

# Random networks

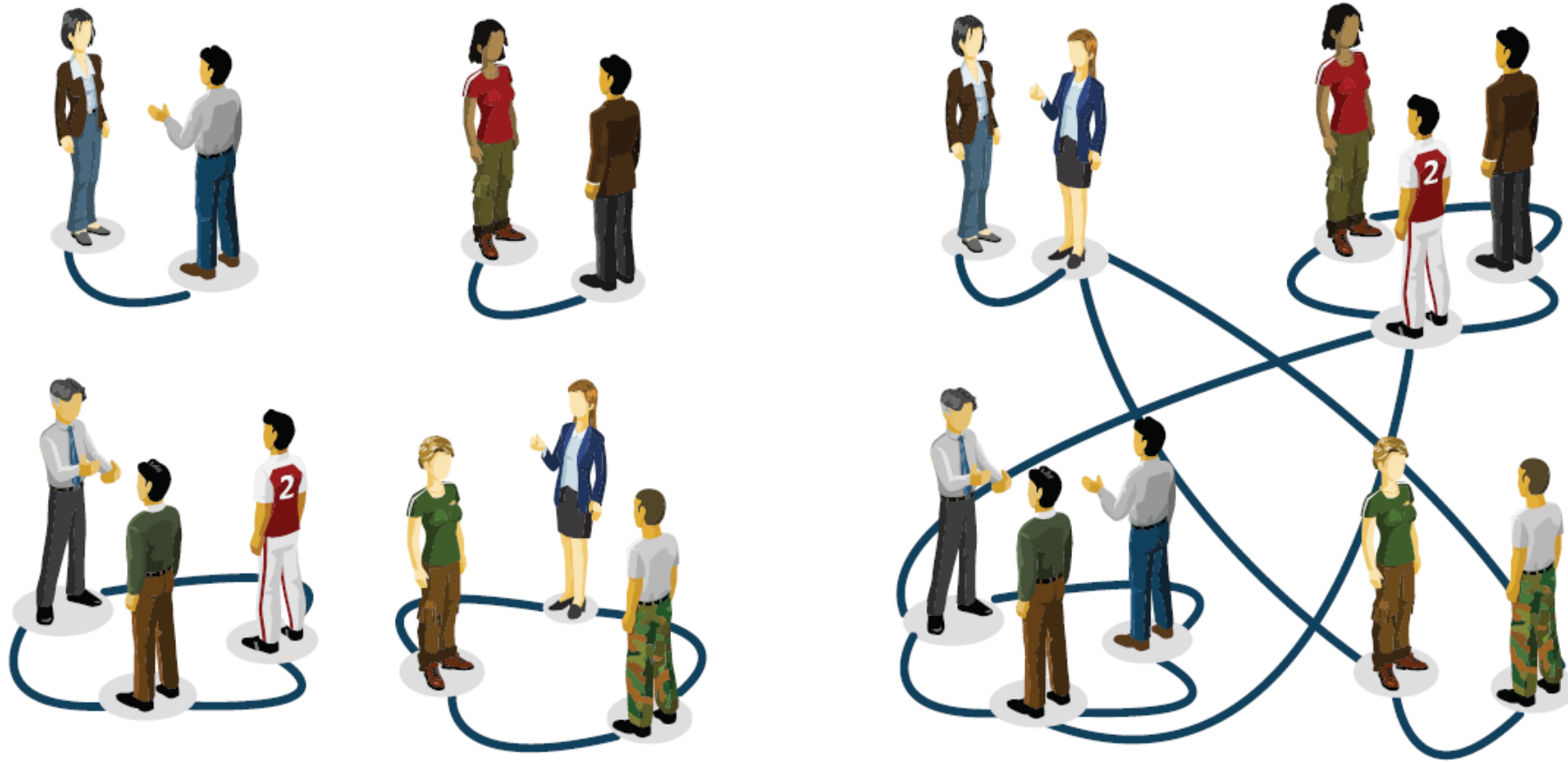


Image 3.1

From a cocktail party to random networks.

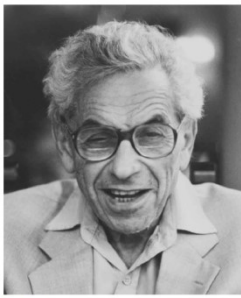


Image 3.2a  
Pál Erdős (1913–1996)



Image 3.2b  
Alfréd Rényi (1921–1970)

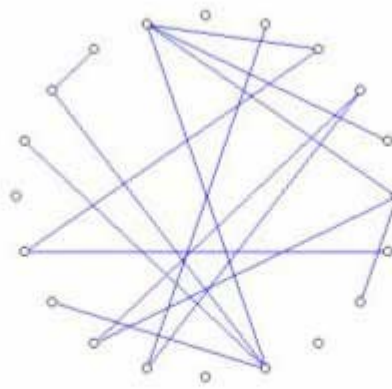
# Erdős–Rényi model

sets an edge between each pair of nodes with equal probability, independently of the other edges

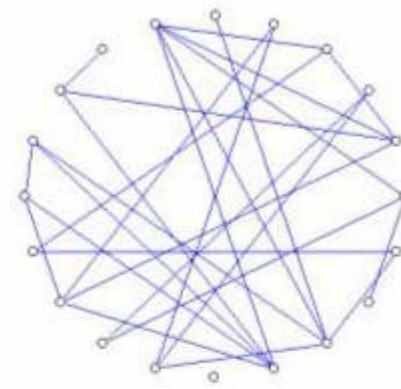
$$G(n, p)$$



$p = 0$   
(a)



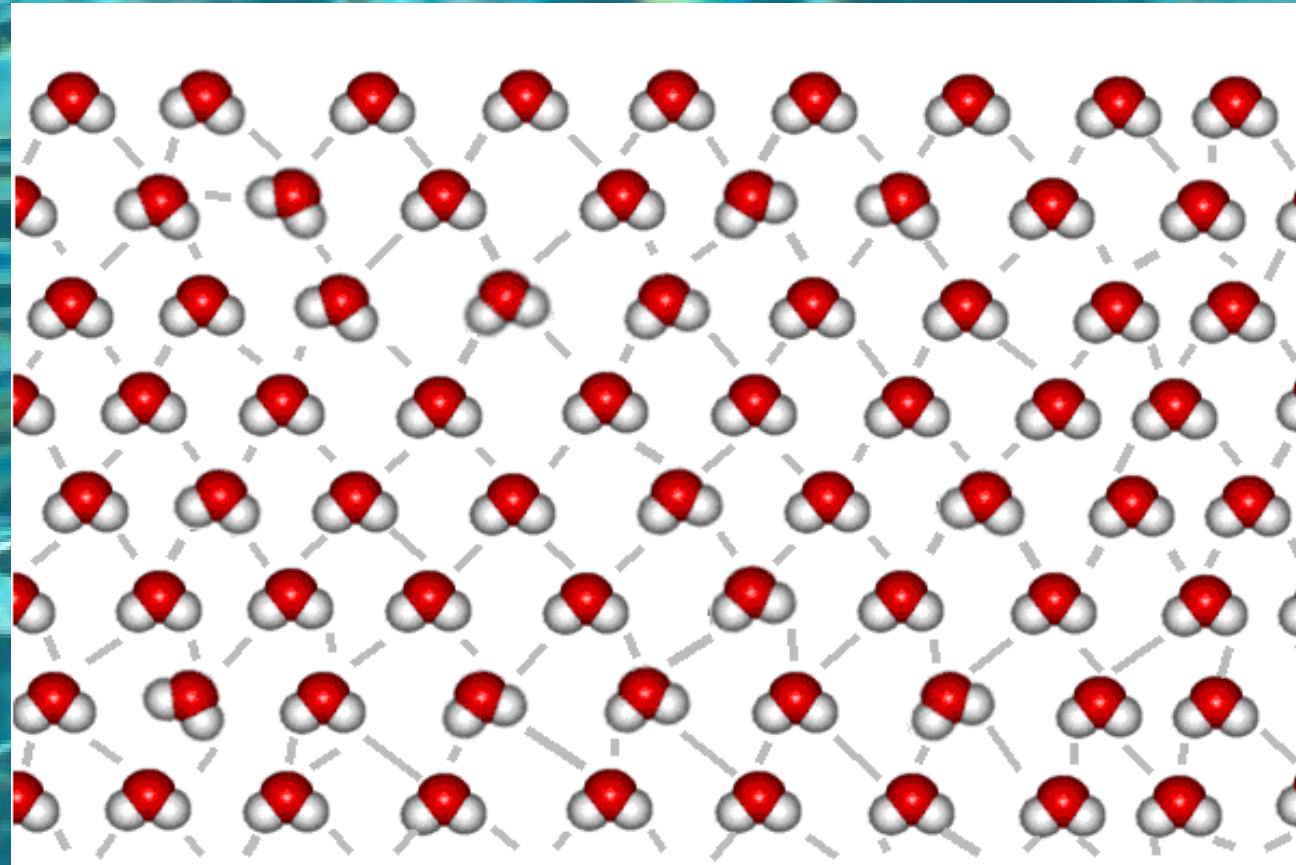
$p = 0.1$   
(b)



$p = 0.2$   
(c)

1. Start with  $N$  isolated nodes.
2. Select a node pair, and generate a random number between 0 and 1. If the random number exceeds  $p$ , connect the selected node pair with a link, otherwise leave them disconnected.
3. Repeat step (2) for each of the  $N(N-1)/2$  node pairs.

# Random networks



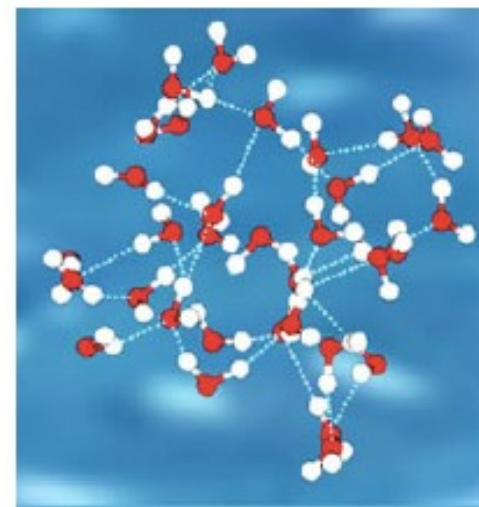
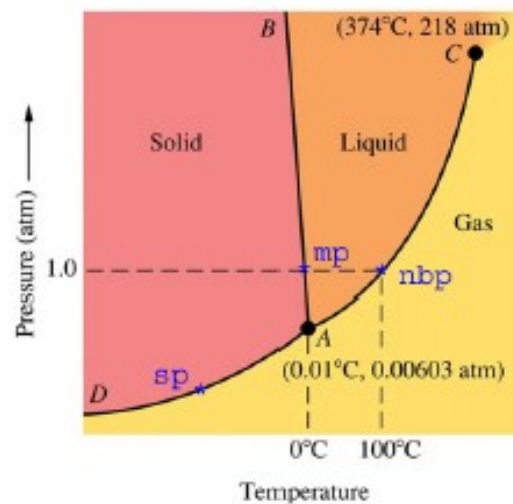
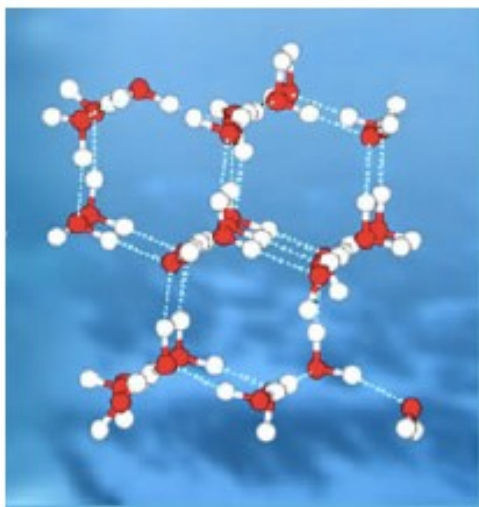


Image 3.22a  
Water-Ice phase transition.

