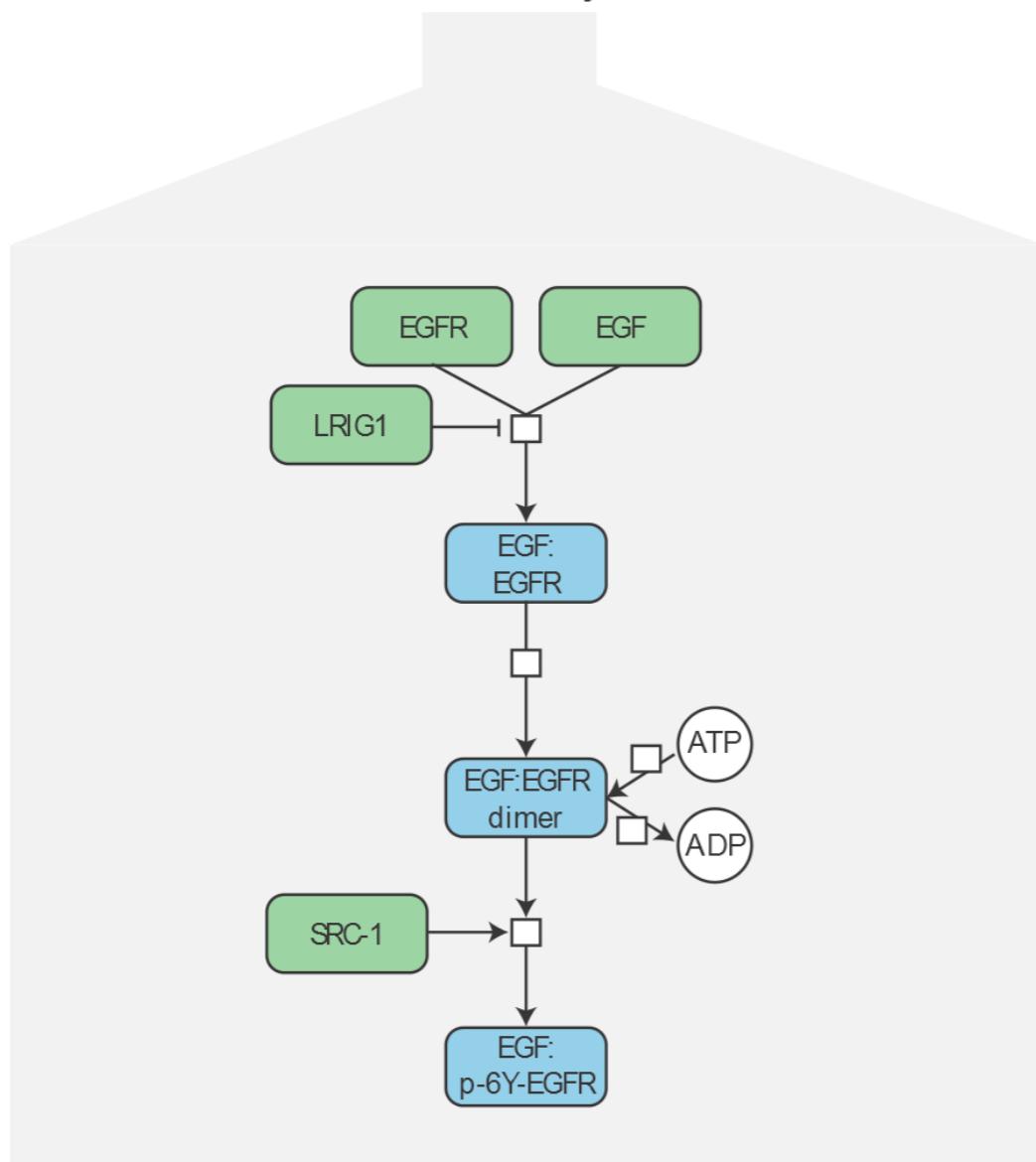
- **Represent biological interactions**
  - ➔ Physical, regulatory, genetic, functional, etc.
- **Useful for discovering relationships in big data**
  - ➔ Better than tables in Excel
- **Visualize multiple heterogenous data types together**
  - ➔ Help highlight and see interesting patterns
- **Network analysis**
  - ➔ Well established quantitative metrics from graph theory

## [Yeast, cell-cycle PPIs]



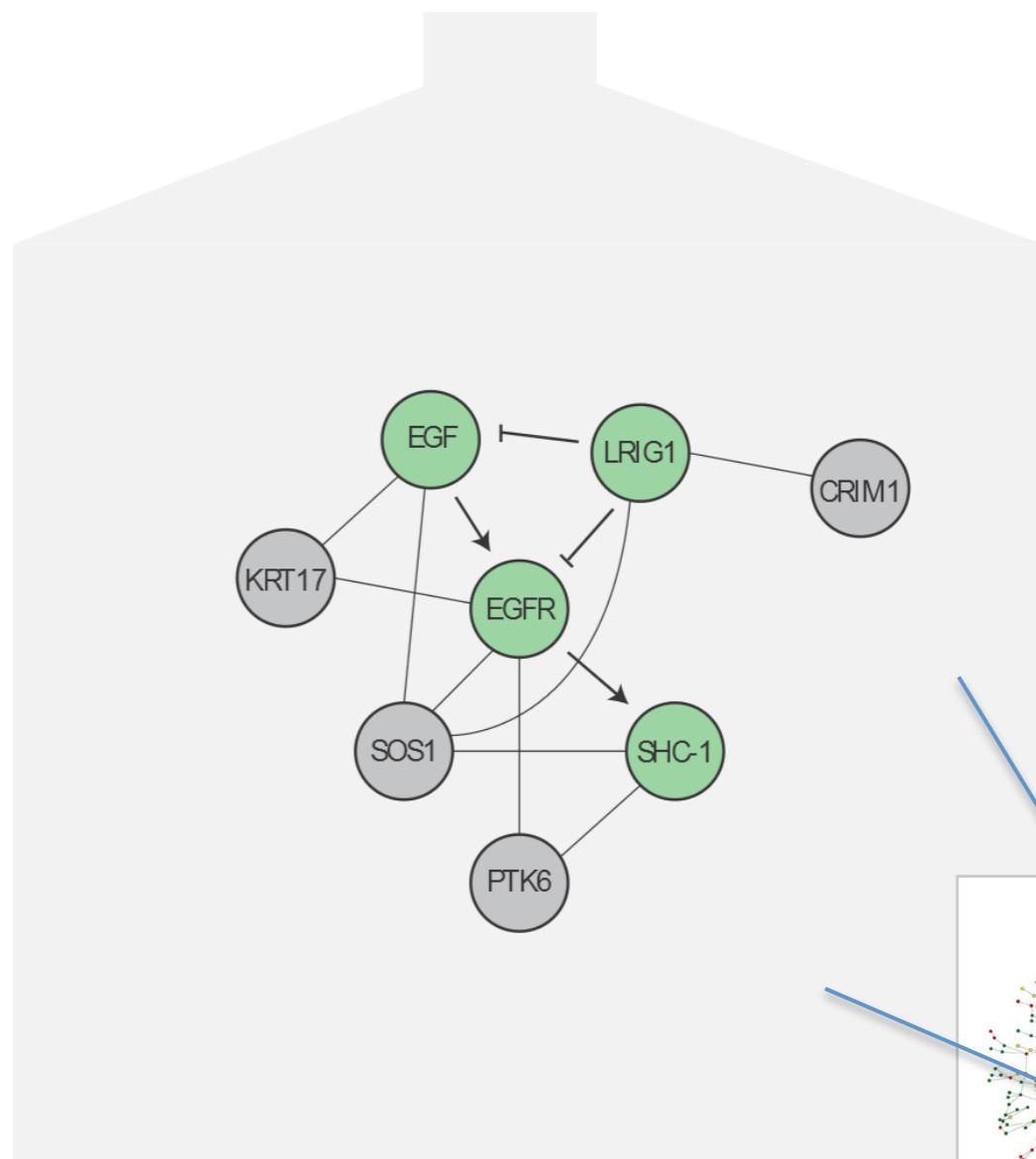
# Pathways vs Networks

EGFR-centered  
Pathway

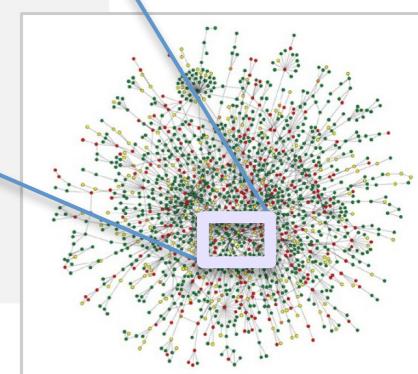


- Detailed, high-confidence consensus
- Biochemical reactions
- Small-scale, fewer genes
- Concentrated from decades of literature

EGFR-centered  
Network



- Simplified cellular logic, noisy
- Abstractions: directed, undirected
- Large-scale, genome-wide
- Constructed from *omics* data integration



# Goal

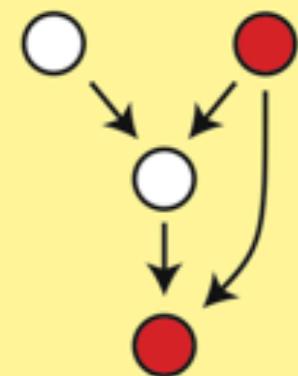
## 1 Enrichment of fixed gene sets

Identification of pre-built pathways or networks that are enriched in a set of mutated or differentially expressed genes

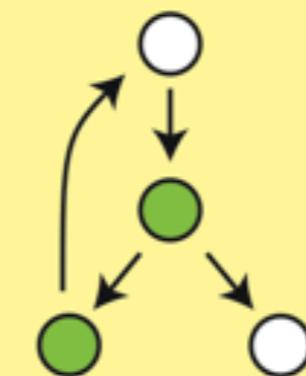
## 2 De novo sub-network construction and clustering

Construction of specific sub-networks from the set of mutated or differentially expressed genes to identify an extended list of putative cancer genes

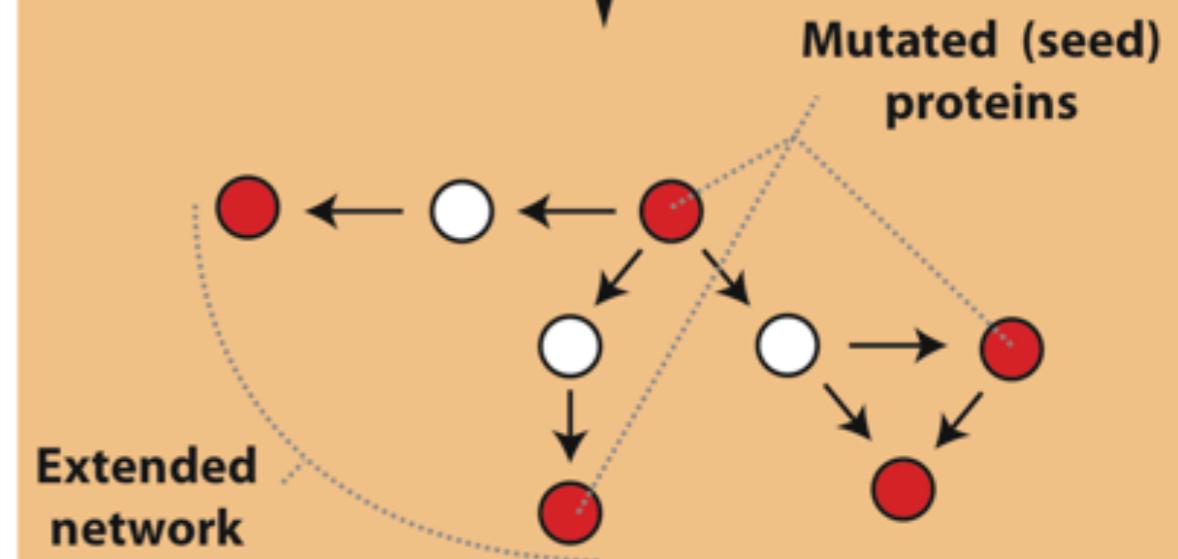
# Output



Enriched network



Depleted network



Extended network

# Goal

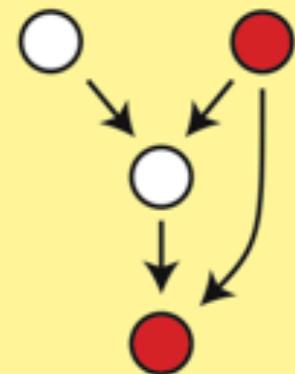
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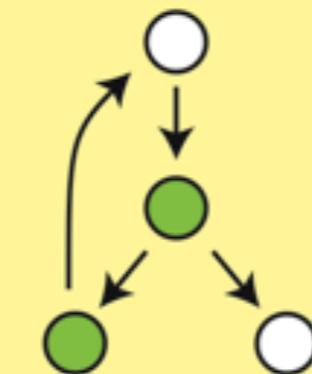
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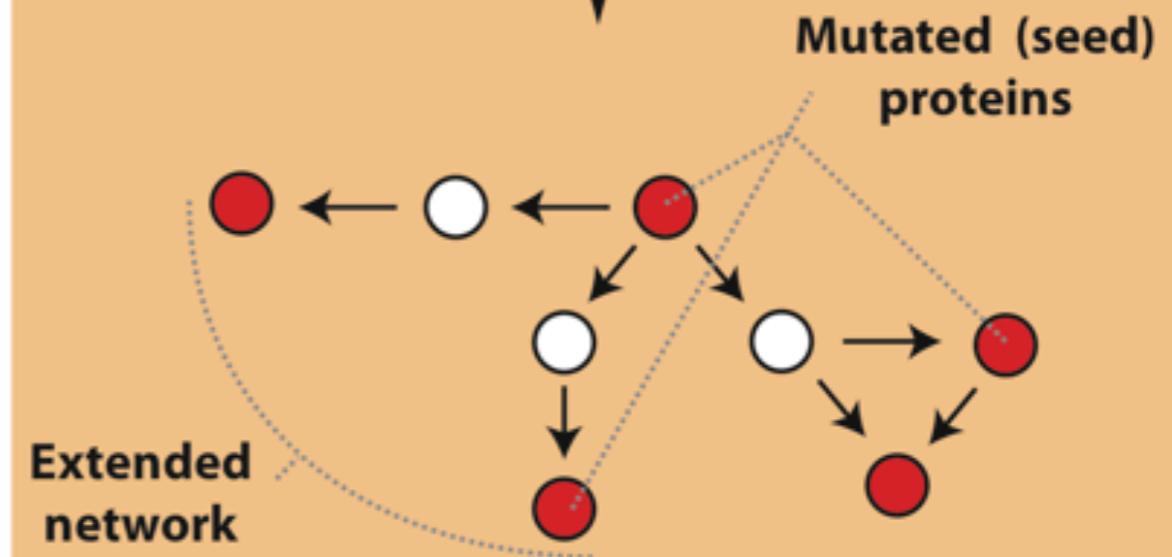
# Output