The hydrogen bonds that hold the water molecules together (dotted lines) are weak, constantly breaking up and re-forming, maintaining partially ordered local structures (left panel). The temperature-pressure phase diagram indicates (center panel) that by lowering the temperature, the water undergoes a phase transition, moving from a liquid (orange) to a frozen solid (red). In the solid phase each water molecule binds rigidly to four other molecules, forming an ice lattice (right panel). After <http://www.lbl.gov/Science-Articles/Archive/sabl/2005/February/water-solid.html>; phase diagram after <http://stevengoddard.wordpress.com/2010/09/02/the-ideal-world-phase-diagrams-part-deux/>.

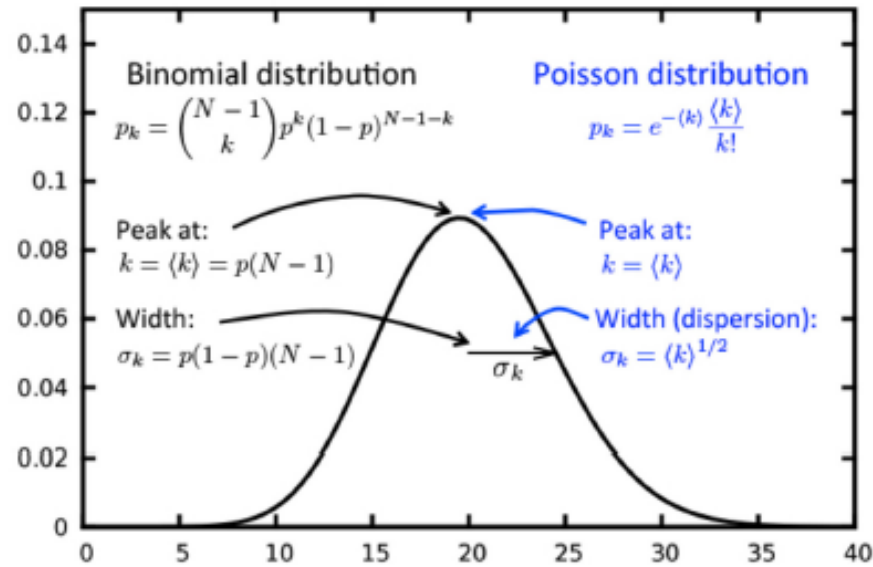


Image 3.4a  
 Anatomy of a binomial and a Poisson degree distribution.

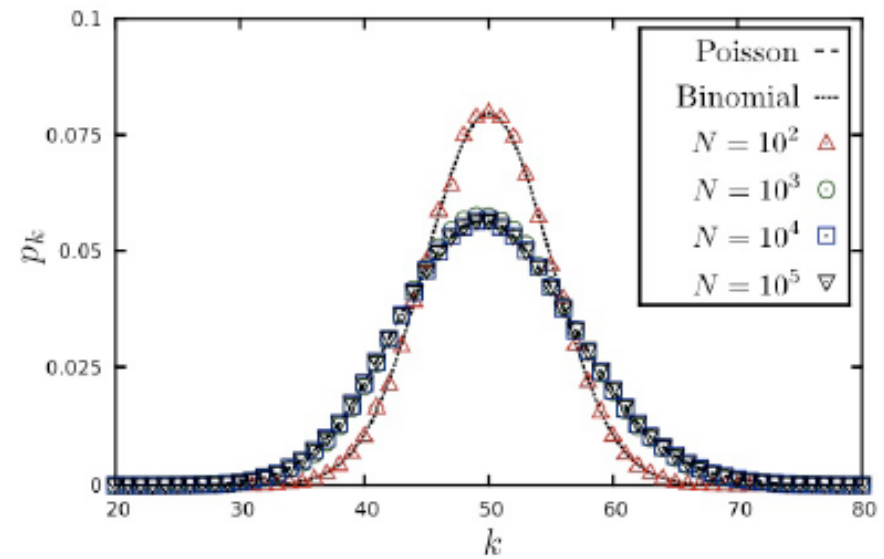


Image 3.4b  
 Degree distribution is independent of the network size.

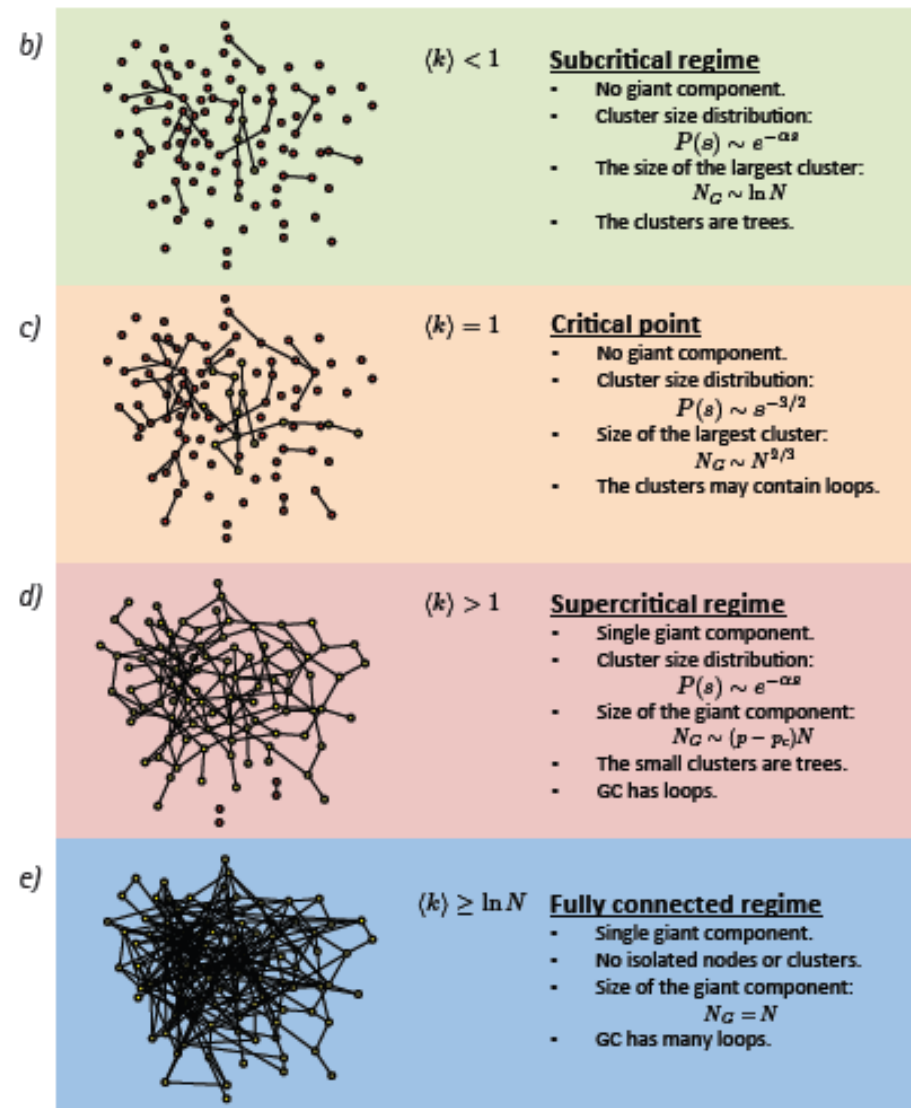


Image 3.6  
Evolution of a random network.

(a) The relative size of the giant component in function of the average degree  $\langle k \rangle$  in the Erdős-Rényi model.

(b)-(e) The main network characteristics in the four regimes that characterize a random network.

# Watts and Strogatz model

- However the ER graphs do not have two important properties observed in many real-world networks:
- They do not generate local clustering and triadic closures. Instead because they have a constant, random, and independent probability of two nodes being connected, ER graphs have a low clustering coefficient.



# Small world



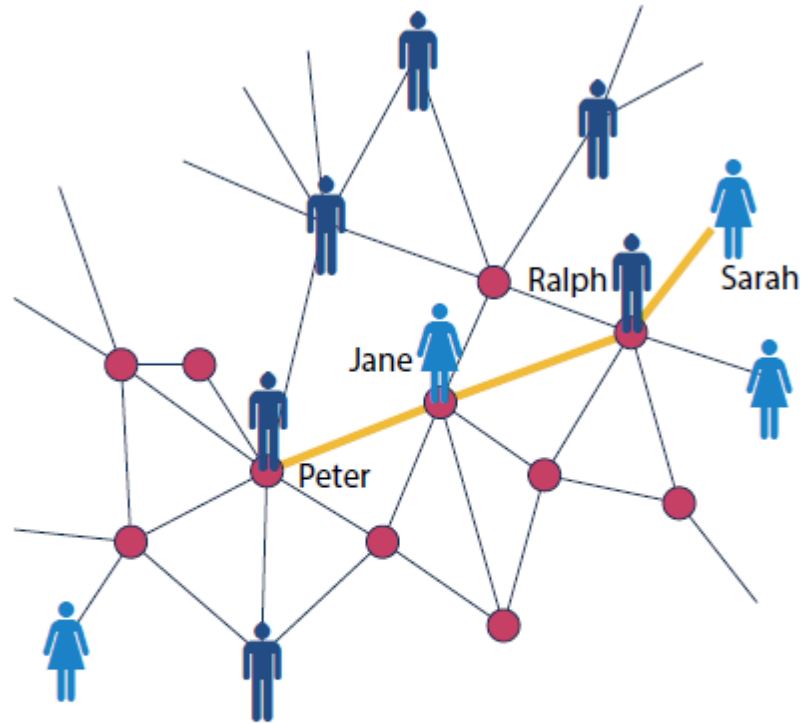


Image 3.9

### Six degrees of separation.

According to six degrees of separation any two individuals, anywhere in the world, can be connected through a chain of six or fewer acquaintances. This means that while Sarah does not know Peter, she knows Ralph, who knows Jane and who in turn knows Peter. Hence Sarah is three degrees from Peter. In the language of network science six degrees, also called the small world property, states that the distance between any two nodes in a network is unexpectedly small.

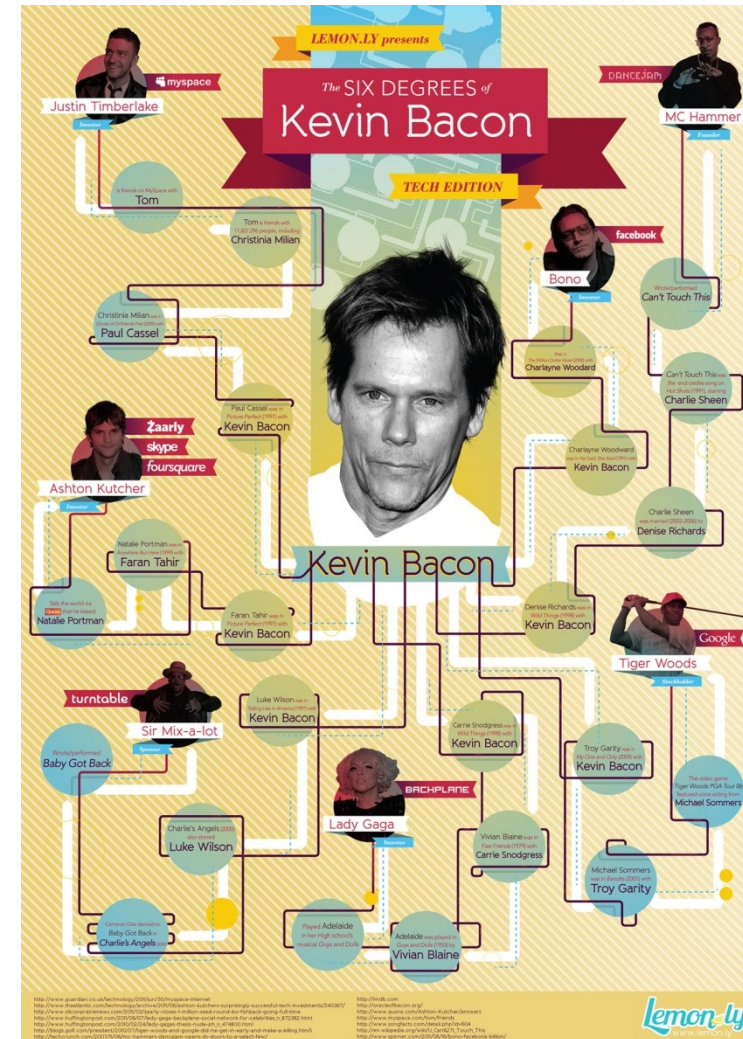


Image 3.13

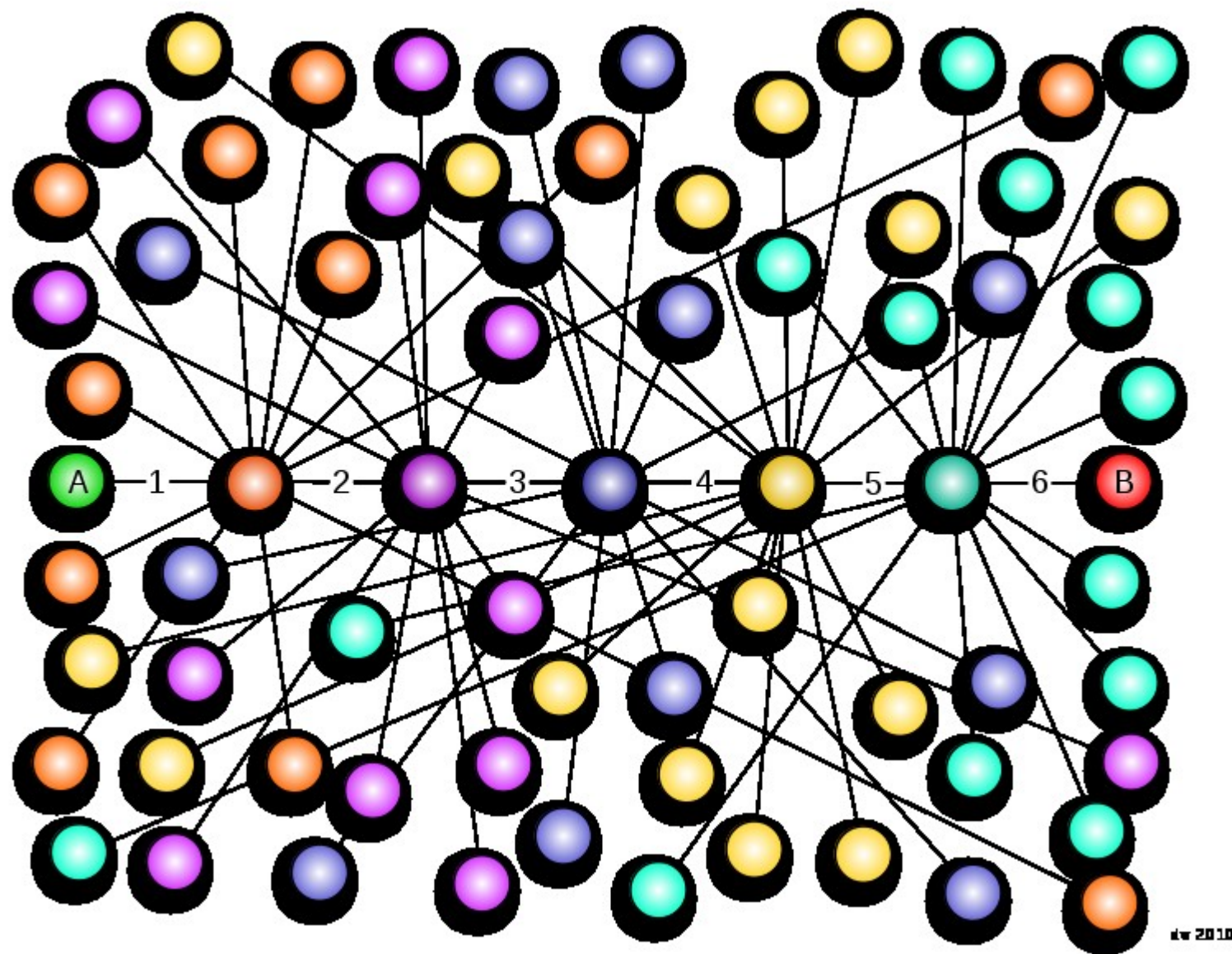
Stanley Milgram (1933-1984)

# Six degree of separation

## Milgram experiment



# Small world



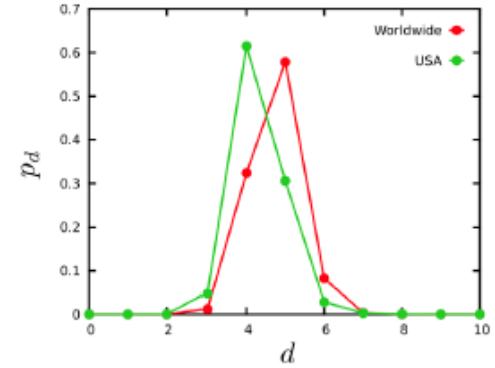
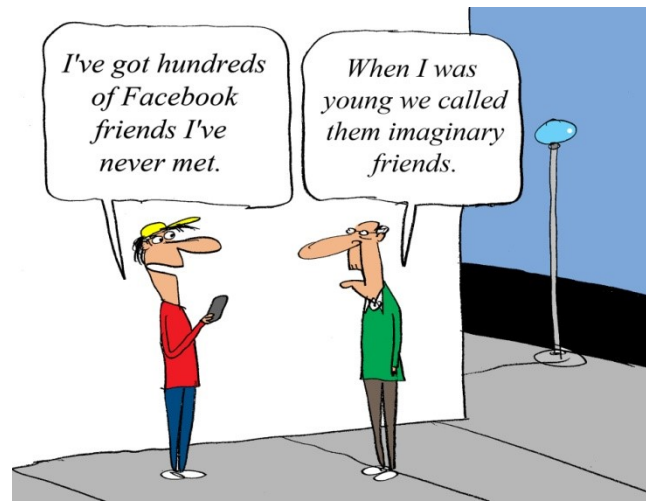


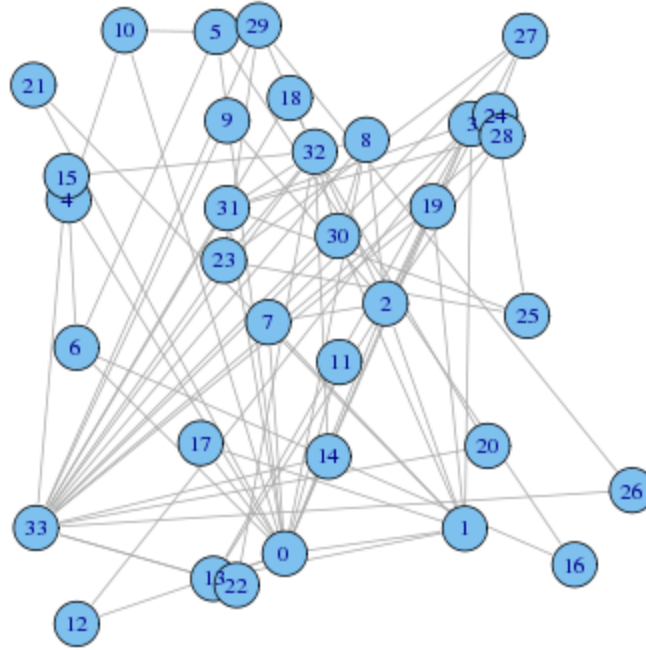
Image 3.11

**Six degrees? Facebook finds only four.**

Milgram's experiment could not detect the true distance between his study's participants, as he lacked an accurate map of the full social network. Today Facebook has the most extensive social network map ever assembled. Using Facebook's social graph of May 2011, consisting of 721 million active users and 68 billion symmetric friendship links, the average distance between the users was 4.74. The figure shows the distance distribution,  $p_d$ , for all pairs of Facebook users worldwide (full dataset) and within the US only. Therefore, instead of 'six degrees' researchers detected only 'four degrees of separation' [4], closer to the prediction of Eq. (20) than to Milgram's six degrees [23]. Using Facebook's  $N$  and  $L$  Eq. (19) predicts the average degree to be approximately 3.90, not far from the reported four degrees.



# WS networks: node degree



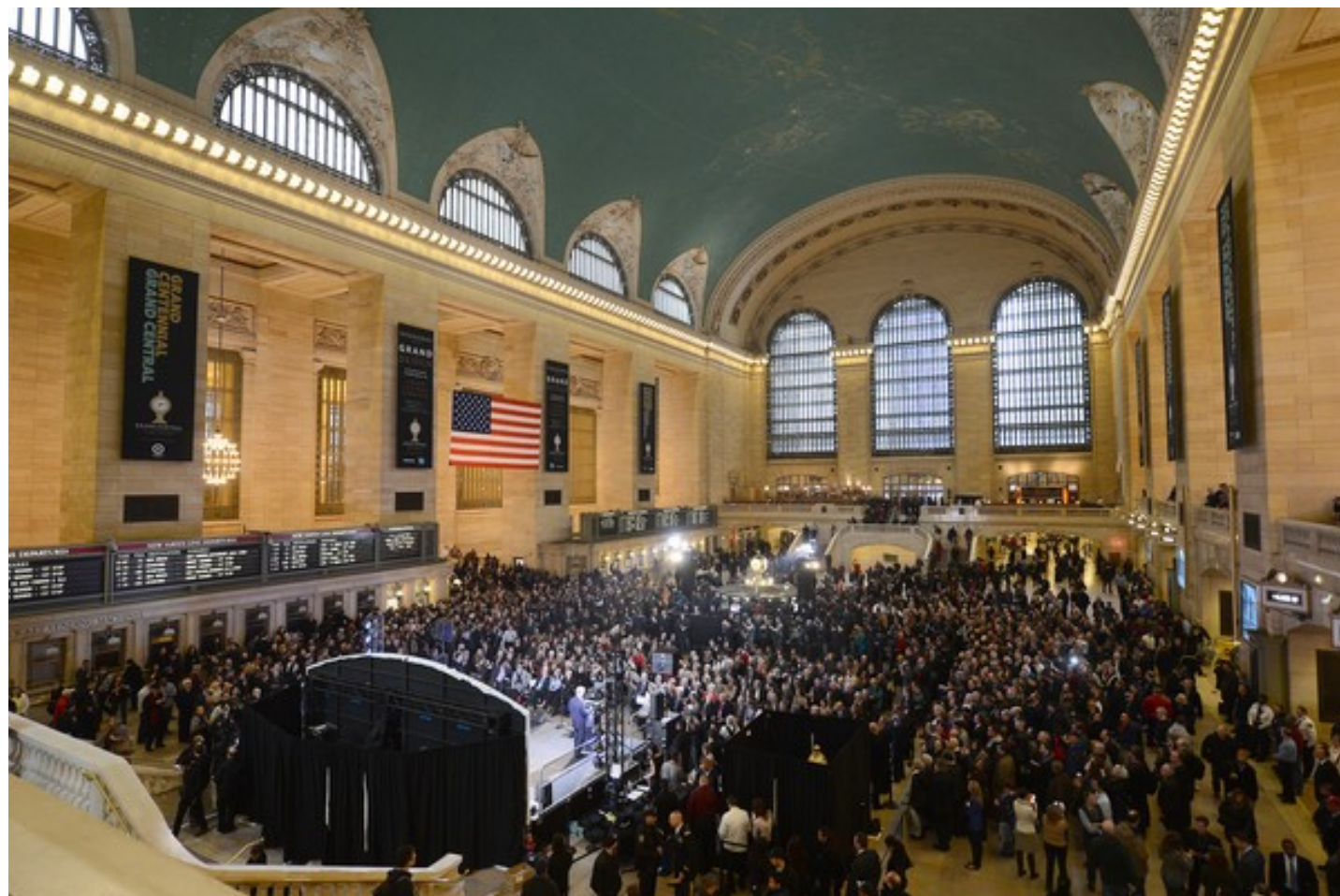
$$P(k) = \sum_{n=0}^{f(k,K)} C_{K/2}^n (1 - \beta)^n \beta^{K/2-n} \frac{(\beta K/2)^{k-K/2-n}}{(k - K/2 - n)!} e^{-\beta K/2}$$