Enriched network



Depleted network



Extended network

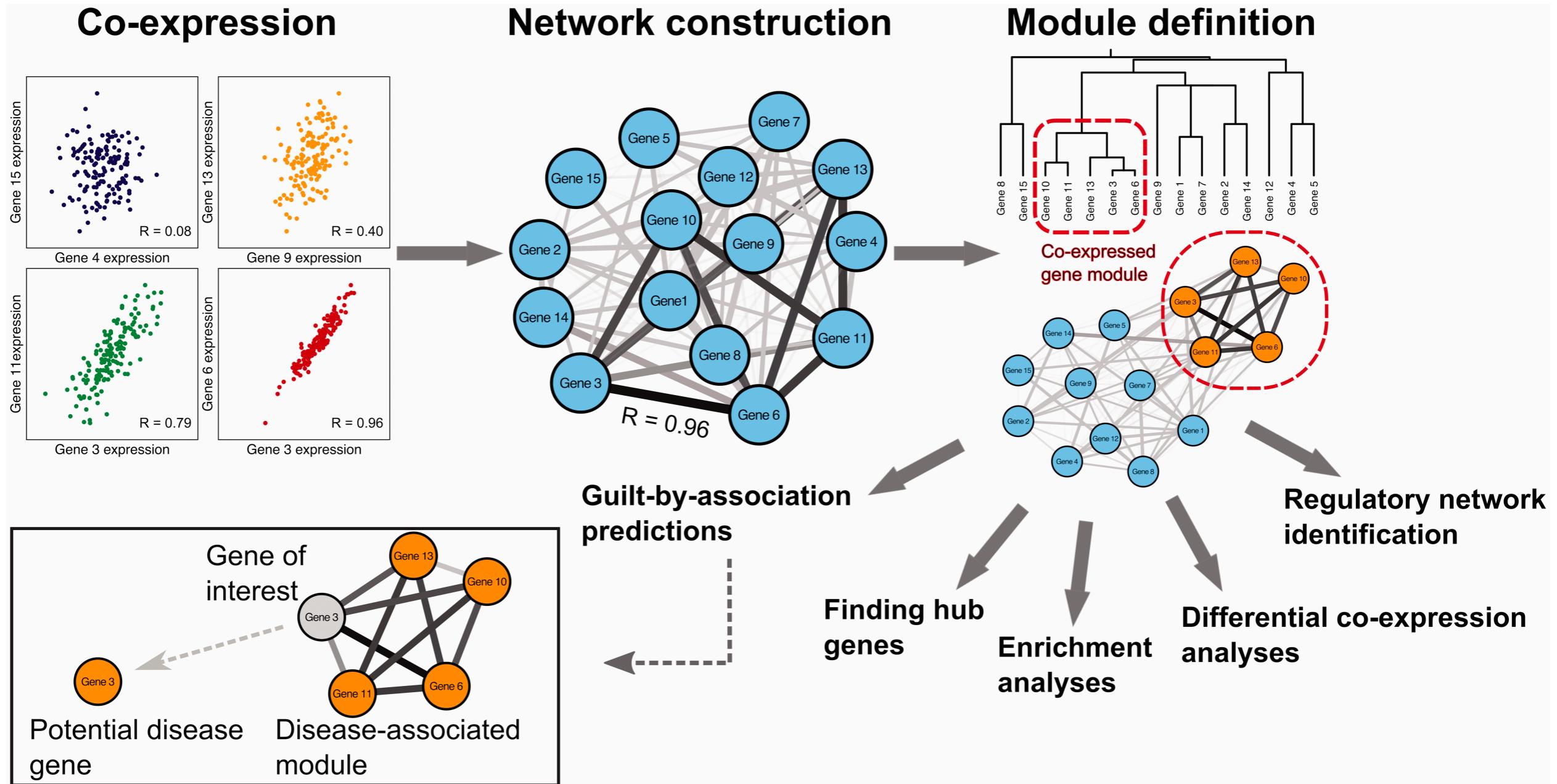
What biological process is altered in this cancer?

Are NEW pathways altered in this cancer? Are there clinically relevant tumor subtypes?

**Network analysis is complementary to pathway analysis and can be used to show how key components of different pathways interact.**

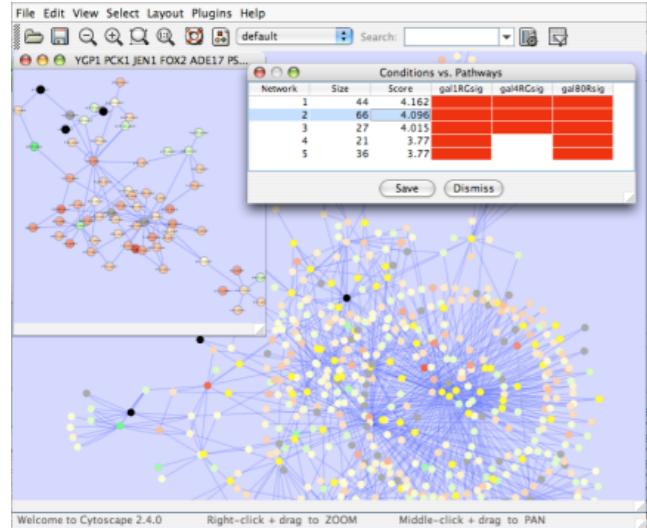
**This can be useful for identifying regulatory events that influence multiple biological processes and pathways**

# Network analysis approaches

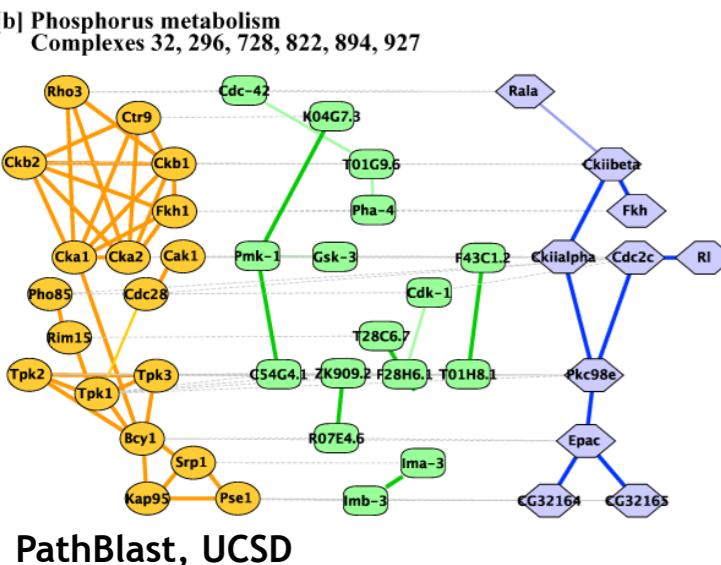


# Applications of Network Biology

- **Gene Function Prediction –** shows connections to sets of genes/proteins involved in same biological process
- **Detection of protein complexes/other modular structures –** discover modularity & higher order organization (motifs, feedback loops)



jActiveModules, UCSD

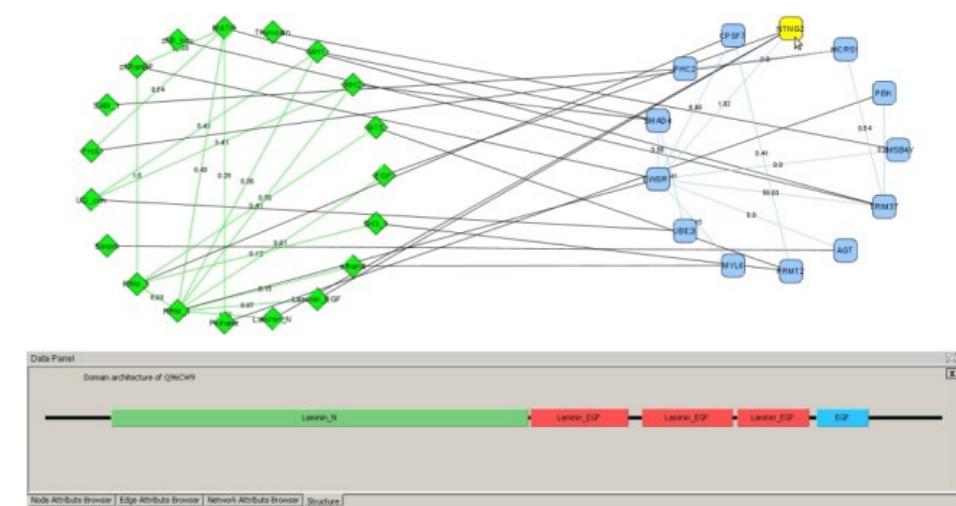


PathBlast, UCSD

- **Network evolution –** biological process(es) conservation across species
- **Prediction of new interactions and functional associations –** Statistically significant domain-domain correlations in protein interaction network to predict protein-protein or genetic interaction; allostery in molecular networks



MCODE, University of Toronto



DomainGraph, Max Planck Institute

# What's missing

- **Dynamics**
  - ➔ Pathways/networks represented as static processes
  - ➔ Difficult to represent a calcium wave or a feedback loop
  - ➔ More detailed mathematical representations exist that handle these e.g. Stoichiometric modeling, Kinetic modeling (VirtualCell, E-cell, ...)
- **Detail** – atomic structures & exclusivity of interactions.
- **Context** – cell type, developmental stage

# What have we learned so far...

- **Networks are useful for seeing relationships in large data sets**
  - ➔ Important to understand what the nodes and edges mean
  - ➔ Important to define the biological question - know what you want to do with your gene list or network
- **Many methods available for network analysis**
  - ➔ Good to determine your question and search for a solution
  - ➔ Or get to know many methods and see how they can be applied to your data

# TODAYS MENU:

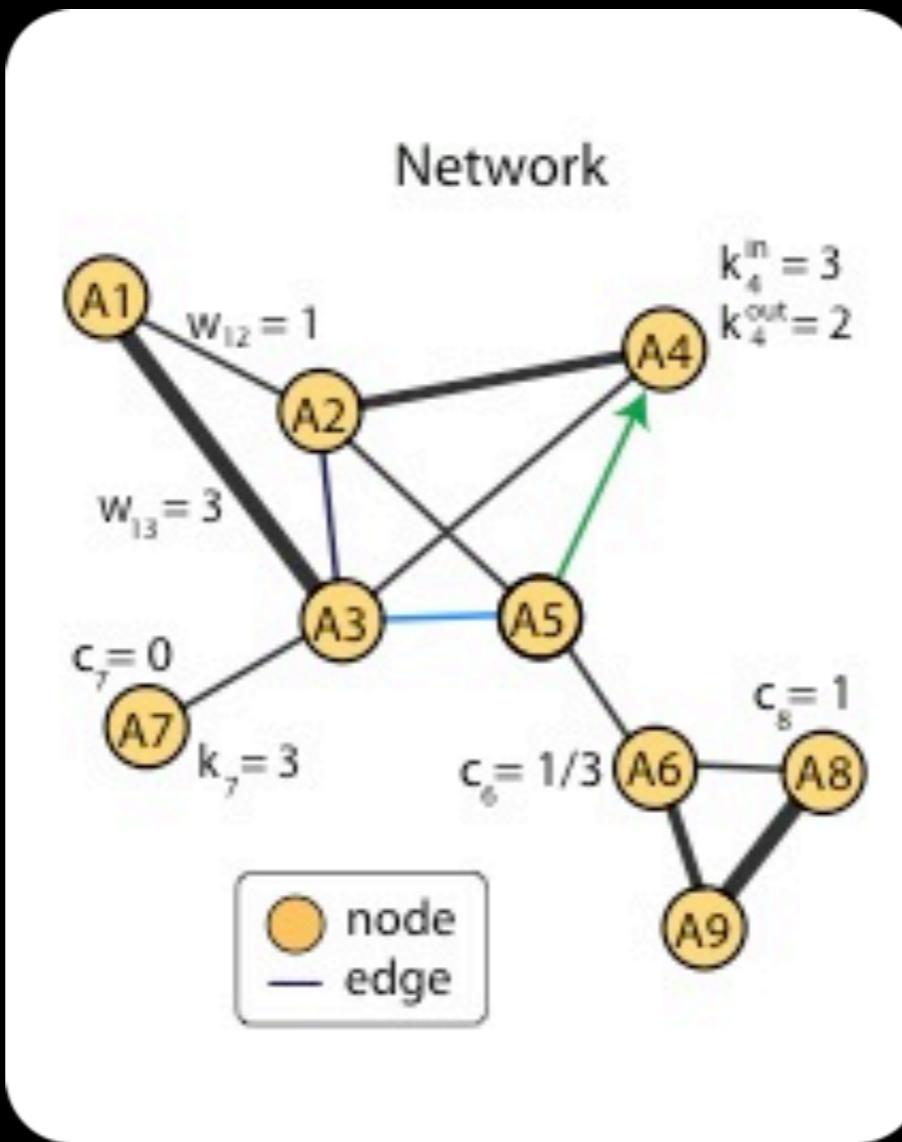
- ▶ Network introduction
- ▶ Network visualization
- ▶ Network analysis
- ▶ Hands-on:  
Cytoscape and R (igraph) software tools  
for network visualization and analysis

# Network Visualization Outline

- Network representations
- Automatic network layout
- Visual features
- Visually interpreting a network

# Network representations

Relationships	Optional weight
A1 ↔ A2	1
A1 ↔ A3	3
A2 ↔ A3	1
A2 ↔ A4	2
A2 ↔ A5	1
A3 ↔ A4	1
A3 ↔ A5	1
A3 ↔ A7	1
A5 → A4	1
A5 ↔ A6	1
A6 ↔ A8	1
A6 ↔ A9	2
A8 ↔ A9	3