# Small-world network

- Specifically, a **small-world network** is defined to be a network where the typical distance  $L$  between two randomly chosen nodes (the number of steps required) grows proportionally to the logarithm of the number of nodes  $N$  in the network, that is:[\[1\]](#)

$$L \propto \log N$$

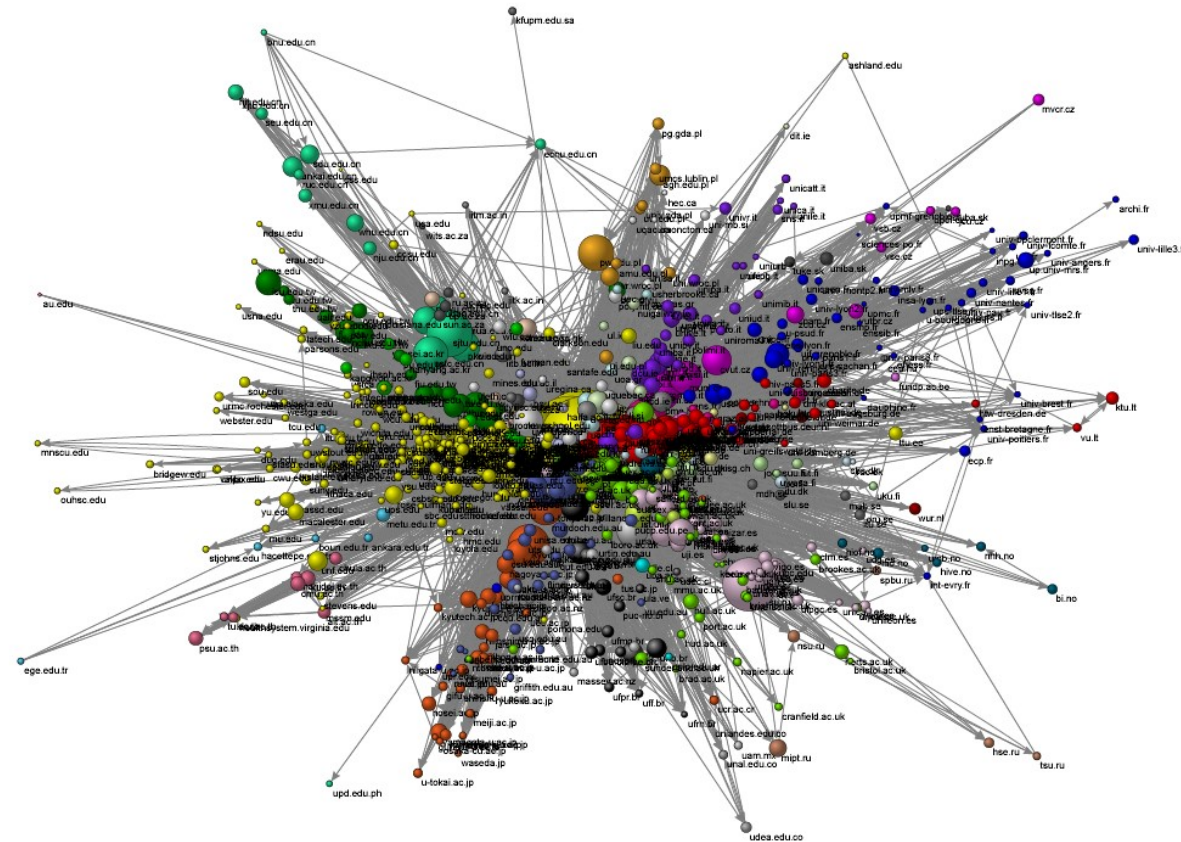
# The hubs



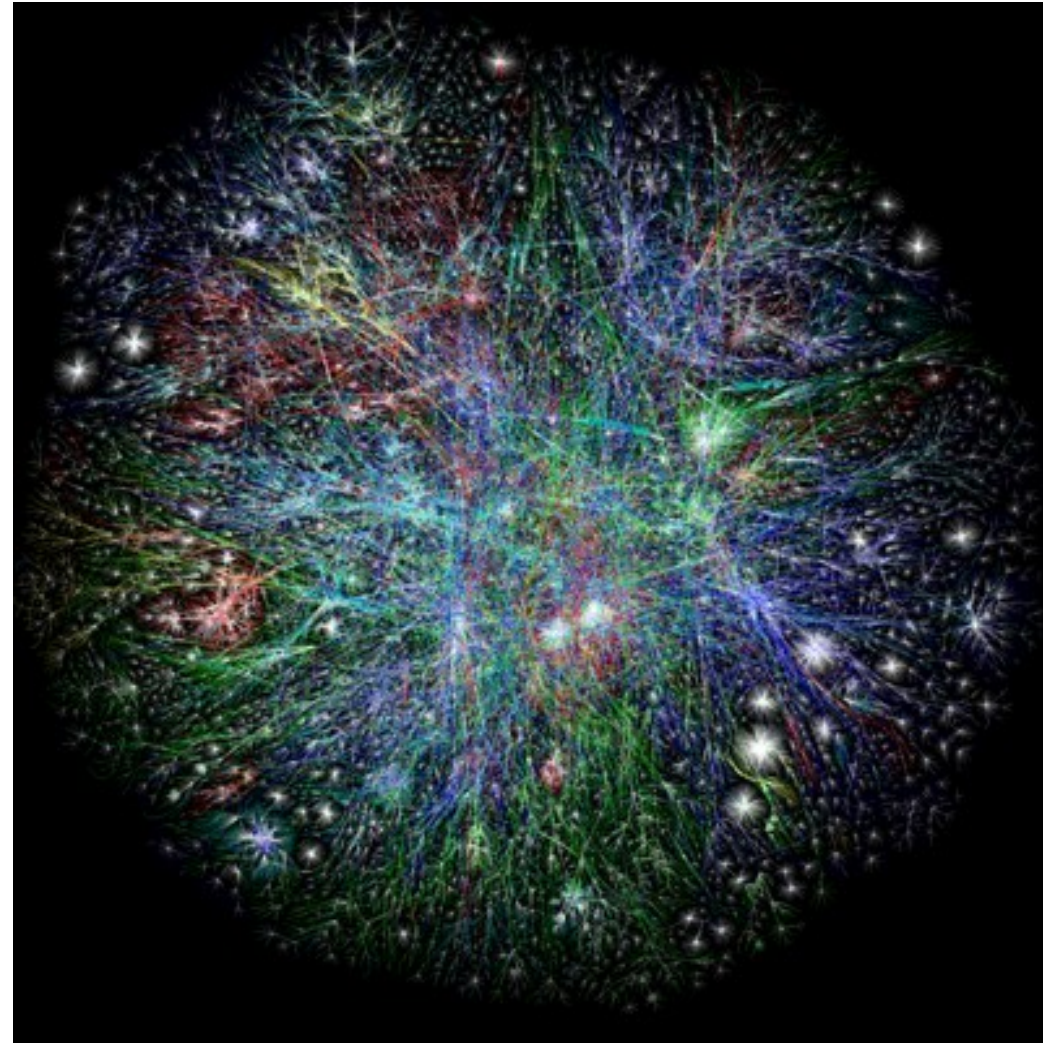
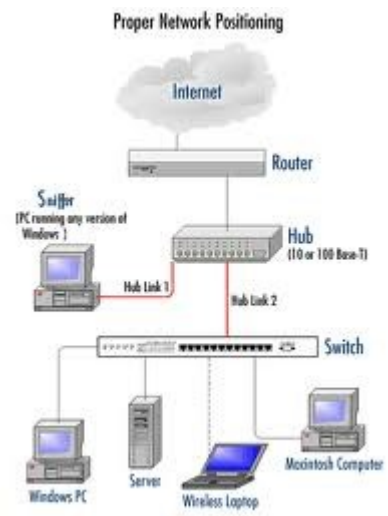