1

List of relationships

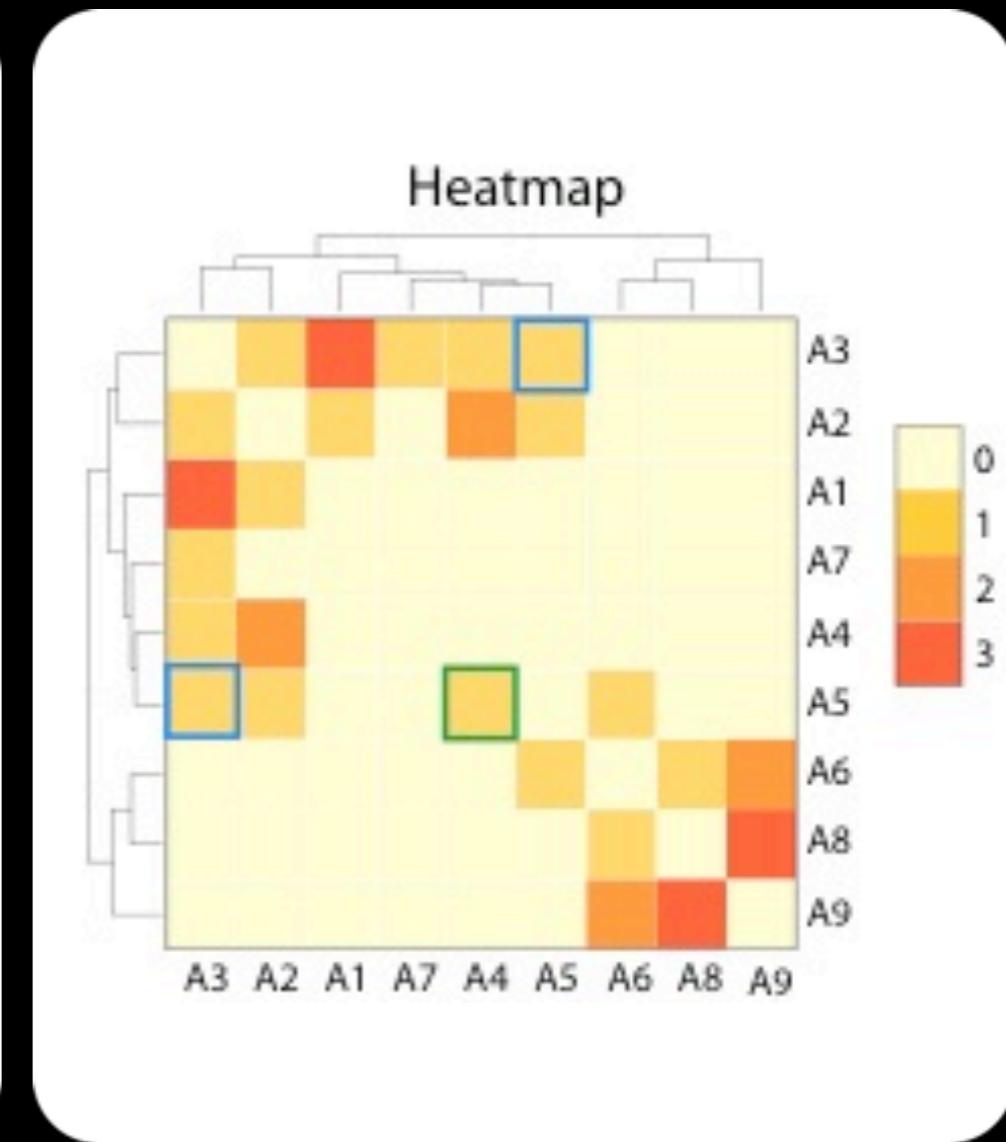
2

Network view

3

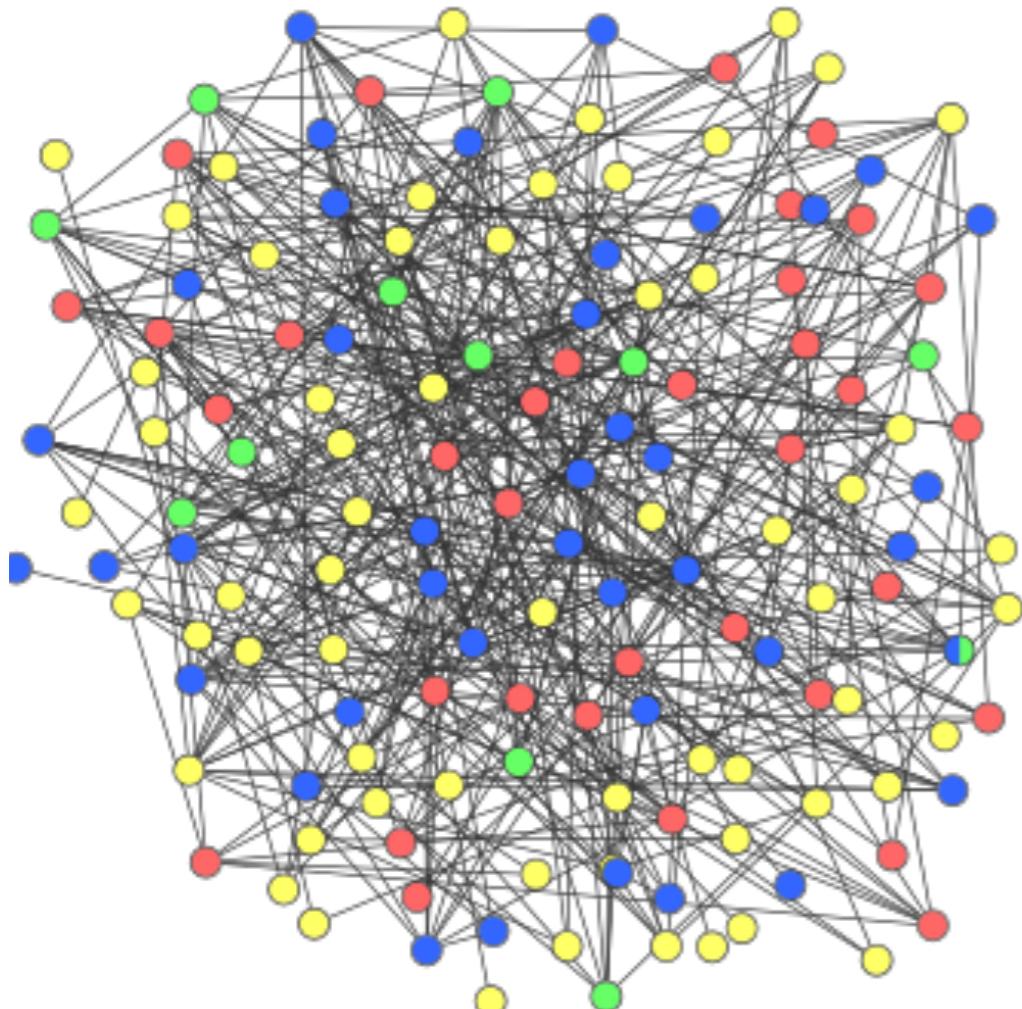
Adjacency matrix view

**Network view is most useful when network is sparse!**

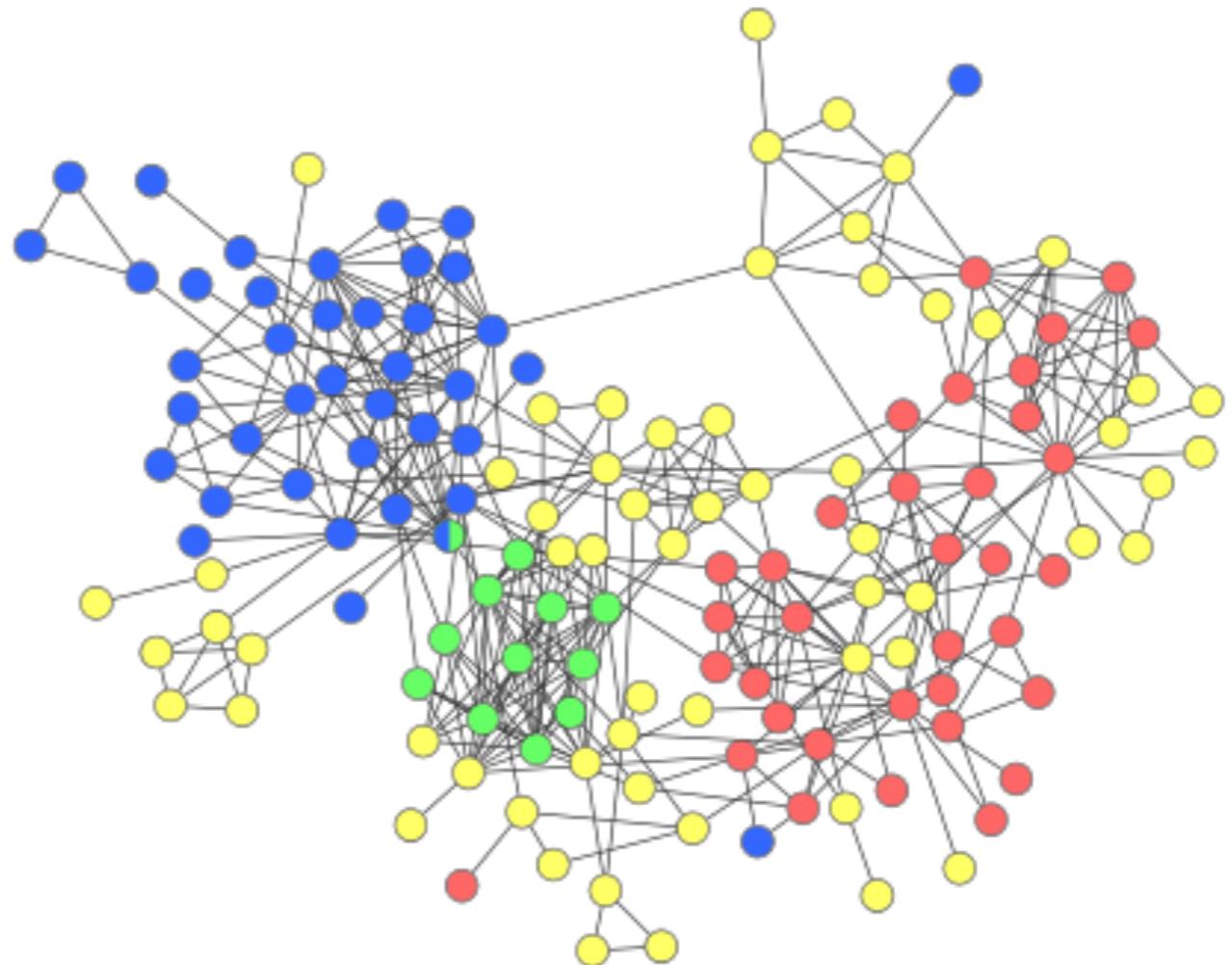


# Automatic network layout

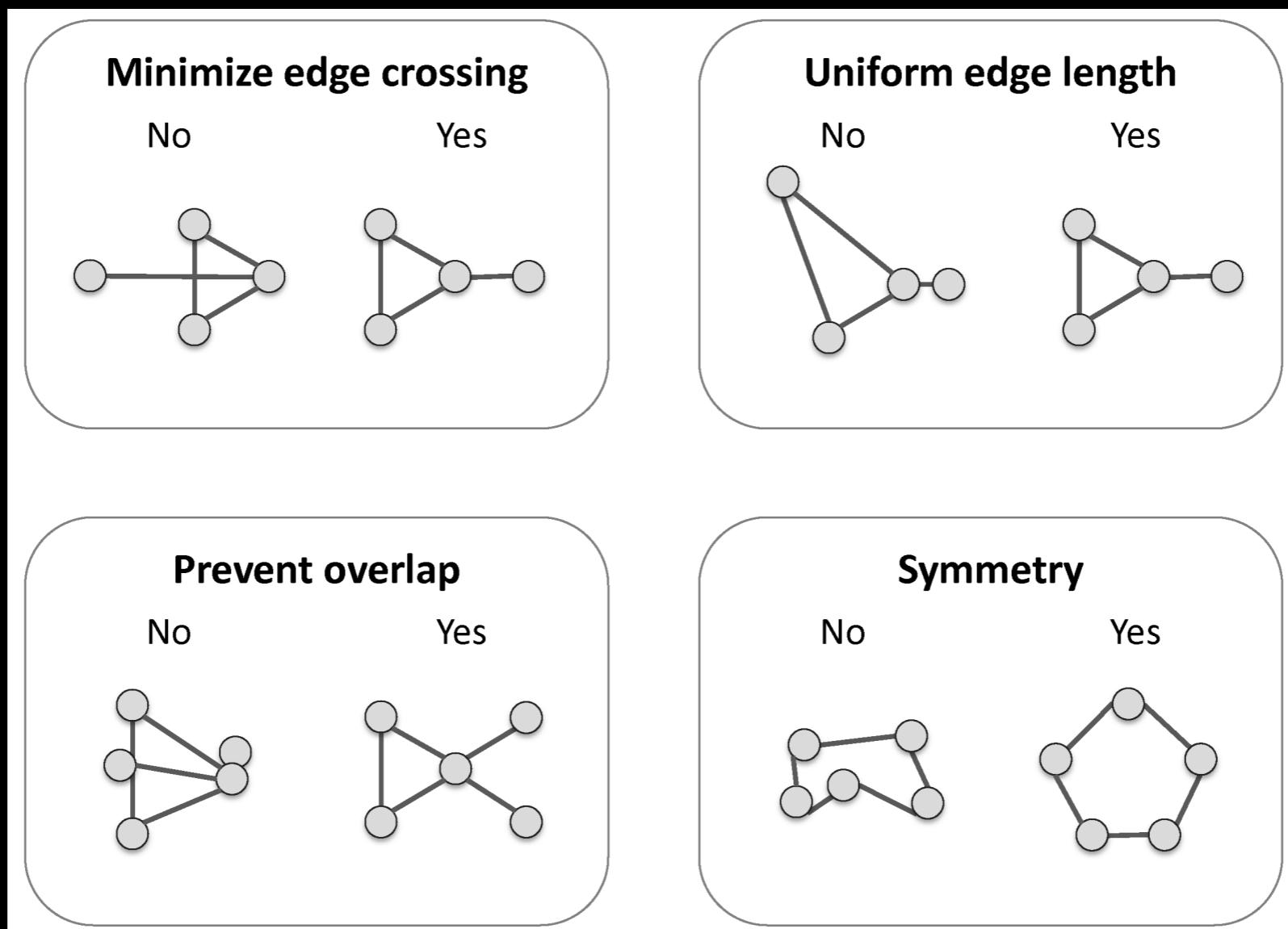
Before layout



After layout



- Modern **graph layouts** are optimized for speed and aesthetics. In particular, they seek to minimize overlaps and edge crossing, and ensure similar edge length across the graph.

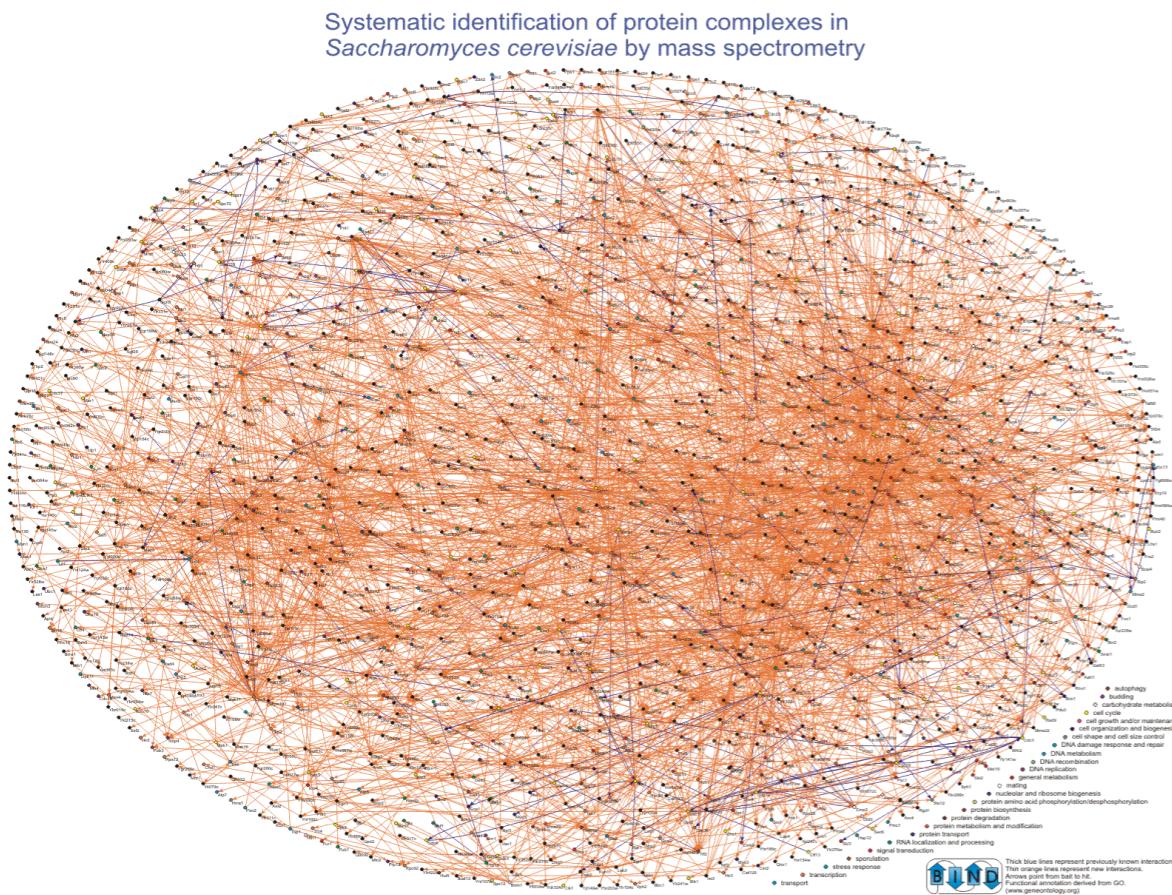


# Force-directed layout:

## Nodes repel and edges pull

- Good for up to 500 nodes
  - ➔ Bigger networks give hairballs
  - ➔ Reduce number of edges
  - ➔ Or just use a heatmap for dense networks
- Advice: try force directed first, or hierarchical for tree-like networks
- Tips for better looking networks
  - ➔ Manually adjust layout
  - ➔ Load network into a drawing program (e.g. Illustrator) and adjust labels