# Barabasi-Albert model

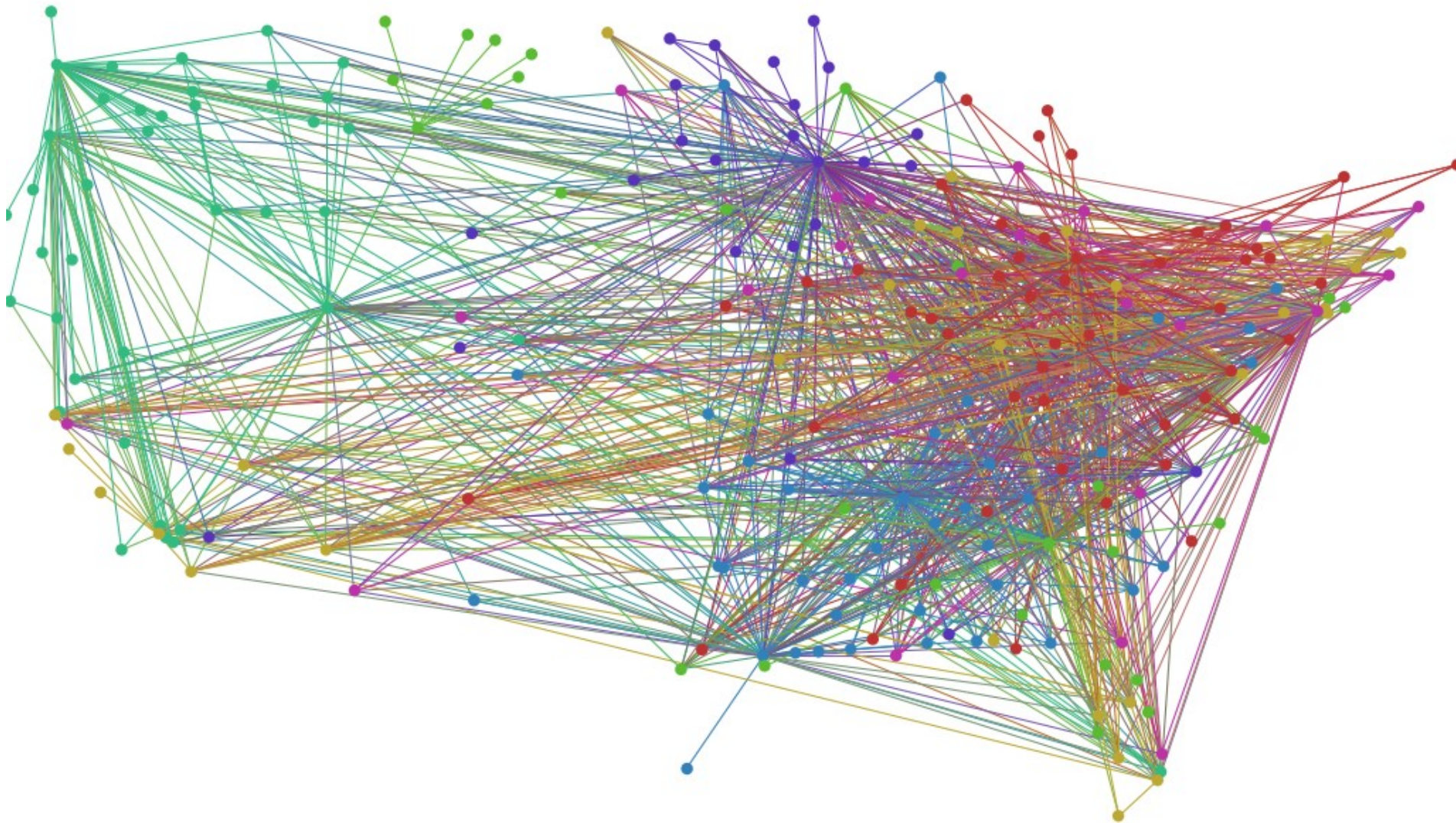
- Node degree:  $y = a x^{-b}$



# WWW

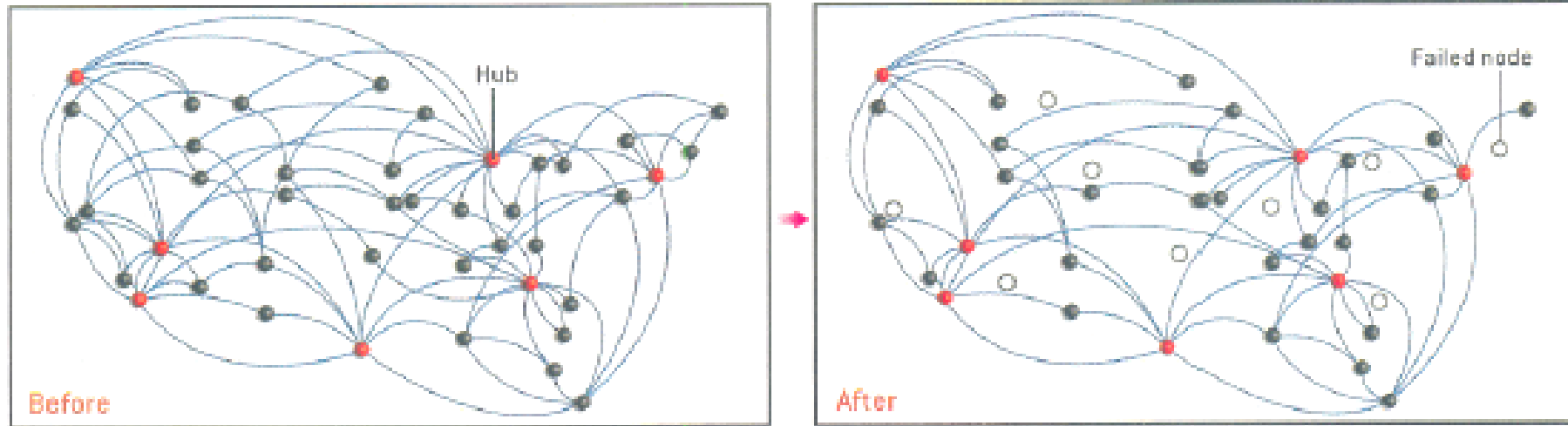


transportation

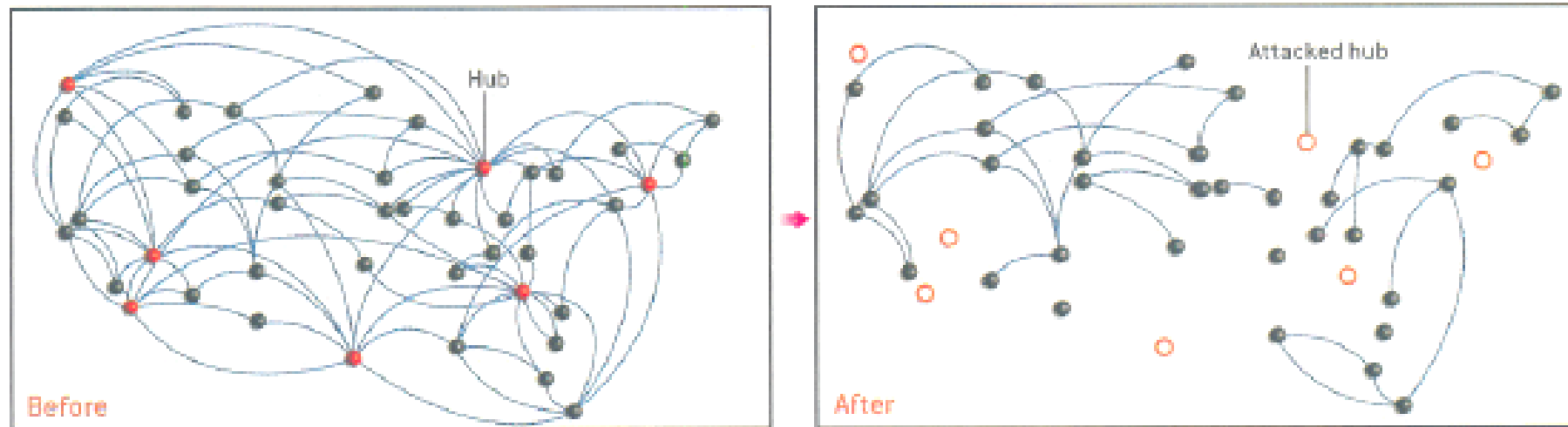


# Robustness against random attacks

Scale-Free Network, Accidental Node Failure



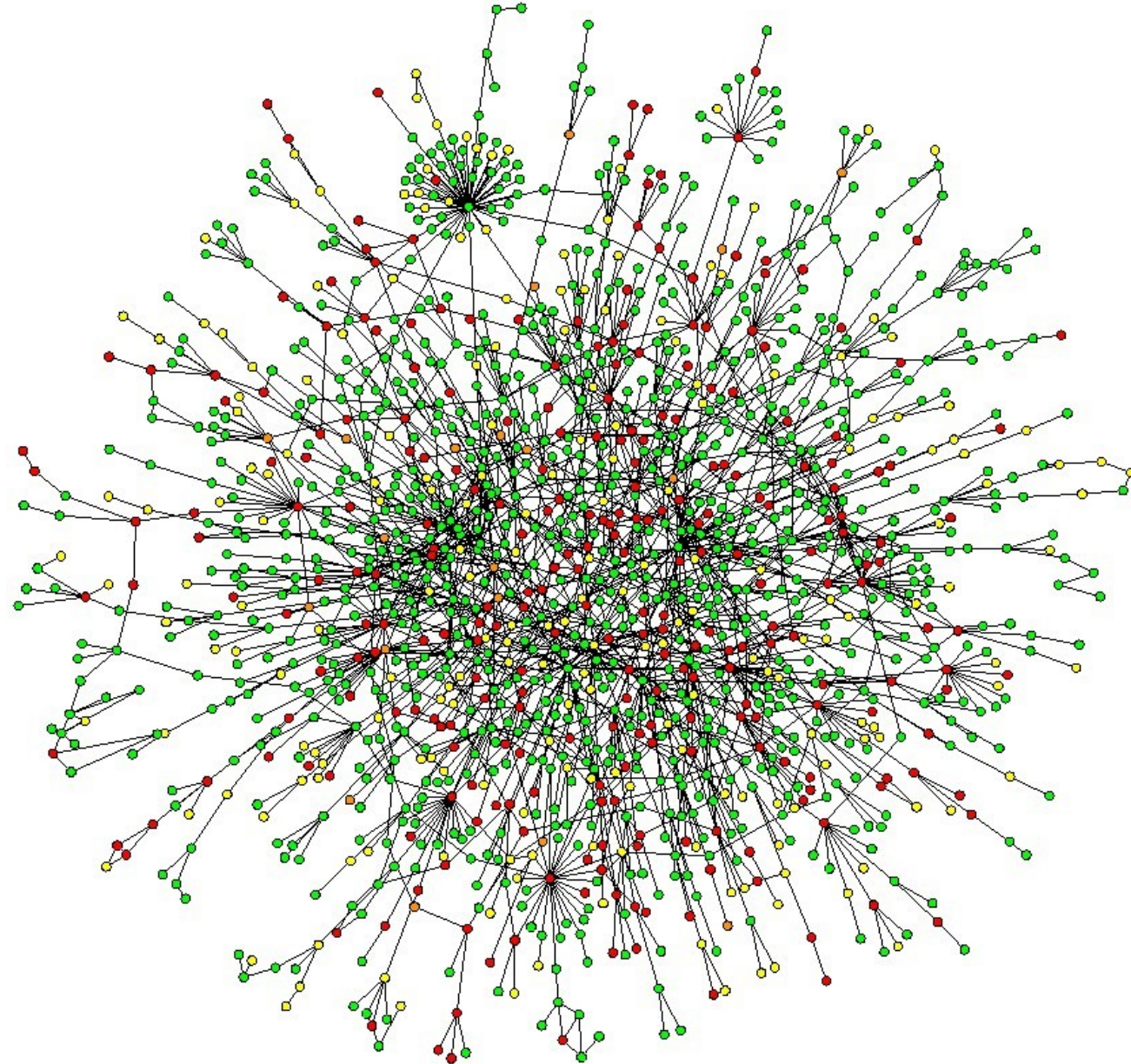
Scale-Free Network, Attack on Hubs



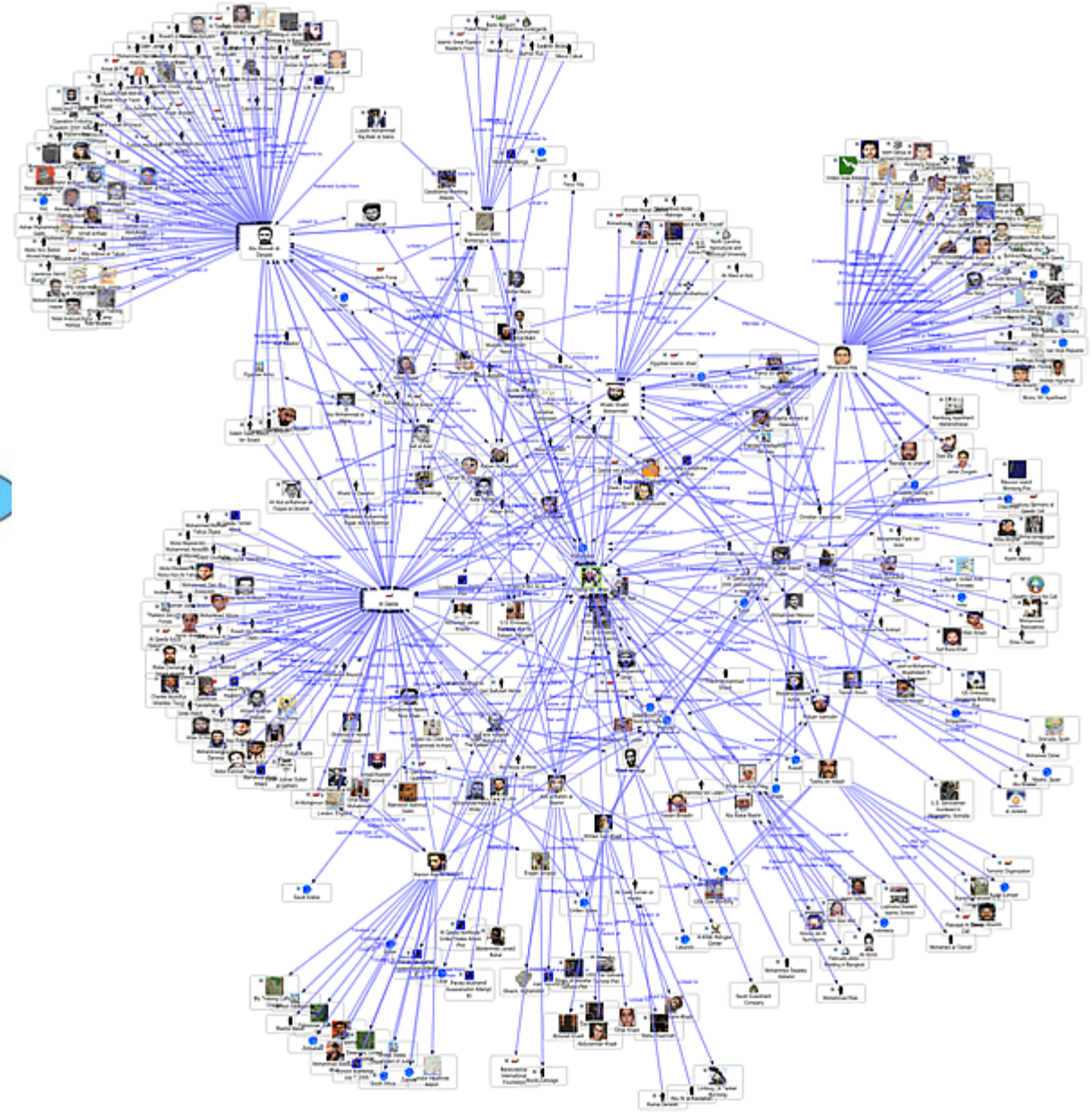
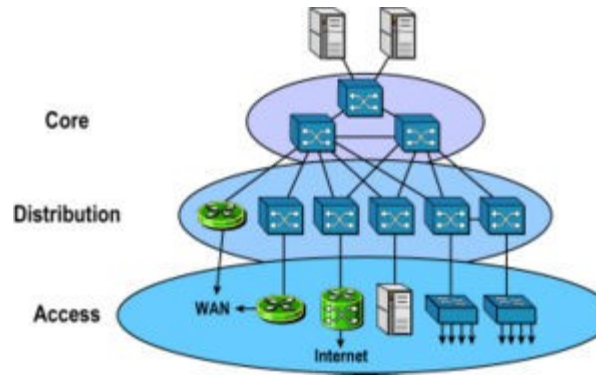
# Targeted attacks



A biological example...