# Dealing with 'hairballs': zoom or filter

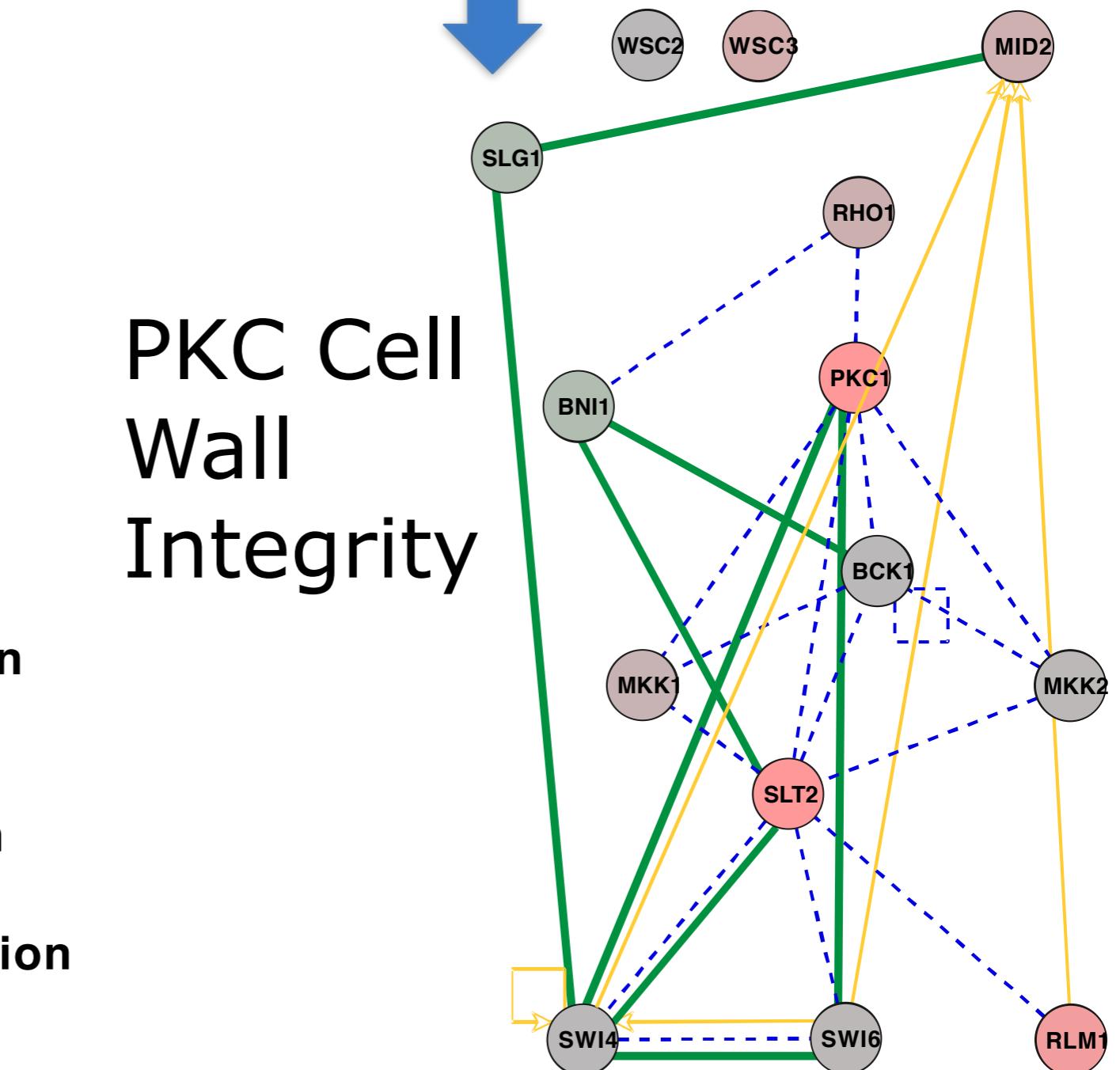


Zoom

Focus

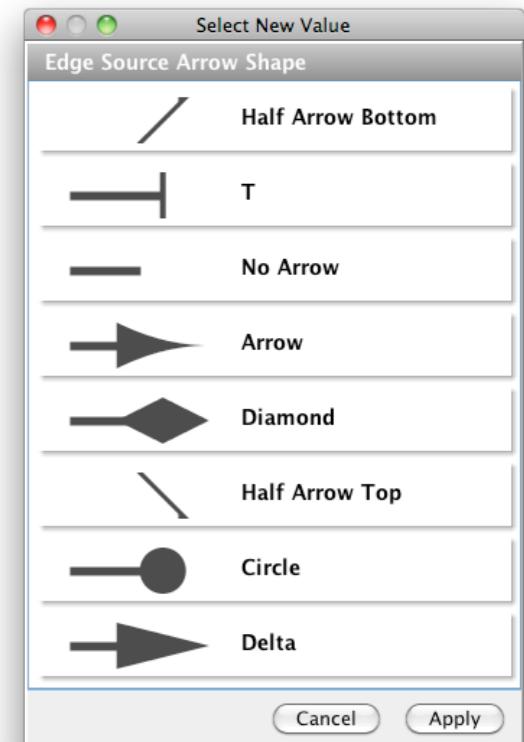
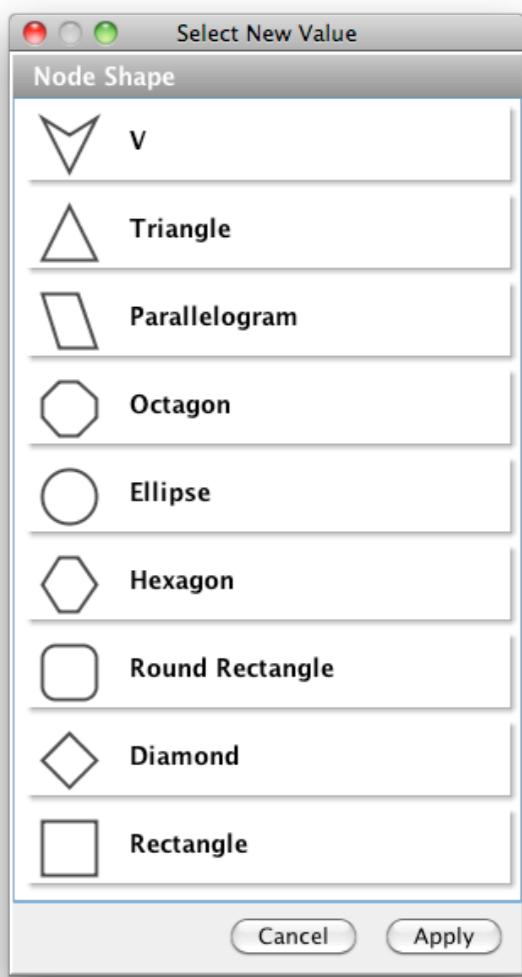
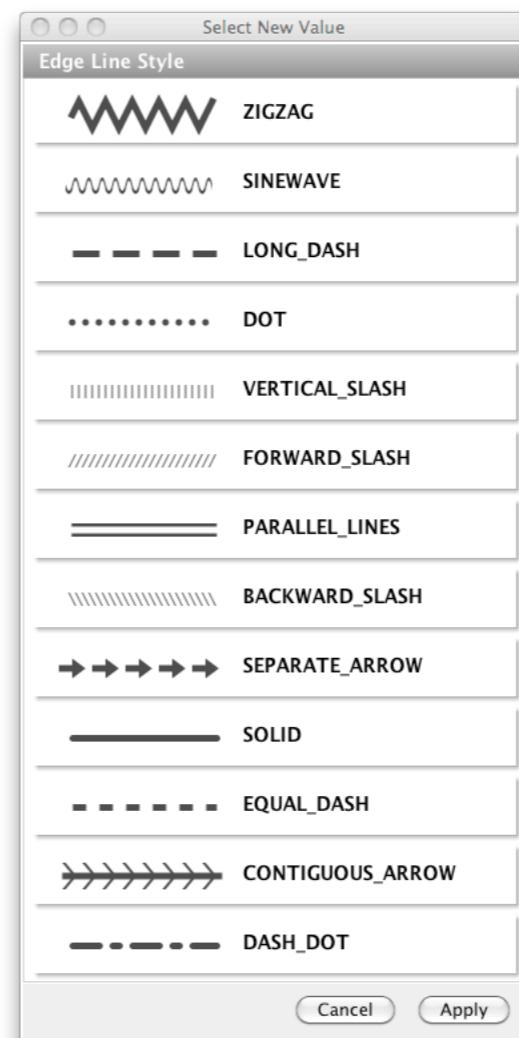
PKC Cell  
Wall  
Integrity

- Synthetic Lethal
- Transcription Factor Regulation
- - - Protein-Protein Interaction
- Up Regulated Gene Expression
- Down Regulated Gene Expression

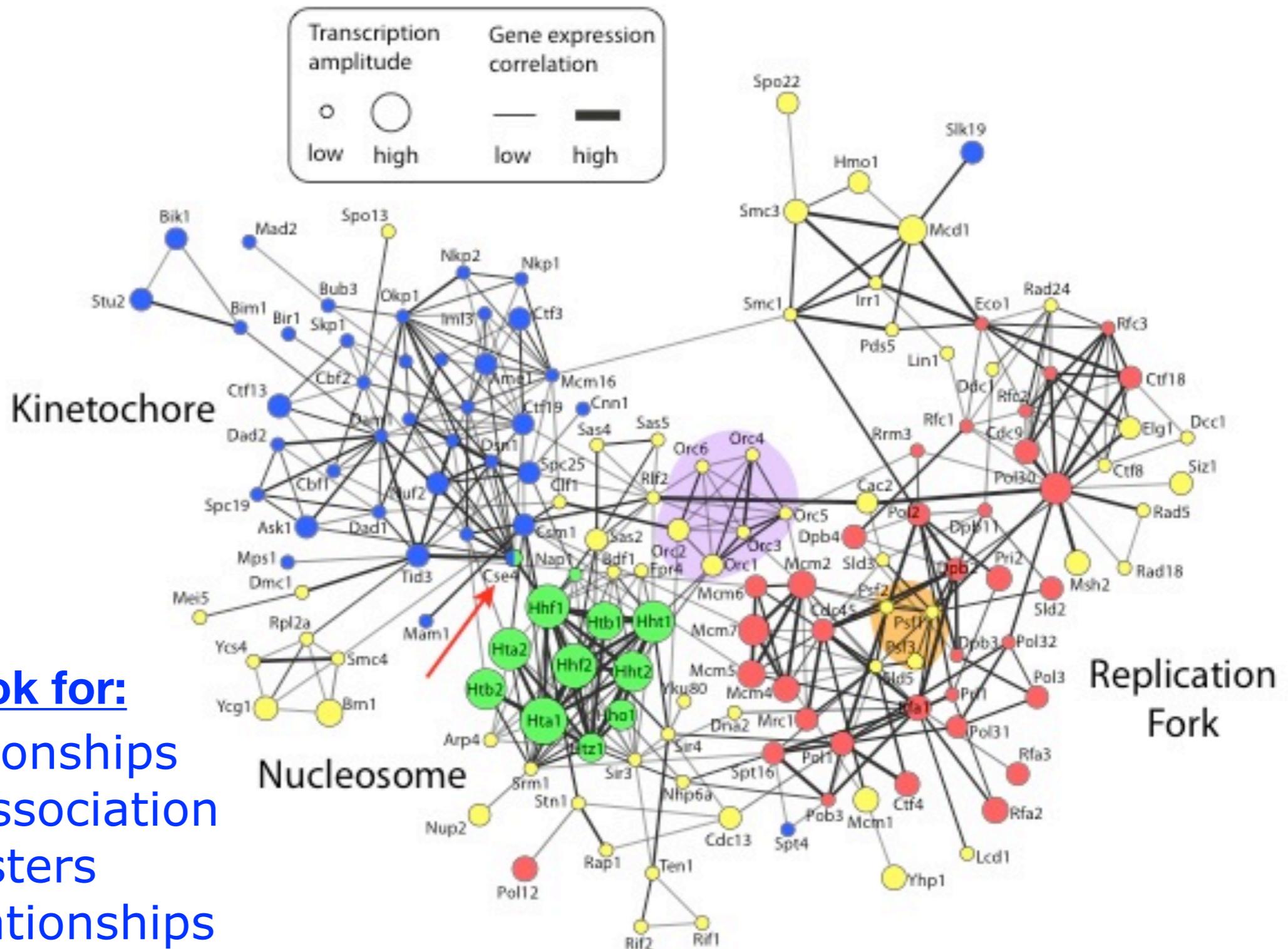


# Visual Features

- Node and edge attributes
  - Text (string), integer, float, Boolean, list
  - E.g. represent gene, interaction attributes
- Visual attributes
  - Node, edge visual properties
  - Color, shape, size, borders, opacity...



# Visually Interpreting a Network



# What have we learned so far...

- Automatic layout is required to visualize networks
- Networks help you visualize interesting relationships in your data
- Avoid hairballs by focusing analysis
- Visual attributes enable multiple types of data to be shown at once – useful to see their relationships

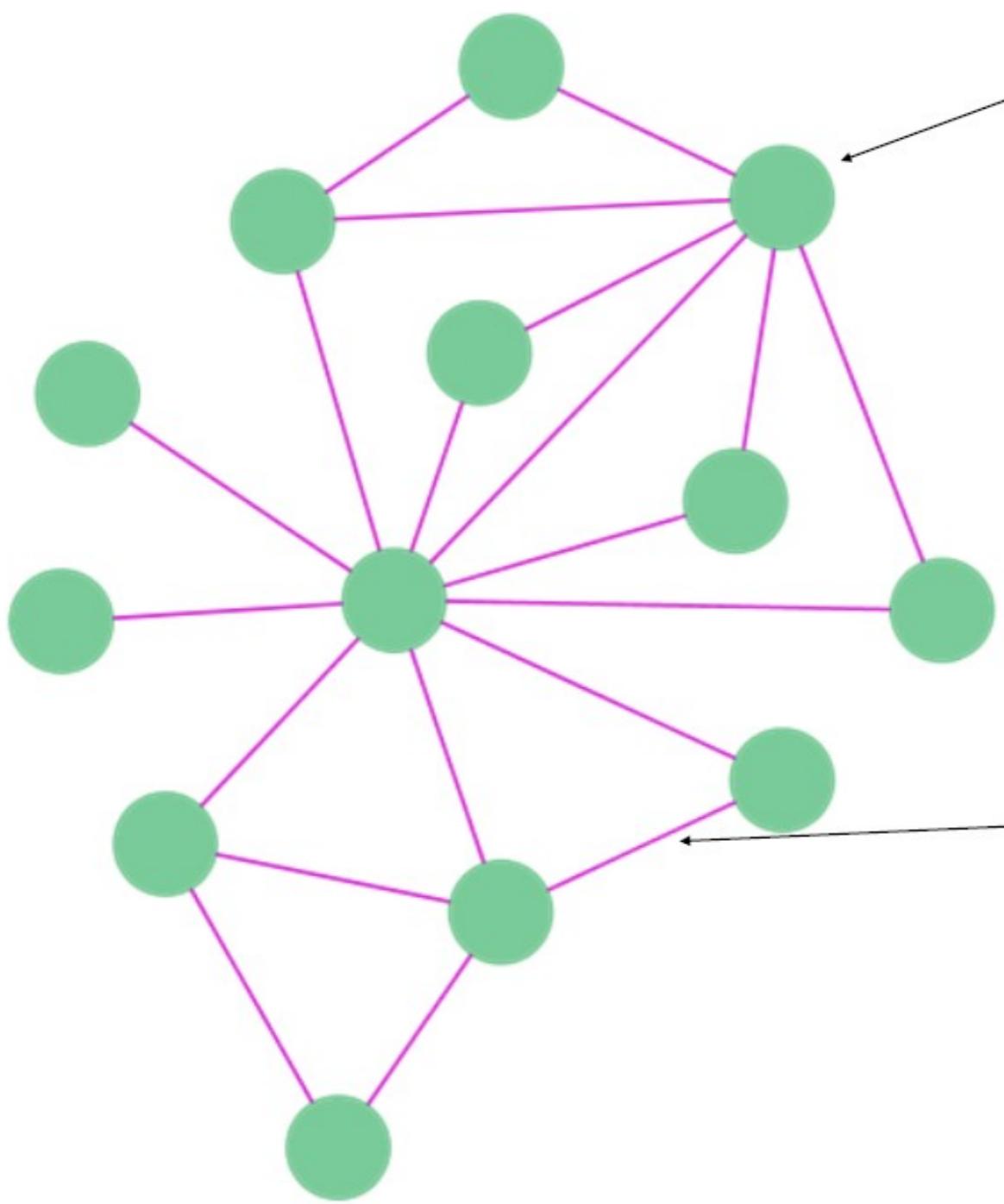
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for network visualization and analysis