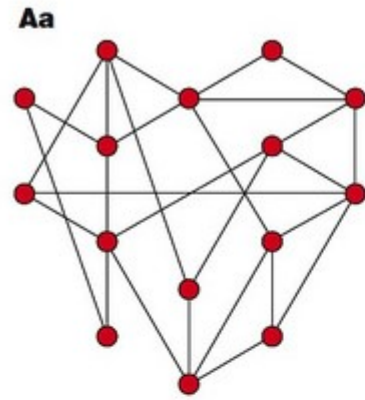


# Hierarchical networks

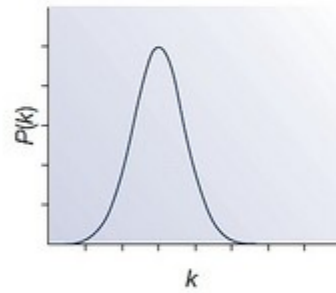


# ... in conclusion

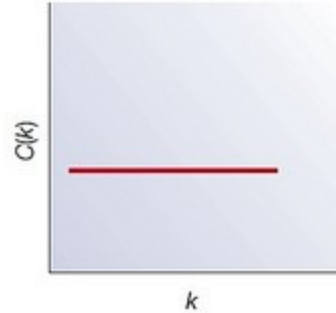
**A** Random network



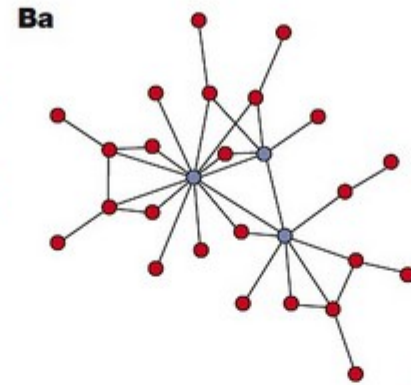
**Ab**



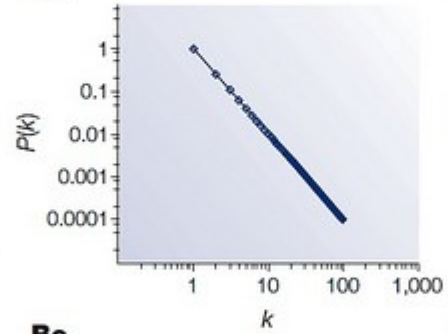
**Ac**



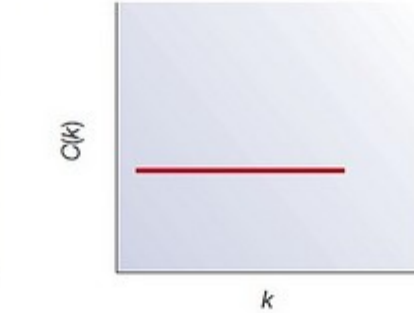
**B** Scale-free network



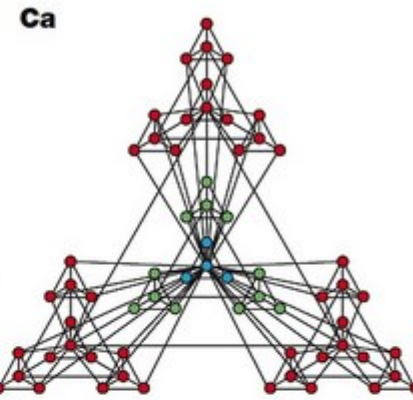
**Bb**



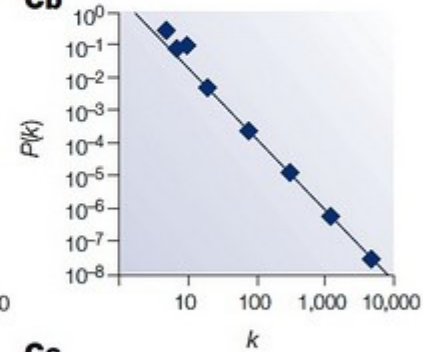
**Bc**



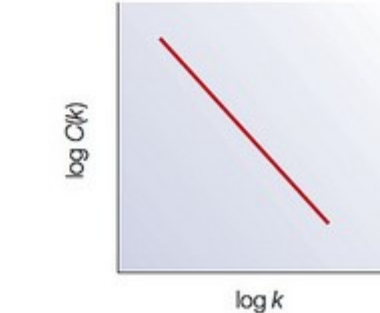
**C** Hierarchical network



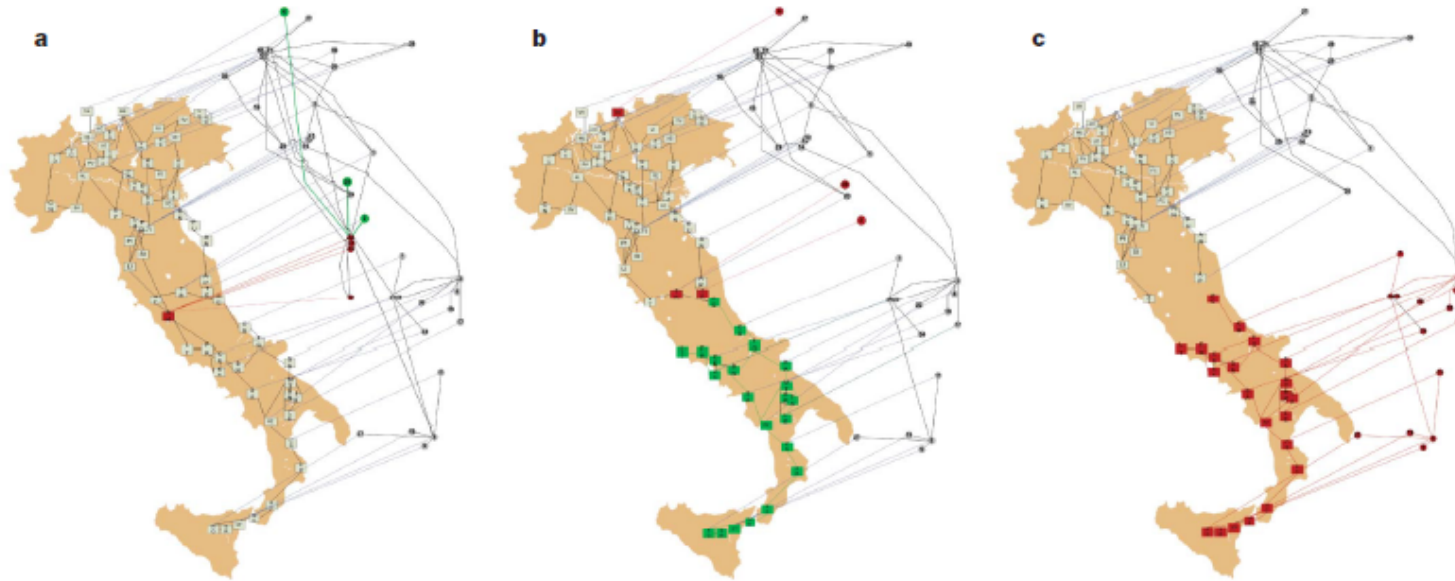
**Cb**



**Cc**



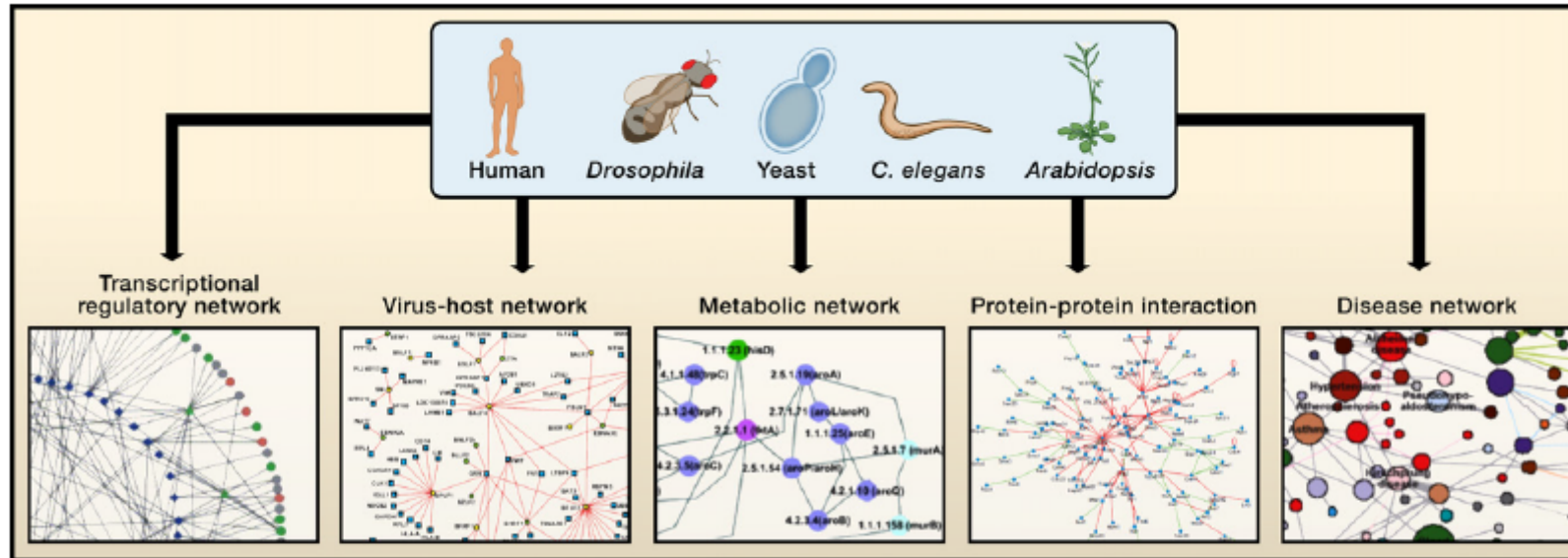




**Figure 1 | Modelling a blackout in Italy.** Illustration of an iterative process of a cascade of failures using real-world data from a power network (located on the map of Italy) and an Internet network (shifted above the map) that were implicated in an electrical blackout that occurred in Italy in September 2003<sup>20</sup>. The networks are drawn using the real geographical locations and every Internet server is connected to the geographically nearest power station. **a**, One power station is removed (red node on map) from the power network and as a result the Internet nodes depending on it are removed from the Internet network (red nodes above the map). The nodes that will be disconnected from the giant cluster (a cluster that spans the entire network)

at the next step are marked in green. **b**, Additional nodes that were disconnected from the Internet communication network giant component are removed (red nodes above map). As a result the power stations depending on them are removed from the power network (red nodes on map). Again, the nodes that will be disconnected from the giant cluster at the next step are marked in green. **c**, Additional nodes that were disconnected from the giant component of the power network are removed (red nodes on map) as well as the nodes in the Internet network that depend on them (red nodes above map).

# In physiology...



**Figure 2. Networks in Cellular Systems**

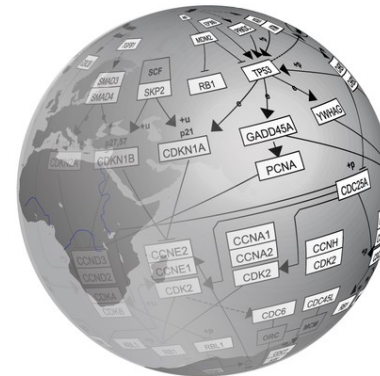
To date, cellular networks are most available for the "super-model" organisms (Davis, 2004) yeast, worm, fly, and plant. High-throughput interactome mapping relies upon genome-scale resources such as ORFeome resources. Several types of interactome networks discussed are depicted. In a protein interaction network, nodes represent proteins and edges represent physical interactions. In a transcriptional regulatory network, nodes represent transcription factors (circular nodes) or putative DNA regulatory elements (diamond nodes); and edges represent physical binding between the two. In a disease network, nodes represent diseases, and edges represent gene mutations of which are associated with the linked diseases. In a virus-host network, nodes represent viral proteins (square nodes) or host proteins (round nodes), and edges represent physical interactions between the two. In a metabolic network, nodes represent enzymes, and edges represent metabolites that are products or substrates of the enzymes. The network depictions seem dense, but they represent only small portions of available interactome network maps, which themselves constitute only a few percent of the complete interactomes within cells.

# Come si costruisce una rete?

Si parte da un database

- depositato e certificato
- creato ad hoc

# Archives on line



WIKIPATHWAYS  
*Pathways for the People*

# For instance...

Alzheimers Disease (Homo sapiens) | www.wiki pathways.org/index.php/Pathway:WP2059

pathway | discussion | view source

## Alzheimers Disease (Homo sapiens)

Nathan Salomonis, Thomas Kelder, Kristina Hanspers

Alzheimers Disease  
Depression: Homo sapiens

Log in to edit pathway | not working? | Download

Contents [hide]

- 1 Curation
- Tags
- 2 Description
  - 2.1 Comments
- 3 Ontology
- Tags
- 4 Bibliography
- 5 Categories
- 6 History
- 7 External references

Microsoft PowerPoi... | Alzheimers Disease (...)

17.15

or... .xls o .xlsx

Human [modalità compatibilità] - Microsoft Excel

Home Inserisci Layout di pagina Formule Dati Revisione Visualizza Componenti aggiuntivi

Incolla Appunti Carattere Allineamento Numeri Formattazione condizionale Stili Formatta come tabella Stili cella Inserisci Elimina Formato Cella Somma automatica Riempimento Cancellazione Ordina e filtra Trova e seleziona Modifica

H1 glucose

	A	B	C	D	E	F	G	H	I
1	glucose	att	Hexokinase	met				glucose	Hexokinase
2	ATP	att	Hexokinase	met				ATP	Hexokinase
3	Hexokinase	att	ADP	met				Hexokinase	ADP
4	Hexokinase	att	glucose 6-phosphate	met				Hexokinase	glucose 6-phosphate
5	glucose 6-phosphate	att	Phosphoglucose isomerase	met				glucose 6-phosphate	Phosphoglucose isomerase
6	Phosphoglucose isomerase	att	fructose 6-phosphate	met				Phosphoglucose isomerase	fructose 6-phosphate
7	fructose 6-phosphate	att	Phosphofructokinase	met				fructose 6-phosphate	Phosphofructokinase
8	ATP	att	Phosphofructokinase	met				ATP	Phosphofructokinase
9	Phosphofructokinase	att	ADP	met				Phosphofructokinase	ADP
10	Phosphofructokinase	att	fructose 1,6-bisphosphate	met				Phosphofructokinase	fructose 1,6-bisphosphate
11	fructose 1,6-bisphosphate	att	Aldolase	met				fructose 1,6-bisphosphate	Aldolase
12	Aldolase	att	dihydroxyacetone phosphate	met				Aldolase	dihydroxyacetone phosphate
13	fructose 1,6-bisphosphate	att	glyceraldehyde 3-phosphate	met				fructose 1,6-bisphosphate	glyceraldehyde 3-phosphate
14	dihydroxyacetone phosphate	att	Triose phosphate isomerase	met				dihydroxyacetone phosphate	Triose phosphate isomerase
15	Triose phosphate isomerase	att	glyceraldehyde 3-phosphate	met				Triose phosphate isomerase	glyceraldehyde 3-phosphate
16	glyceraldehyde 3-phosphate	att	Glyceraldehyde phosphate dehydrogenas	met				glyceraldehyde 3-phosphate	Glyceraldehyde phosphate dehydrogenas
17	glyceraldehyde 3-phosphate	att	NAD+	met				glyceraldehyde 3-phosphate	NAD+
18	Glyceraldehyde phosphate dehydrogenas	att	NADH	met				Glyceraldehyde phosphate dehydrogenas	NADH
19	Glyceraldehyde phosphate dehydrogenas	att	1,3-bisphosphoglycerate	met				Glyceraldehyde phosphate dehydrogenas	1,3-bisphosphoglycerate
20	1,3-bisphosphoglycerate	att	phosphoglycerate kinase	met				1,3-bisphosphoglycerate	phosphoglycerate kinase
21	phosphoglycerate kinase	att	3-phosphoglycerate	met				phosphoglycerate kinase	3-phosphoglycerate
22	3-phosphoglycerate	att	Phosphoglyceromutase	met				3-phosphoglycerate	Phosphoglyceromutase
23	Phosphoglyceromutase	att	2-phosphoglycerate	met				Phosphoglyceromutase	2-phosphoglycerate
24	2-phosphoglycerate	att	Enolase	met				2-phosphoglycerate	Enolase
25	Enolase	att	phosphoenolpyruvate	met				Enolase	phosphoenolpyruvate
26	phosphoenolpyruvate	att	Pyruvate kinase	met				phosphoenolpyruvate	Pyruvate kinase
27	ADP	att	Pyruvate kinase	met				ADP	Pyruvate kinase
28	Pyruvate kinase	att	pyruvate	met				Pyruvate kinase	pyruvate
29	Pyruvate kinase	att	ATP	met				Pyruvate kinase	ATP
30	pyruvate	att	pyruvate dehydrogenase	met				pyruvate	pyruvate dehydrogenase
31	NAD+	att	pyruvate dehydrogenase	met				NAD+	pyruvate dehydrogenase
32	pyruvate dehydrogenase	att	acetyl CoA	met				pyruvate dehydrogenase	acetyl CoA
33	pyruvate dehydrogenase	att	NADH	met				pyruvate dehydrogenase	NADH
34	acetyl CoA	att	citrate synthase	met				acetyl CoA	citrate synthase
35	citrate synthase	att	citrate	met				citrate synthase	citrate
36	citrate	att	aconitase	met				citrate	aconitase
37	aconitase	att	cis-aconitate	met				aconitase	cis-aconitate

Pronto Conteggio: 410 90%

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# Or .txt

```
uomo - Blocco note
File Modifica Formato Visualizza ?
glucose Hexokinase
ATP Hexokinase
Hexokinase ADP
Hexokinase glucose 6-phosphate
glucose 6-phosphate Phosphoglucose isomerase
Phosphoglucose isomerase fructose 6-phosphate
fructose 6-phosphate Phosphofruktokinase
ATP Phosphofruktokinase
Phosphofruktokinase ADP
Phosphofruktokinase fructose 1,6-bisphosphate
fructose 1,6-bisphosphate Aldolase
Aldolase dihydroxyacetone phosphate
fructose 1,6-bisphosphate glyceraldehyde 3-phosphate
dihydroxyacetone phosphate Triose phosphate isomerase
Triose phosphate isomerase glyceraldehyde 3-phosphate
glyceraldehyde 3-phosphate Glyceraldehyde phosphate dehydrogenase
glyceraldehyde 3-phosphate NAD+
Glyceraldehyde phosphate dehydrogenase NADH
Glyceraldehyde phosphate dehydrogenase 1,3-bisphosphoglycerate
1,3-bisphosphoglycerate phosphoglycerate kinase
phosphoglycerate kinase 3-phosphoglycerate
3-phosphoglycerate Phosphoglyceromutase
Phosphoglyceromutase 2-phosphoglycerate
2-phosphoglycerate Enolase
Enolase phosphoenolpyruvate
phosphoenolpyruvate Pyruvate kinase
ADP Pyruvate kinase
Pyruvate kinase pyruvate
Pyruvate kinase ATP
pyruvate pyruvate dehydrogenase
NAD+ pyruvate dehydrogenase
pyruvate dehydrogenase acetyl CoA
pyruvate dehydrogenase NADH
acetyl CoA Citrate synthase
citrate synthase citrate
citrate aconitase
aconitase cis-aconitate
cis-aconitate aconitase
aconitase isocitrate
isocitrate isocitrate dehydrogenase
NAD+ isocitrate dehydrogenase
isocitrate dehydrogenase NADH
isocitrate dehydrogenase oxalosuccinate
oxalosuccinate oxalosuccinate dehydrogenase
oxalosuccinate dehydrogenase a-ketoglutarate
a-ketoglutarate a-ketoglutarate dehydrogenase
NAD+ a-ketoglutarate dehydrogenase
a-ketoglutarate dehydrogenase NADH
a-ketoglutarate dehydrogenase succinyl CoA
succinyl CoA succinyl CoA synthase
GDP succinyl CoA synthase
succinyl CoA synthase GTP
succinyl CoA synthase succinate
succinate succinate dehydrogenase
```

# Network creation and analysis

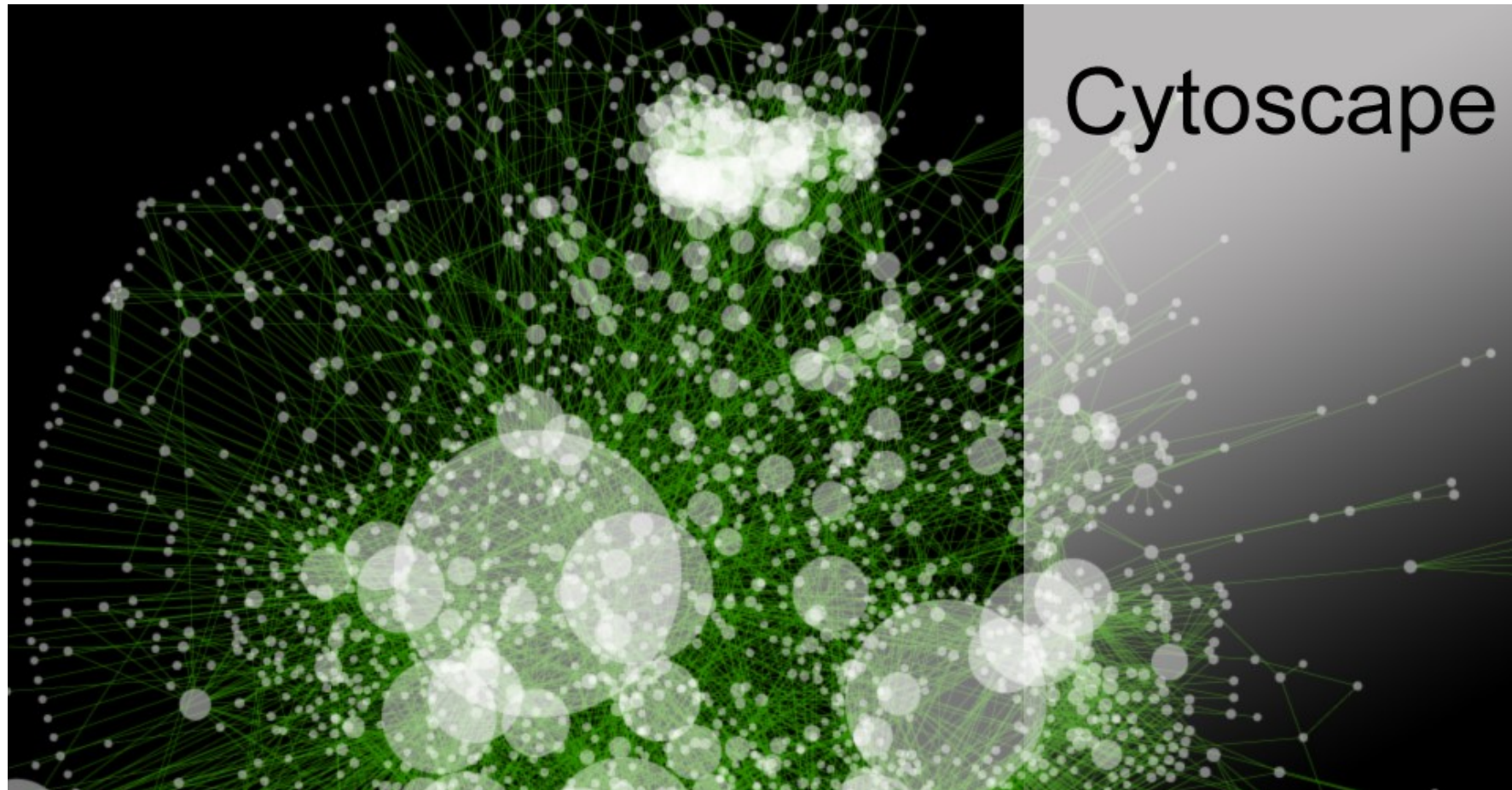
The screenshot shows the Cytoscape website homepage. At the top, it says "Cytoscape: An Open Source Platform for Complex Network Analysis and Visualization". Below this, there are navigation tabs for Home, Introduction, Download, Plugins, Documentation, Community, Report a Bug, and Getting Help. The main content area features a large network graph visualization with green nodes and red edges. To the right of the graph, there is a section titled "Network Data Integration, Analysis, and Visualization in a Box" with a "Download Cytoscape Now" button and a "Learn More" button. Below the graph, there are sections for "Cytoscape New Features" and "What Can You Do With Cytoscape?".