# Introduction to graph theory

- Biological network analysis historically originated from the tools and concepts of **social network analysis** and the application of **graph theory** to the social sciences.
- Wikipedia defines graph theory as:
  - ➔ “[...] the study of graphs used to model pairwise relations between objects. A graph in this context is made up of **vertices** connected by **edges**”.
- In practical terms, it is the set of concepts and methods that can be used to visualize and analyze networks

## Network or graph



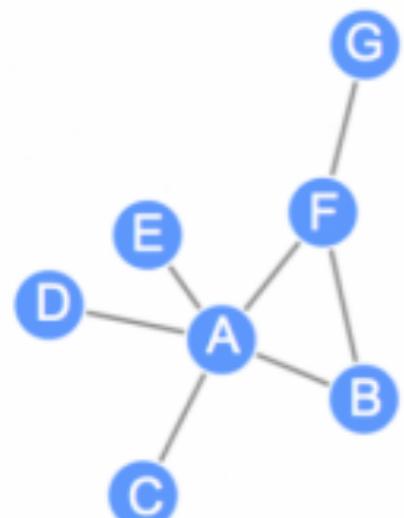
Node or vertex: protein, gene, drug, disease

Edge or link: relation between nodes

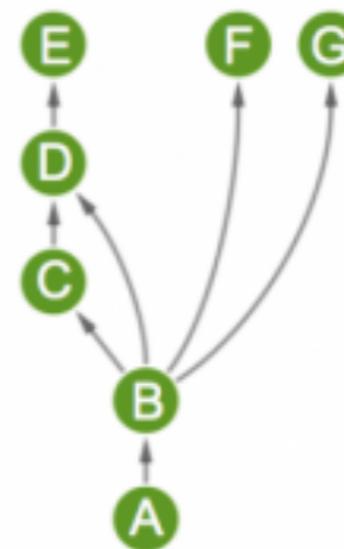
- Binary or continuous
- Directed or undirected
- Edge types

# Types of network edges

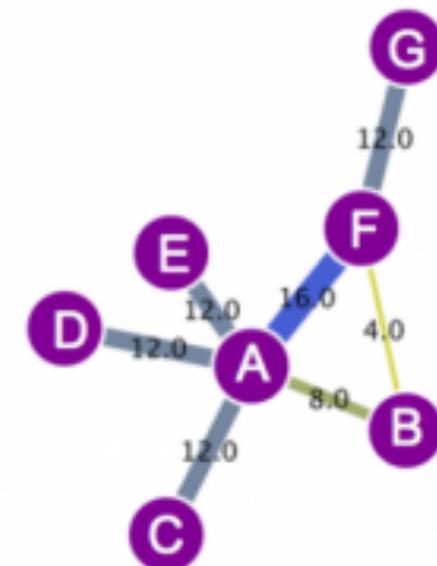
Undirected



Directed



Weighted



Connection,  
without a given  
'flow' implied

(e.g. protein A  
binds protein B)

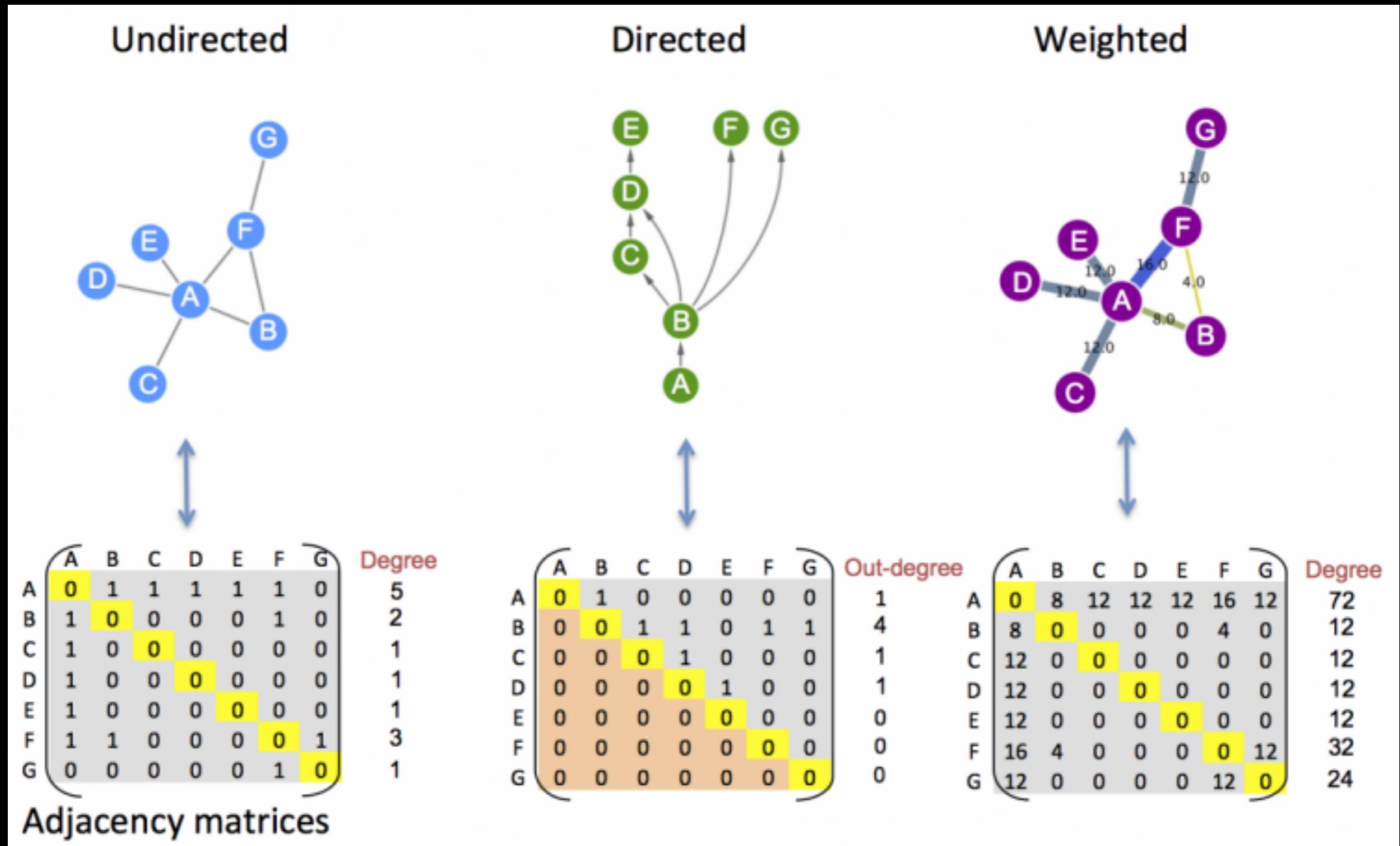
There is directional  
flow/signal implied

(e.g. metabolic or  
gene networks)

Edges can also  
have weight

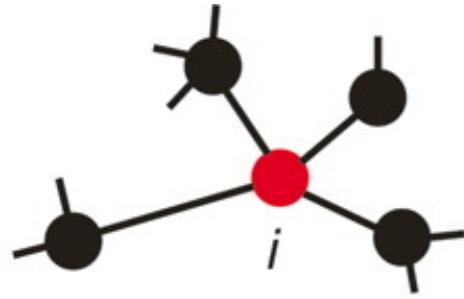
(i.e. a 'strength' of  
interaction).

- Every network can be expressed mathematically in the form of an adjacency matrix



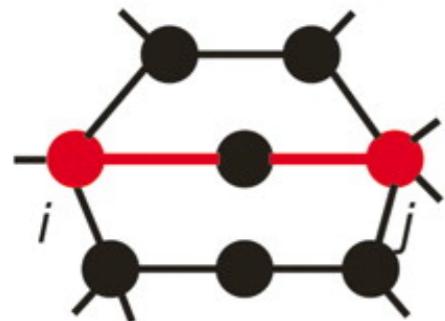
# Network topology

- Topology is the way in which the nodes and edges are arranged within a network.
- The most used topological properties and concepts include:
  - ➔ **Degree** (i.e. how many node neighbors)
  - ➔ **Communities** (i.e. clusters of well connected nodes)
  - ➔ **Shortest Paths** (i.e. shortest distance between 2 nodes)
  - ➔ **Centralities** (i.e. how ‘central’ is a given node?)
  - ➔ **Betweenness** (a measure of centrality based on shortest paths)



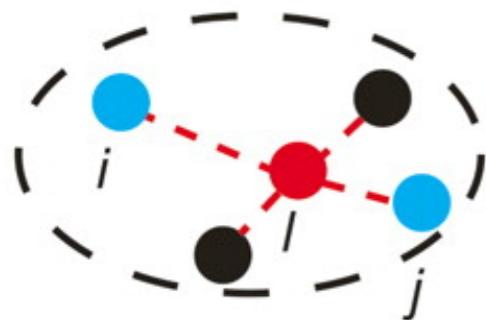
Degree

$k_i$  = number of links connected to node  $i$



Distance

$d_{ij}$  = shortest path length between node  $i$  and  $j$



Betweenness

$b_l = \sum_{ij} p_{ij}(l)/p_{ij}$

$p_{ij}$

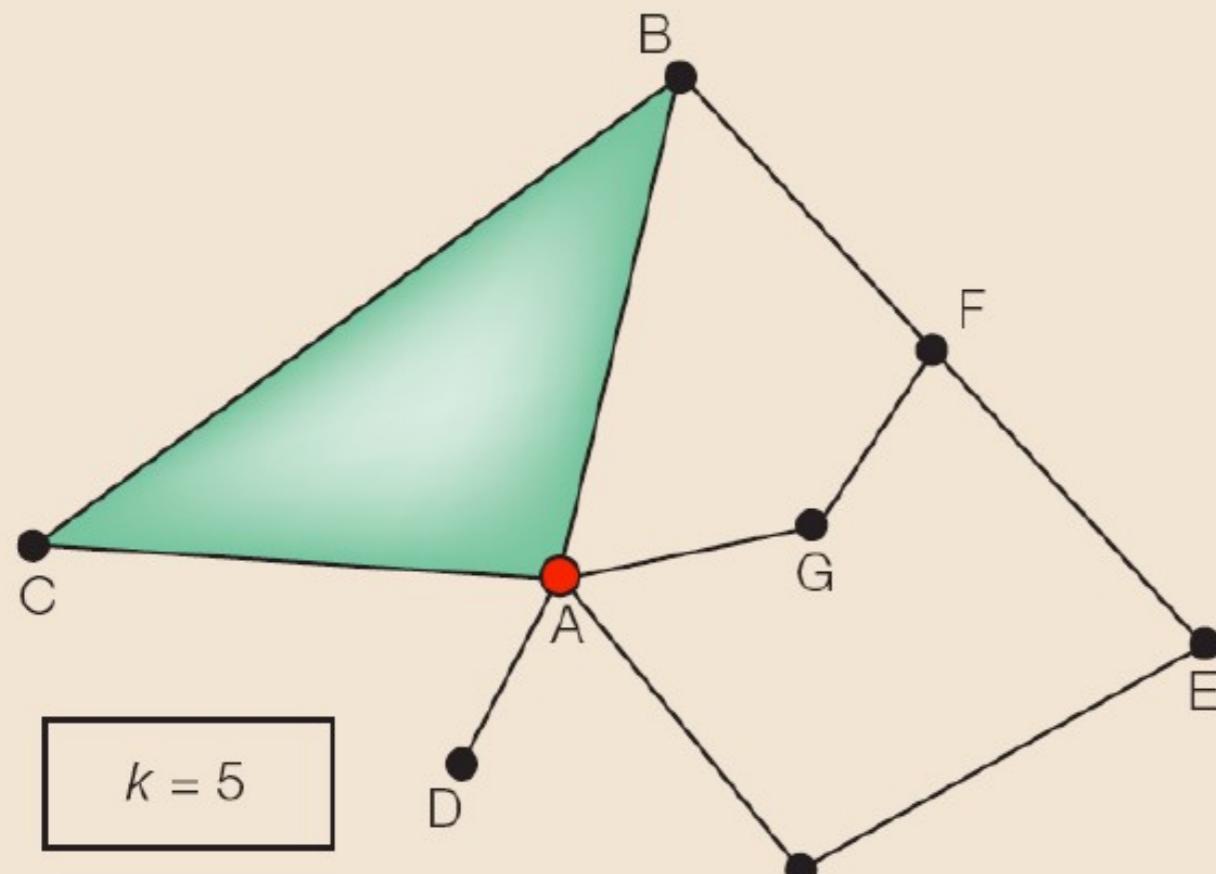
: number of shortest paths between  
 $i$  and  $j$

$p_{ij}(l)$

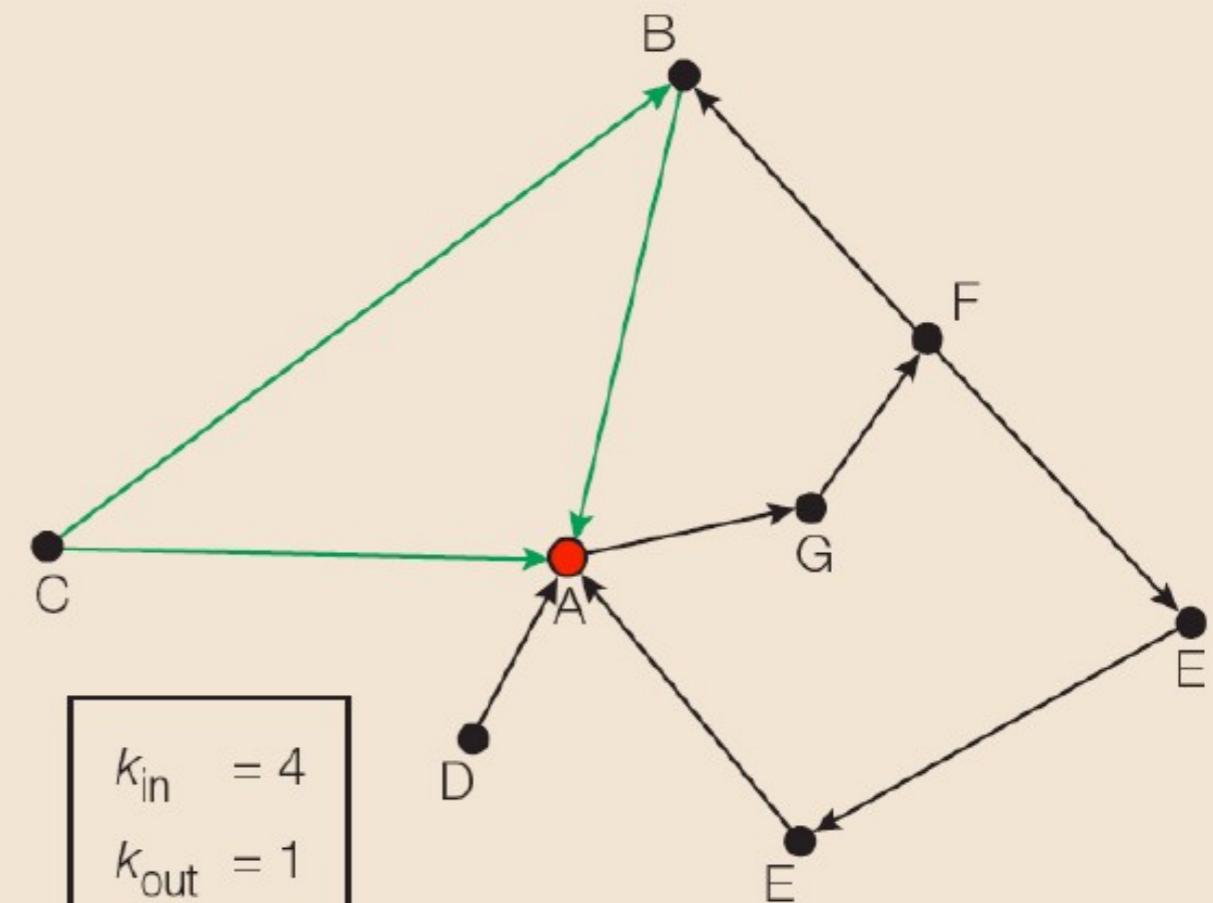
: number of shortest paths between
 $i$  and  $j$  going through node  $l$

# Network Measures: Degree

a Undirected network

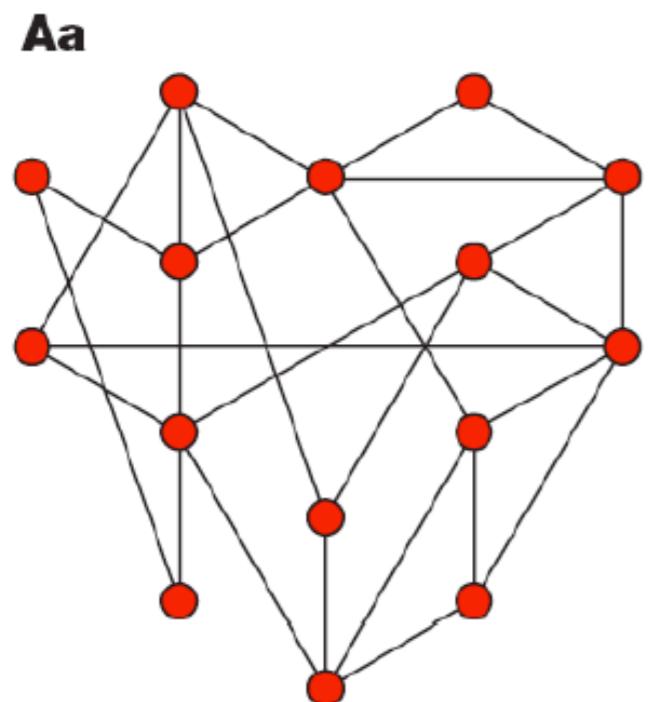


b Directed network

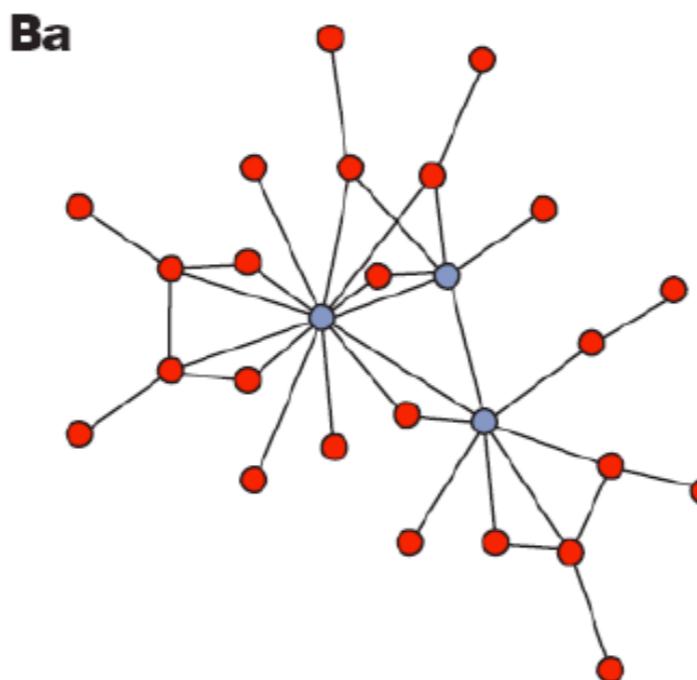


# Degree Distribution

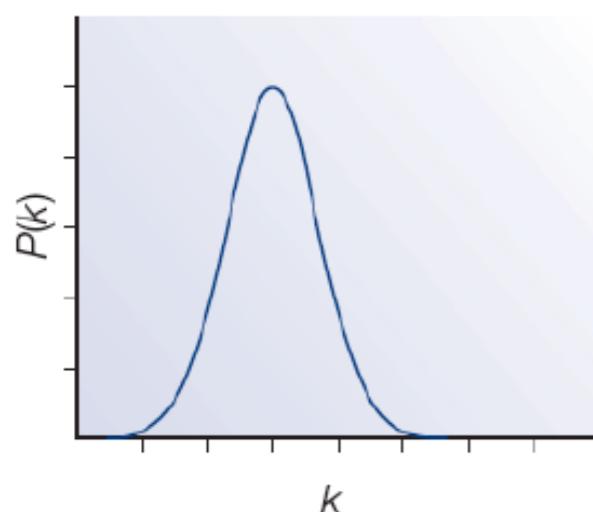
A Random network



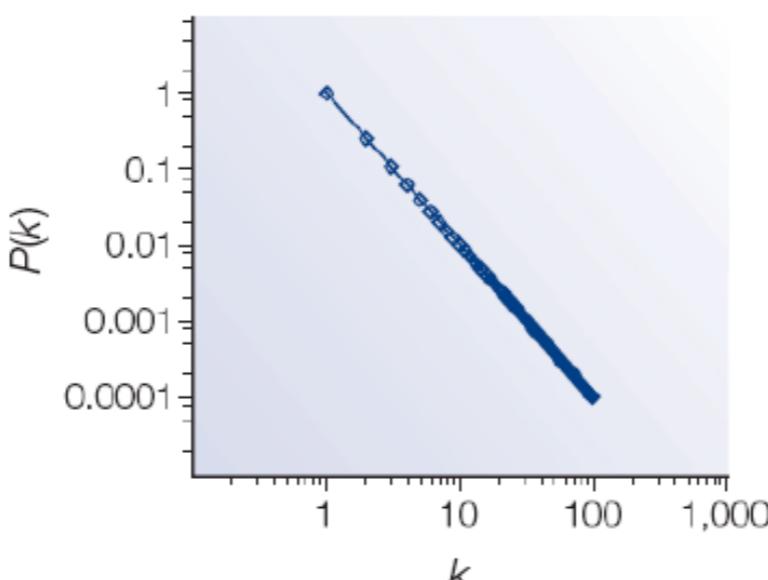
B Scale-free network



Ab



Bb



$P(k)$  is probability of each degree  $k$ , i.e fraction of nodes having that degree.

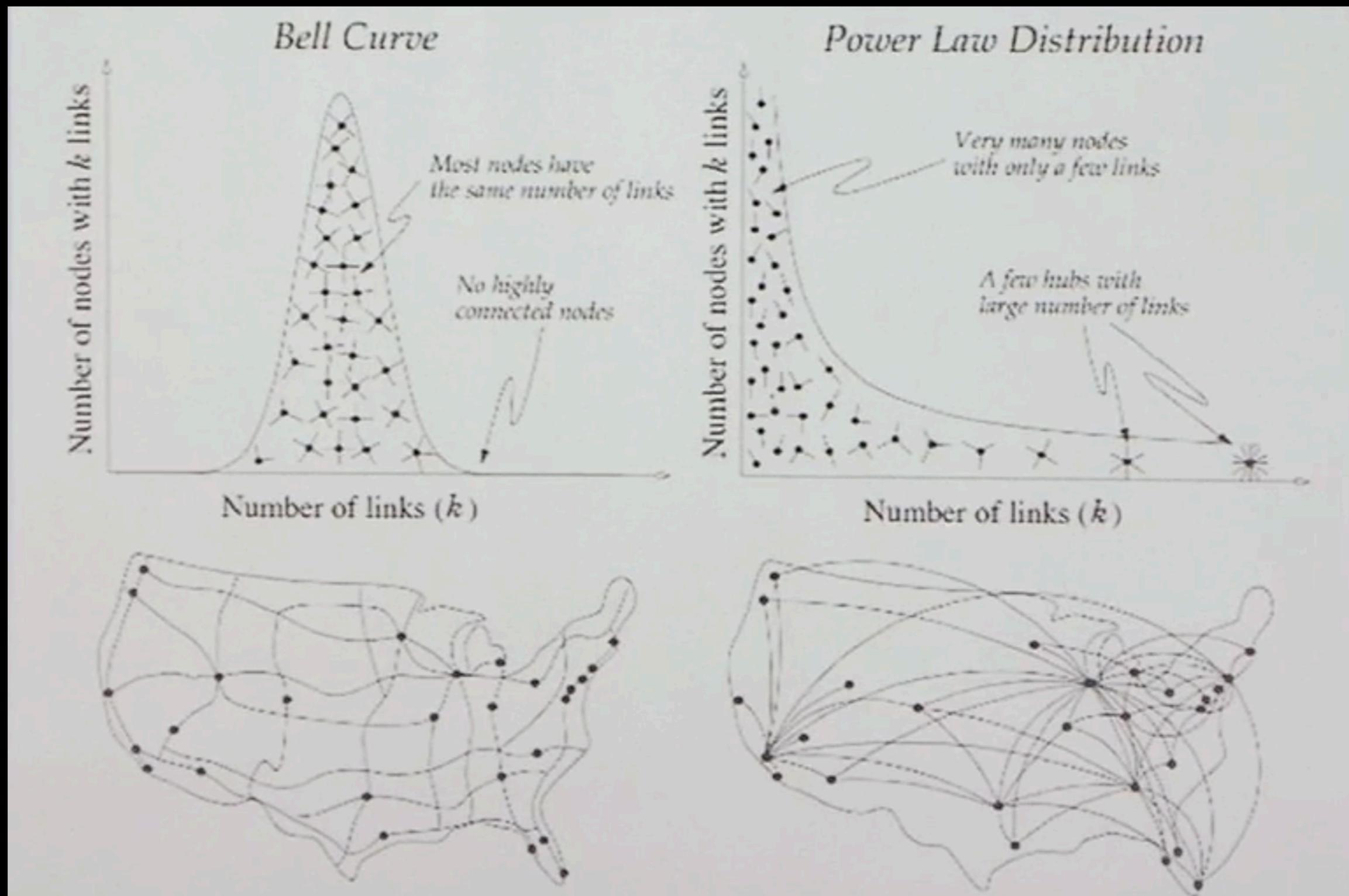
For random networks,  $P(k)$  is normally distributed.

For real networks the distribution is often a power-law:

$$P(k) \sim k^{-\gamma}$$

Such networks are said to be **scale-free**

# Random graphs vs scale free



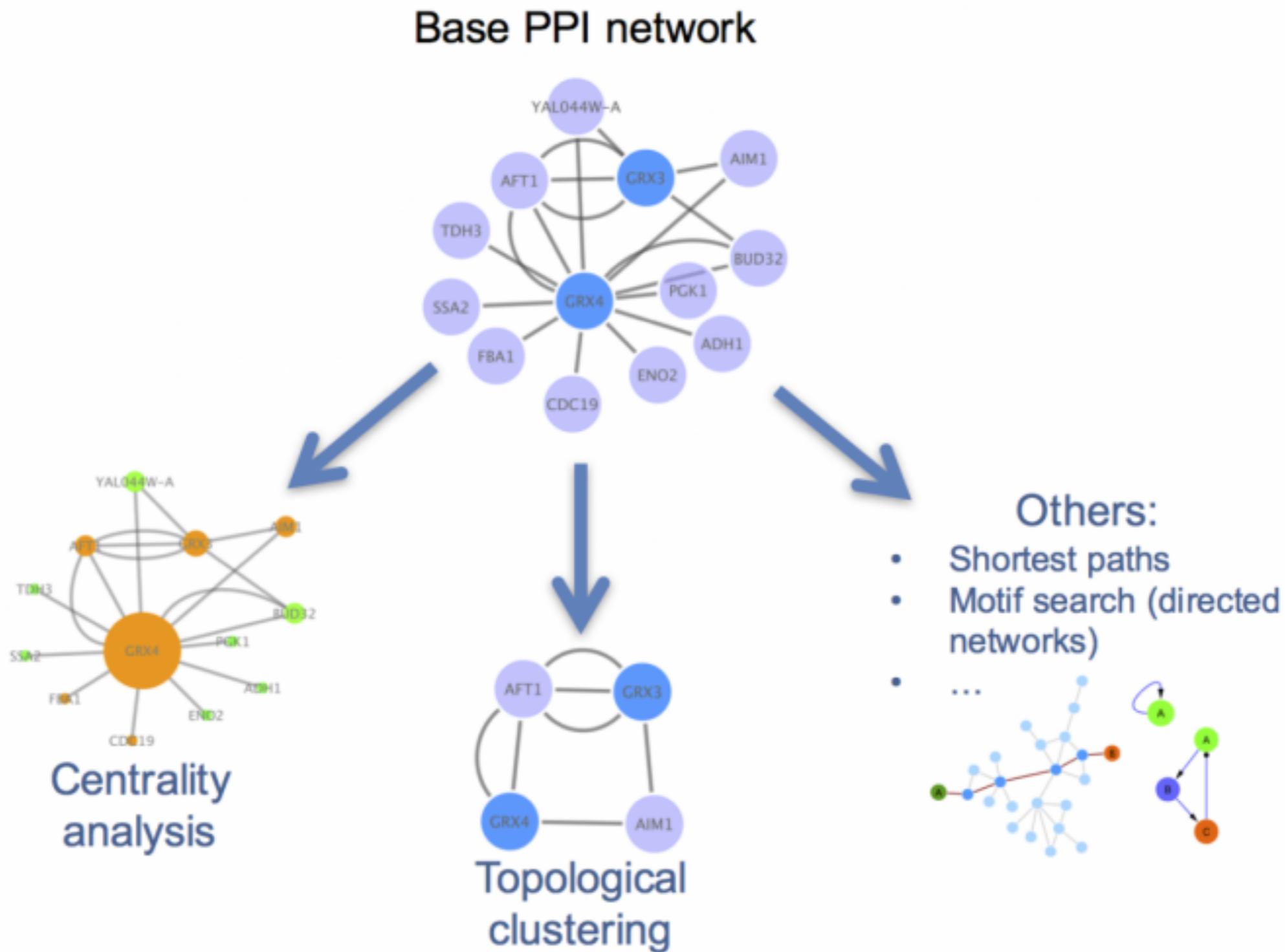
# Scale-Free Networks are Robust

- Complex systems (cell, internet, social networks), are resilient to component failure
- Network topology plays an important role in this robustness
  - Even if ~80% of nodes fail, the remaining ~20% still maintain network connectivity
- *Attack vulnerability* if hubs are selectively targeted
- In yeast, only ~20% of proteins are lethal when deleted, and are 5 times more likely to have degree  $k > 15$  than  $k < 5$ .

# Implications

- Many biological networks (protein-protein interaction networks regulatory networks, etc...) are thought to have hubs, or nodes with high degree.
- For protein-protein interaction networks (PPIs) these hubs have been shown to be older [1] and more essential than random proteins [2]
  - ➔ [1] Fraser et al. *Science* (2002) 296:750
  - ➔ [2] Jeoung et al. *Nature* (2001) 411:41

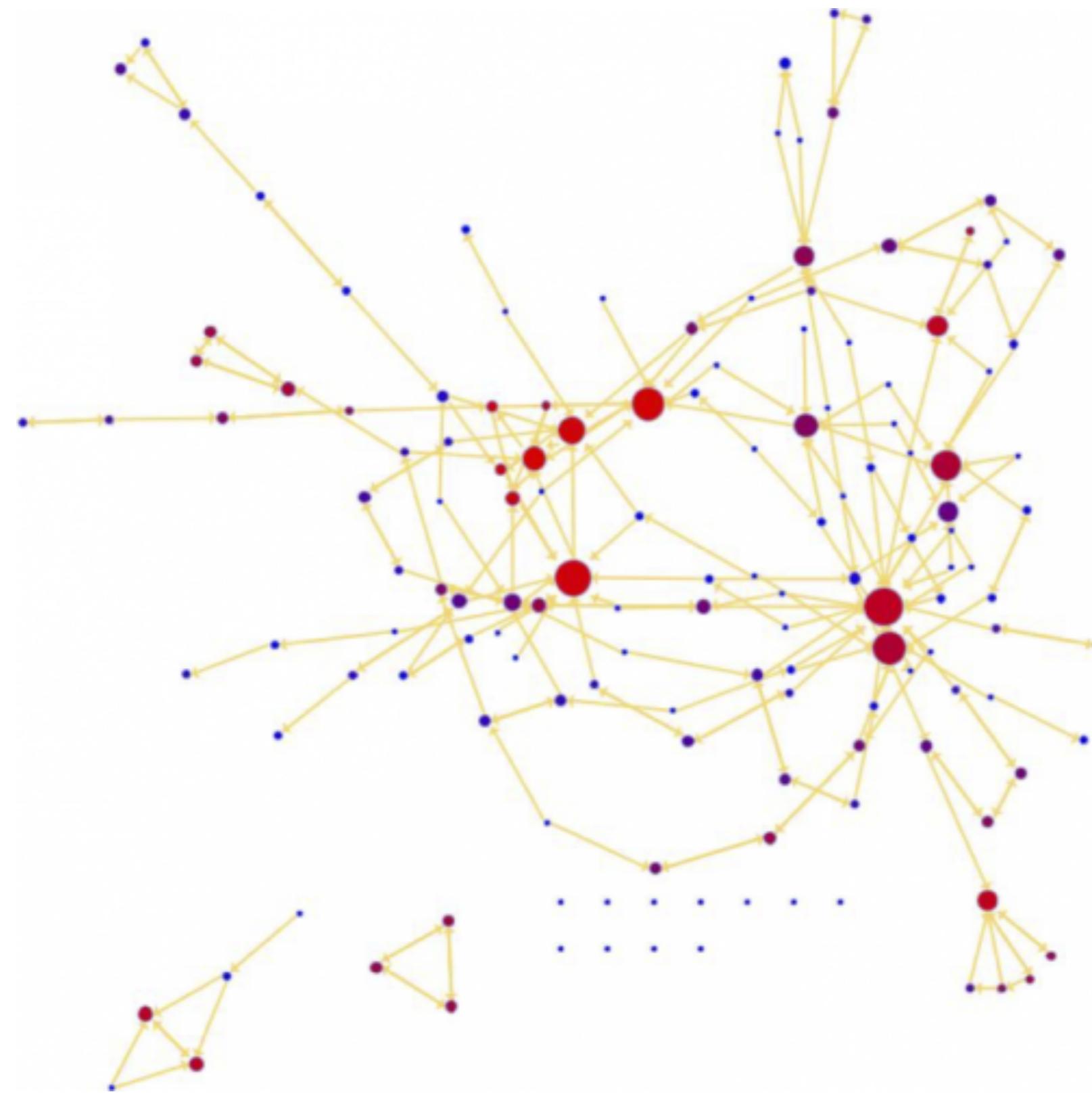
Analyzing the topological features of a network is a useful way of identifying relevant participants and substructures that may be of biological significance.



# Centrality analysis

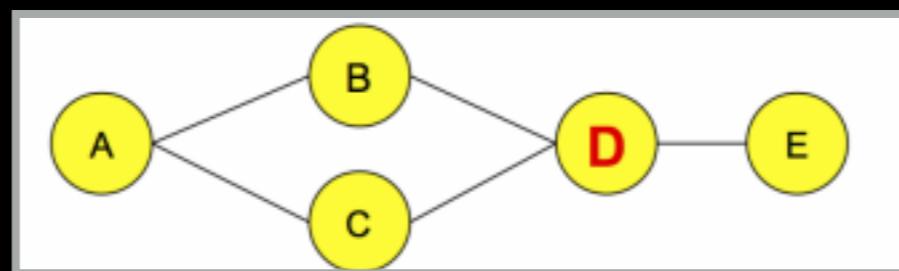
- Centrality gives an estimation on how important a node or edge is for the connectivity or the information flow of the network
- It is a useful parameter in signalling networks and it is often used when trying to find drug targets.
- Centrality analysis in PPINs usually aims to answer the following question:
  - ➔ Which protein is the most important and why?

Bigger, redder nodes have higher **centrality values** in this representation.



# Betweenness centrality

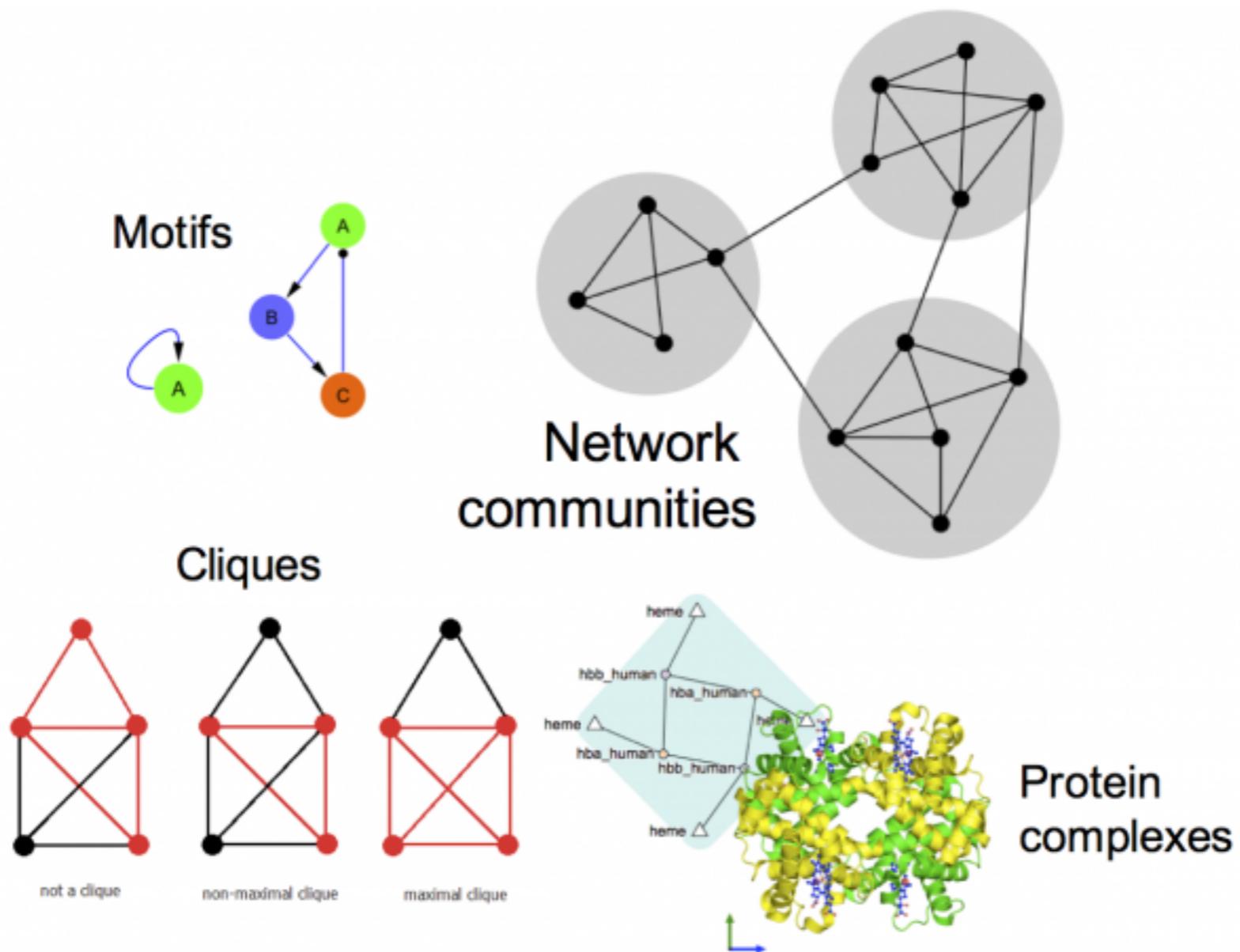
- Nodes with a high betweenness centrality are interesting because they lie on communication paths and can control information flow.
- The number of shortest paths in the graph that pass through the node divided by the total number of shortest paths.
- Betweenness centrality measures how often a node occurs on all shortest paths between two nodes.



# Community analysis

- **Community:** A general, catch-all term that can be defined as a group (i.e. *cluster*) of nodes that are more connected within themselves than with the rest of the network. The precise definition for a community will depend on the method or algorithm used to define it.

Looking for communities in a network is a nice strategy for reducing network complexity and extracting functional modules (e.g. protein complexes) that reflect the biology of the network.



# TODAYS MENU:

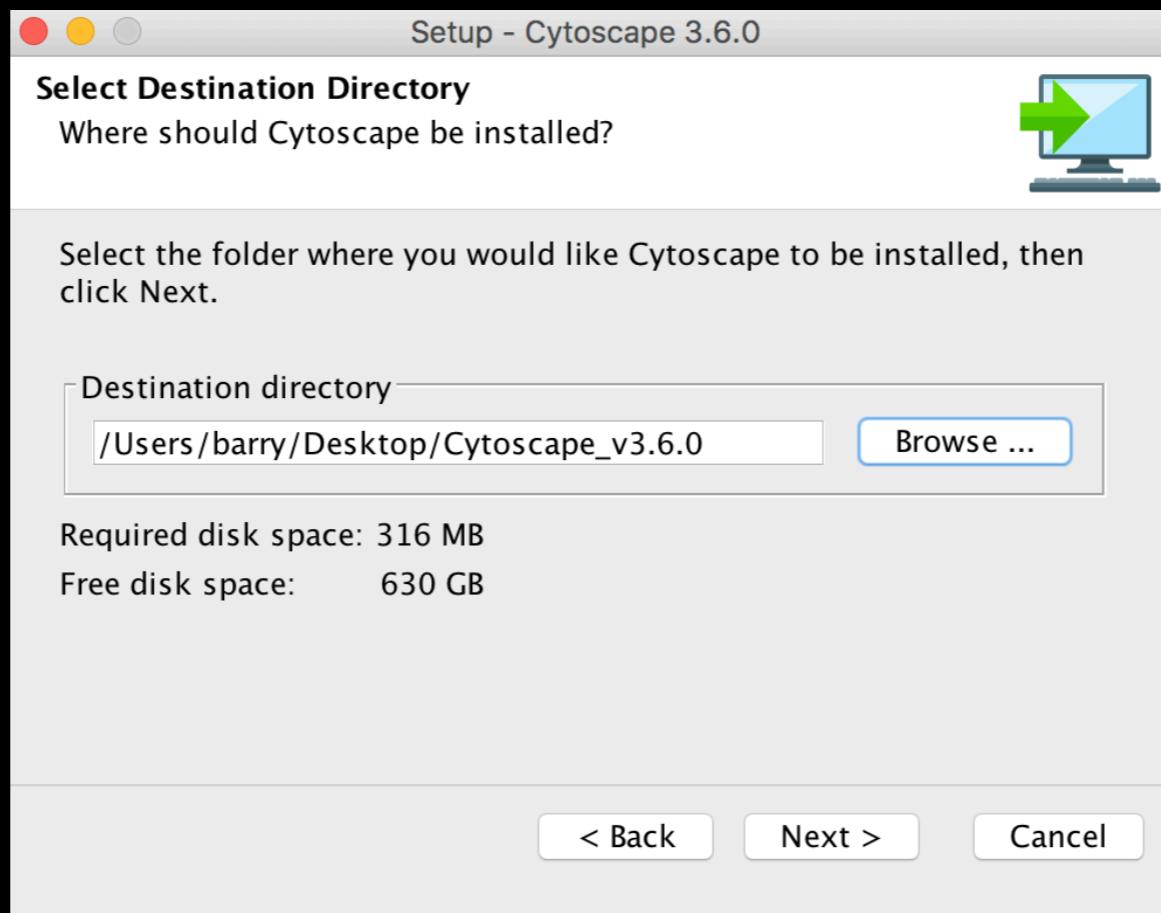
- ▶ Network introduction
- ▶ Network visualization
- ▶ Network analysis
- ▶ Hands-on:
  - Cytoscape and R (igraph) software tools for network visualization and analysis

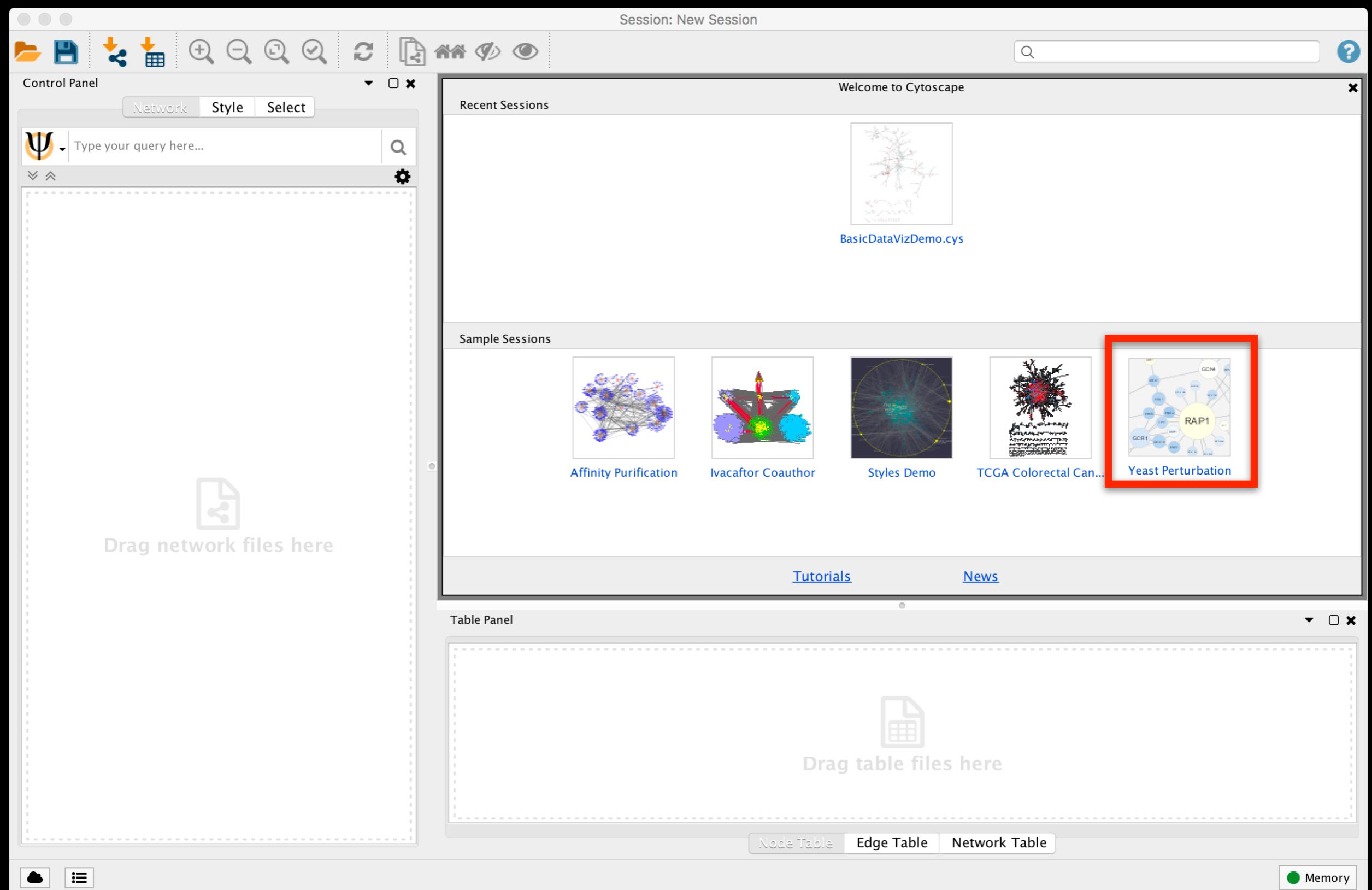
# Practical issues

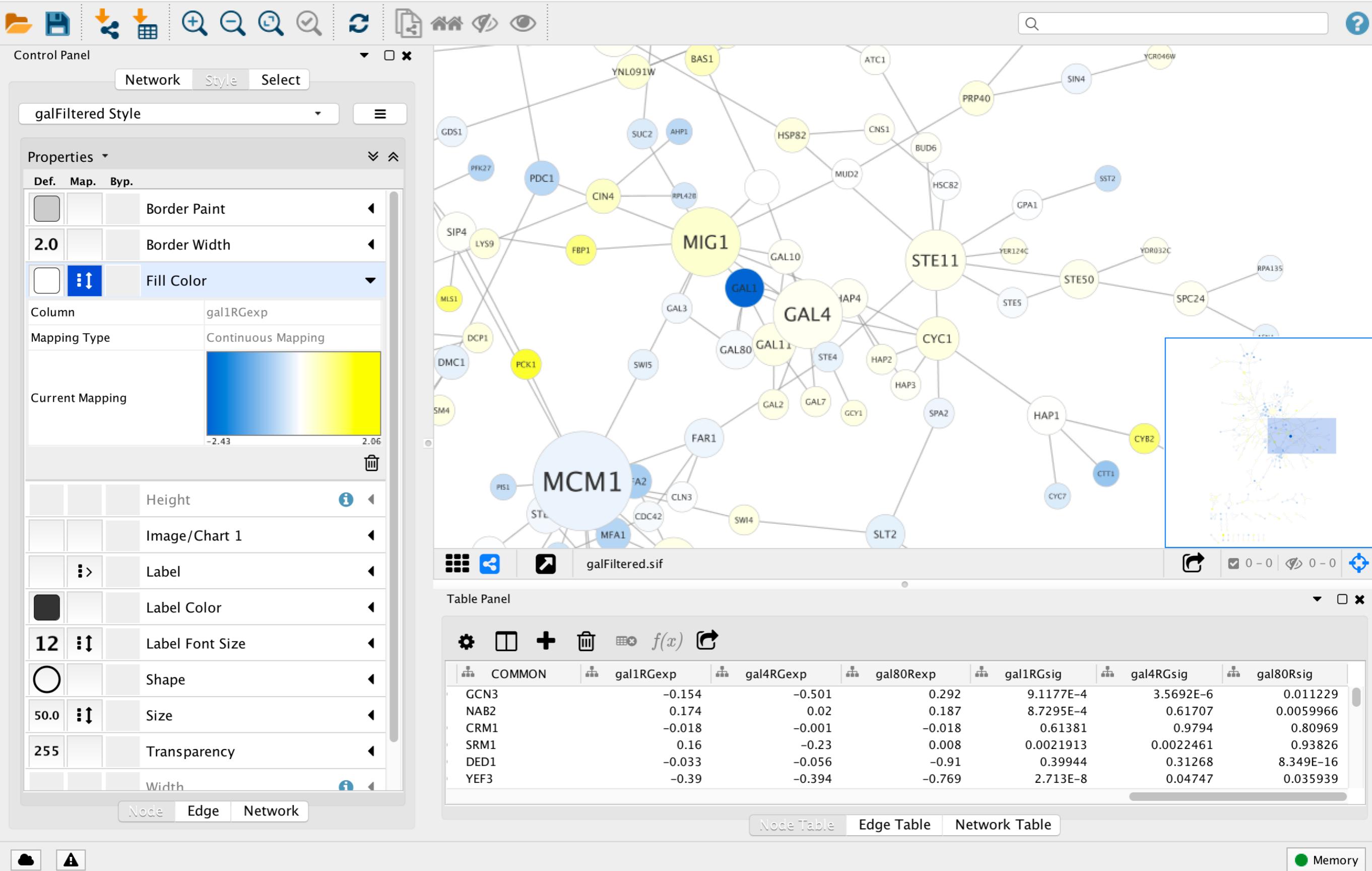
- Major tools for the **creation, manipulation** and **visualization** of biological networks include:
  - ➔ Cytoscape,
  - ➔ Gephi
  - ➔ R packages (igraph, graph, tidygraph)
- Tools for network analysis and modeling include:
  - ➔ Cytoscape apps/plugins
  - ➔ R packages (igraph and others)
  - ➔ NetworkX (for Python)
  - ➔ ByoDyn, COPASI

<http://cytoscape.org/download.php>

**Note:** If you are on a classroom Mac please check if Cytoscape is already installed. If not then please be sure to install to your **Desktop** directory!







# Cytoscape Memory Issues

- Cytoscape uses lots of memory and doesn't like to let go of it
  - ➔ An occasional restart when working with large networks is a good thing
  - ➔ Destroy views when you don't need them
- Since version 2.7, Cytoscape does a much better job at “guessing” good default memory sizes than previous versions but it still not great!
  - ➔ Java doesn't give us a good way to get the memory right at start time

# Cytoscape Sessions

- Sessions save pretty much everything:
  - ➔ Networks
  - ➔ Properties
  - ➔ Visual styles
  - ➔ Screen sizes
- Saving a session on a large screen may require some resizing when opened on your laptop

# Hands-on: Part 1

[https://bioboot.github.io/bggn213\\_W19/lectures/#17](https://bioboot.github.io/bggn213_W19/lectures/#17)

- The data used in **part 1** is from yeast, and the genes Gal1, Gal4, and Gal80 are all yeast transcription factors. The experiments all involve some perturbation of these transcription factor genes.
- In this network view, the following node attributes have been mapped to visual style properties in cytoscape:
  - ➔ The "gal80exp" expression values are used for Node Fill Color.
  - ➔ The Default Node Color, for nodes with no data mapping, is dark grey.
  - ➔ Nodes with expression values that are significant are rendered as rectangles, others are ovals.
  - ➔ The common name for each gene is used as the Node Label.

Skip for today!

# Hands-on: Part 2

[https://bioboot.github.io/bggn213\\_W19/lectures/#17](https://bioboot.github.io/bggn213_W19/lectures/#17)

- The data used in **part 2** is from an ocean metagenomic sequencing project - where all the genetic material in a sample of ocean water is sequenced.
- We will use the R package **igraph** and the bioconductor package **RCy3** together with Cytoscape.
- Many of these microbial species in these types of studies have not yet been characterized in the lab.
  - ➔ Thus, to know more about the organisms and their interactions, we can observe which ones occur at the same sites.
  - ➔ One way to do that is by using **co-occurrence networks** where you examine which organisms occur together at which sites.

*Do this now next day!*

# Revisit Lecture 11

[https://bioboot.github.io/bggn213\\_W19/lectures/#11](https://bioboot.github.io/bggn213_W19/lectures/#11)

Muscle setup instructions (at your command line TERMINAL)

## Windows install and setup cmd:

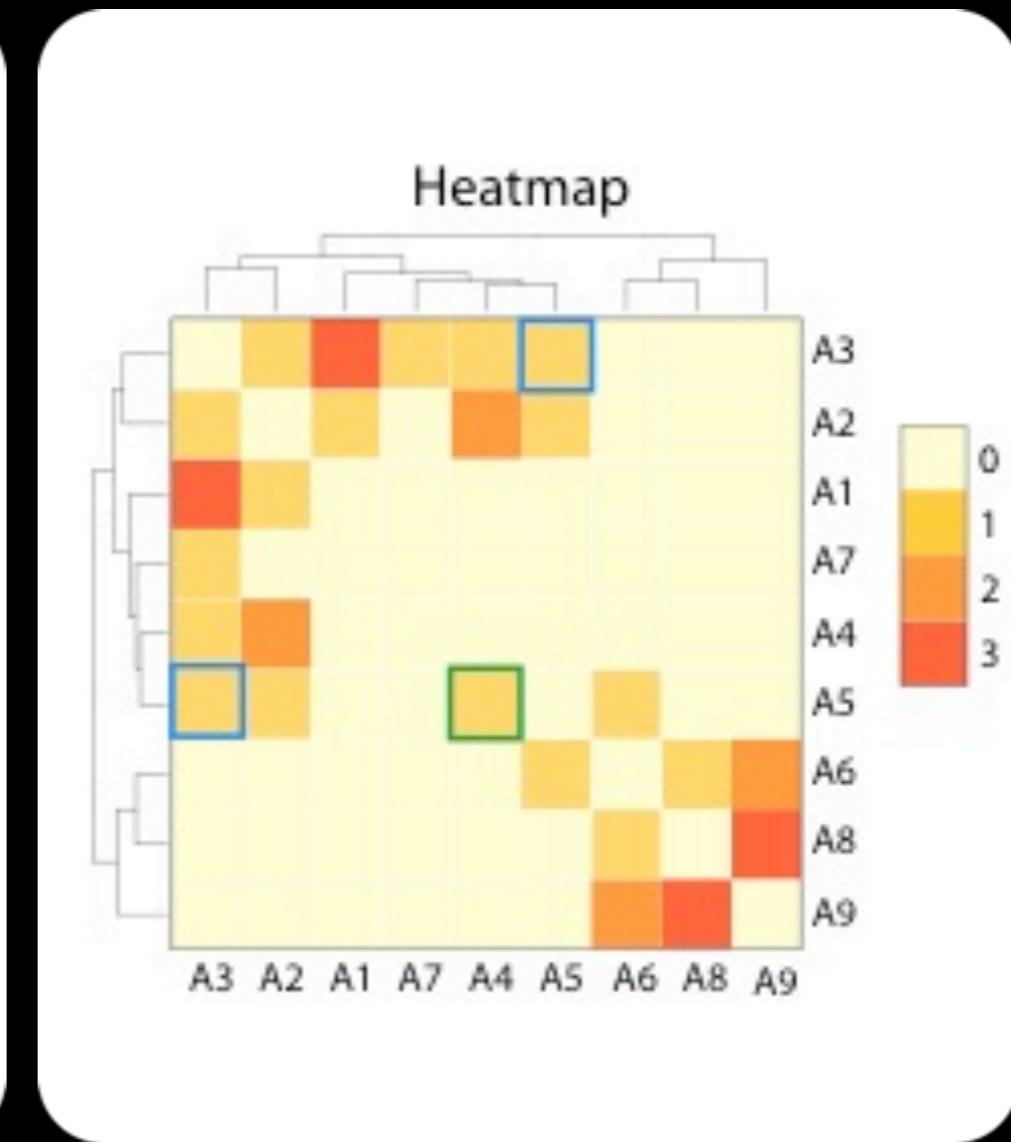
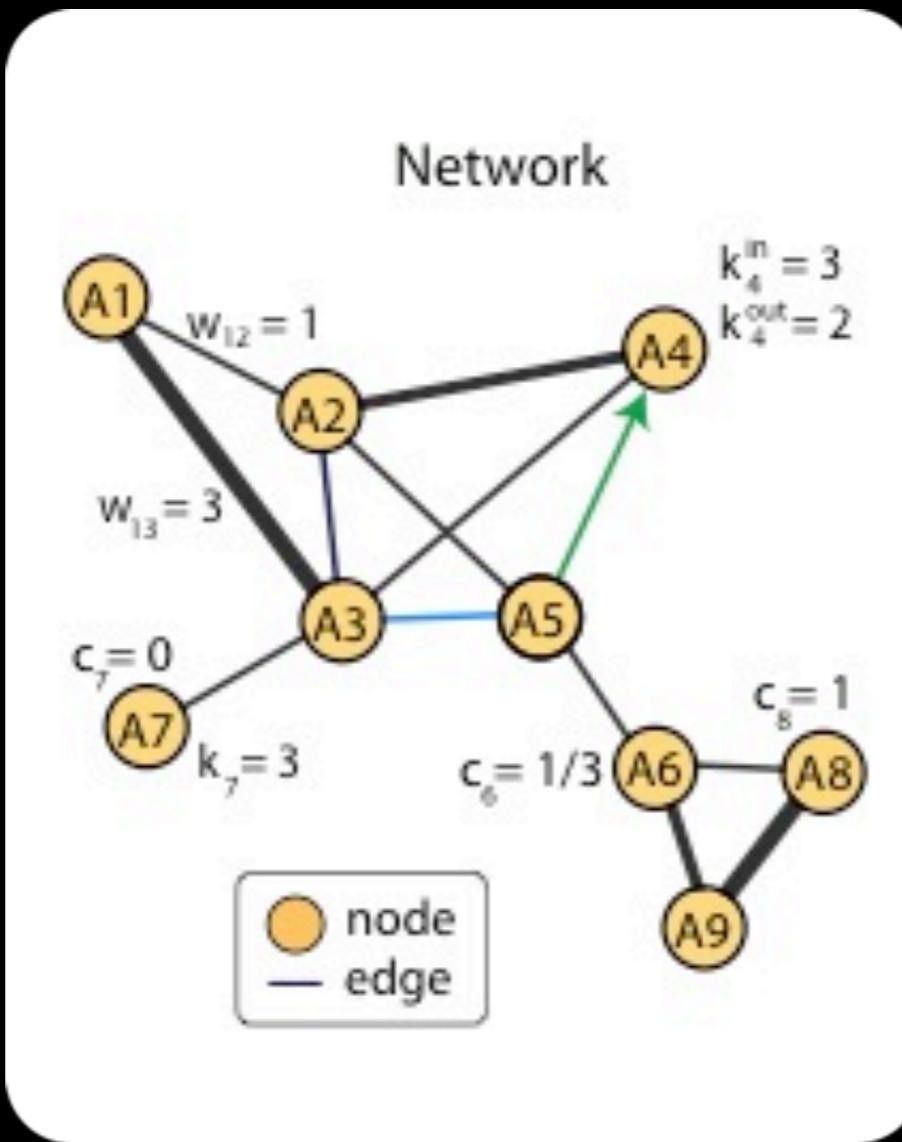
```
cd ~/Desktop  
curl -o "muscle.exe" "https://www.drive5.com/muscle/downloads3.8.31/muscle3.8.31_i86win32.exe"
```

## Mac install and setup cmd:

```
curl -o "/usr/local/bin/muscle" "http://thegrantlab.org/misc/muscle"  
chmod +x /usr/local/bin/muscle
```

# Network representations

Relationships	Optional weight
A1 ↔ A2	1
A1 ↔ A3	3
A2 ↔ A3	1
A2 ↔ A4	2
A2 ↔ A5	1
A3 ↔ A4	1
A3 ↔ A5	1
A3 ↔ A7	1
A5 → A4	1
A5 ↔ A6	1
A6 ↔ A8	1
A6 ↔ A9	2
A8 ↔ A9	3



1

List of relationships

2

Network view

3

Adjacency matrix view

**Network view is most useful when network is sparse!**

# Summary

- Network biology makes use of the tools provided by **graph theory** to represent and analyze complex biological systems.
- Major types of biological networks include: genetic, metabolic, cell signaling etc.
- Networks are represented by **nodes** and **edges**.
- Biological networks have a number of characteristics, mainly:
  - ➔ **Scale-free**: A small number of nodes (hubs) are a lot more connected than the average node.
  - ➔ **Transitivity**: The networks contain communities of nodes that are more connected internally than they are to the rest of the network.
- Major tools for network analysis include: **Cytoscape**, **igraph**, Gephi and NetworkX.
- Two of the most used topological methods to analyze PPINs are:
  - ➔ **Centrality analysis**: Which identifies the most important nodes in a network, using different ways to calculate centrality.
  - ➔ **Community detection**: Which aims to find heavily inter-connected components that may represent protein complexes and machineries

# Summary cont. . .

- **Cytoscape** is a useful, free software tool for network visualization and analysis
  - ➔ Provides basic network manipulation features
  - ➔ Plugins/Apps are available to extend the functionality
- The R **igraph** package has extensive network analysis functionality beyond that in Cytoscape
- The R bioconductor package **RCy3** package allows us to bring networks and associated data from R to Cytoscape so we can have the best of both worlds.

# Network Analysis Overview