The screenshot shows the BiologicalNetworks website homepage. The header includes the logo "BIOLOGICAL NETWORKS" and the tagline "Integrated Research Environment". Below the header, there is a search bar and a "Free download" button. The main content area is divided into several sections: "BiologicalNetworks research environment enables integrative analysis of" followed by a list of features (Interaction networks, Gene regulatory modules, Genomic sequences, Comparative genomics, 3D protein structures, Multiple ontologies); "The database currently integrates over 100 curated and publicly contributed data sources"; and "BiologicalNetworks system has been used by thousands of researchers world-wide". There are also buttons for "PathwayCollection", "Use Case #1", and "Homology Wizard".

The screenshot shows the BioLayout Express3D website homepage. The header features the logo "BioLayout Express3D" and a navigation menu with buttons for HOME, ABOUT, SUPPORT, DOWNLOAD, and LAUNCH. The main content area is titled "Welcome" and contains a paragraph describing the tool as a powerful tool for the visualization and analysis of network graphs. To the right, there is a "Latest News" section with a sub-heading "Version 2.2 of BioLayout Express3D released" and a list of new features including CAD-style Model Shape Editor, updated mEPN-3D Scheme, and support for OpenGL 1.1.1. At the bottom, it states "BioLayout Express3D is free and directly funded by the BBSRC".

The screenshot shows the Networks / Pajek website. The header includes the title "Networks / Pajek" and a sub-heading "Program for Large Network Analysis". Below the header, there is a paragraph stating "In January 2008 this page was replaced by Pajek Wai." and a "DOWNLOAD Pajek" button. The main content area is a list of links and resources, including "Data: test networks, GPHs, GEDs, POB files", "Screenshots, History, Manual (pdf), Papers/presentations, Applications, in News, Examples: SVG, PDF", "How to 7 English / Slovene / Japanese (problems with IE - download and use Acrobat reader)", "Pajek: kindly runs on Linux via Wine", "Slides from NICTA workshop", "Pajek workshop at XXVIII Sunbelt Conference", "Network analysis course at ECPR Summer School in Methods and Techniques", "W. de Hooy, A. Mvri, V. Batagelj: Exploratory Social Network Analysis with Pajek", "Chapter about Pajek: V. Batagelj, A. Mvri: Pajek - Analysis and Visualization of Large Networks", and "An improved version of the paper presented at Sunbelt'97 was published in Connections 21(1998): 47-57 - V. Batagelj, A. Mvri: Pajek - Program for Large Network Analysis (PDF, FRIDON.VSI)".

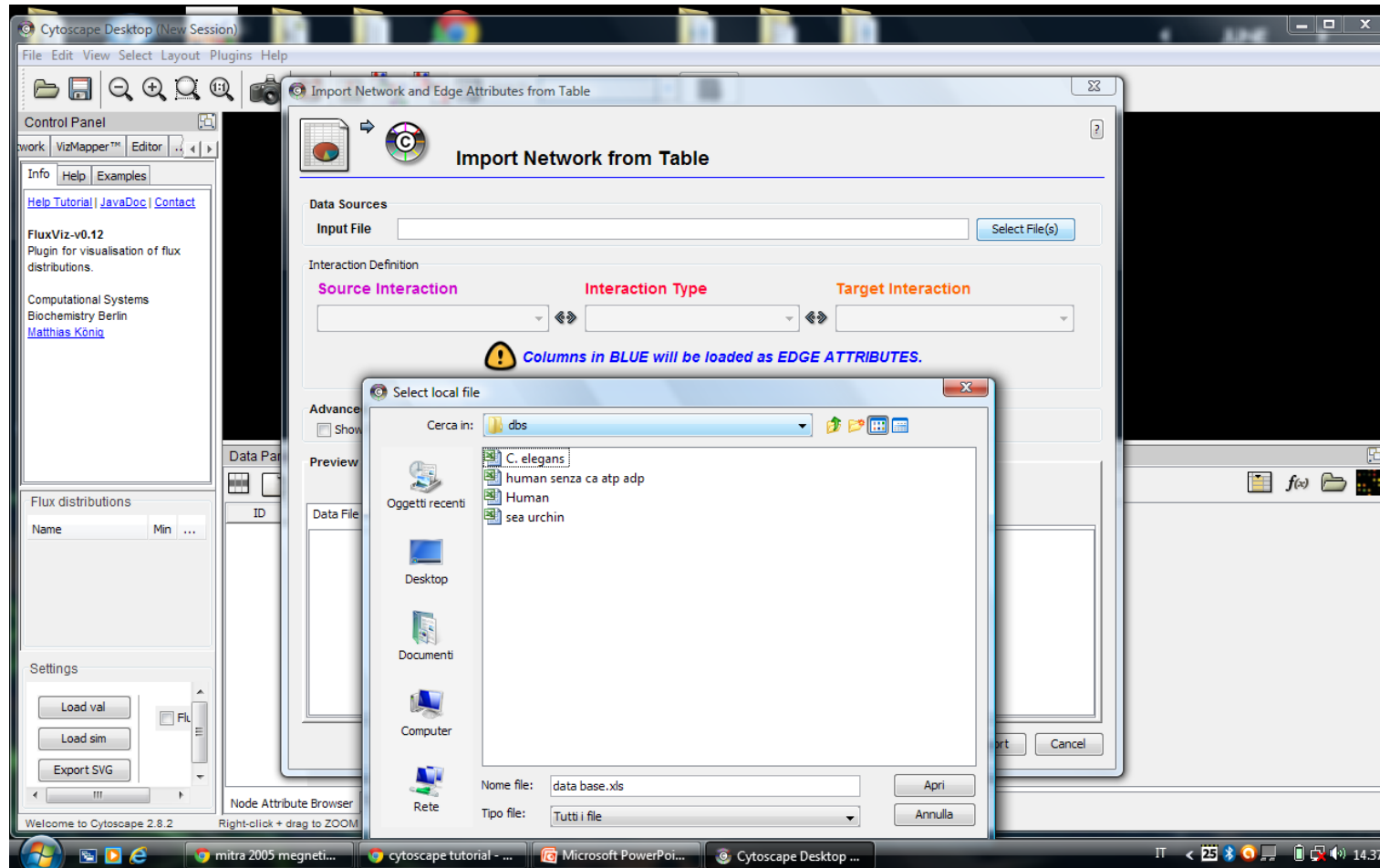




# File formats

- Simple interaction file (SIF or .sif format)
- Graph Markup Language (GML or .gml format)
- XGMML (extensible graph markup and modelling language).
- SBML
- BioPAX
- PSI-MI Level 1 and 2.5
- Delimited text
- Excel Workbook (.xls)

# Network realization I



# Network realization II

Cytoscape Desktop (New Session)

File Edit View Select Layout Plugins Help

Control Panel

work VizMapper™ Editor

Info Help Examples

[Help Tutorial](#) | [JavaDoc](#) | [Contact](#)

FluxViz-v0.12  
Plugin for visualisation of flux distributions.

Computational Systems  
Biochemistry Berlin  
[Matthias König](#)

Flux distributions

Name Min ...

Settings

Load val  Flk

Load sim

Export SVG

Node Attribute Browser Edge Attribute Browser Network Attribute Browser

Import Network and Edge Attributes from Table

Import Network from Table

Data Sources

Input File file:/C:/Users/Fisiologia/Desktop/ECS/data%20base.xls

Interaction Definition

Source Interaction Interaction Type Target Interaction

Column 1 Column 2 Column 3

Columns in BLUE will be loaded as EDGE ATTRIBUTES.

Advanced

Show Text File Import Options

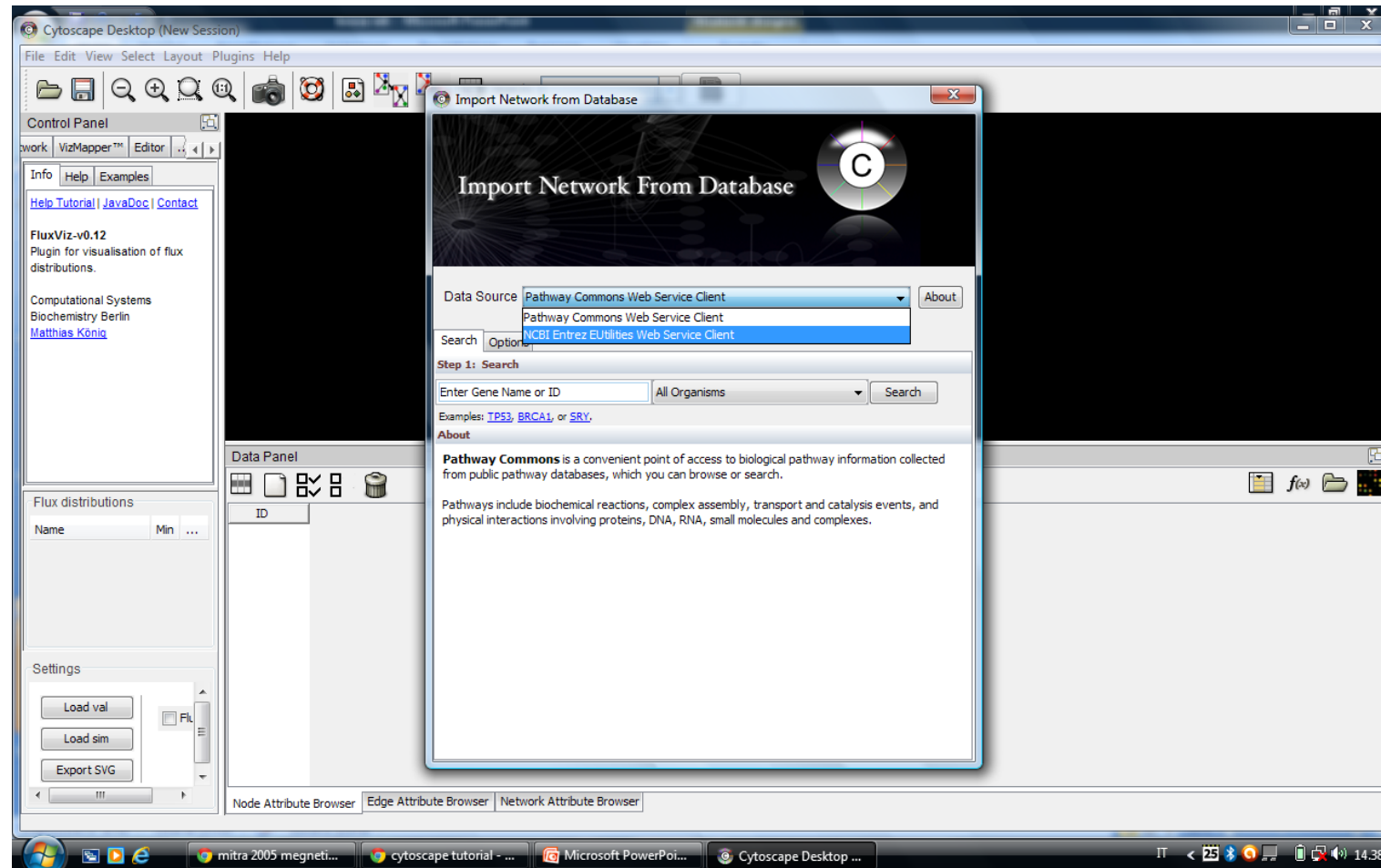
Preview

Excel™ Workbook **Left Click: Enable/Disable Column, Right Click: Edit Column**

Foglio1

Column 1	Column 2	Column 3	Column 4	Column 5
[Ca2+]i	activates	sn1-specific DG lipase		
[Ca2+]i	inhibits	Monoglyceride lipase		
[Na+]i	activates	membrane depolarization		
2AG	activates	CB1		
2AG	activates	p38 (MAP kinase)		
2AG	activates	PPARalfa		
2AG	activates	PPARgamma		
2AG	binds	opioid receptors		

# Network realization III



# Layout

Cytoscape Desktop (New Session)

File Edit View Select Layout Plugins Help

Control Panel

work VizMapper™ Editor

Info Help Examples

[Help Tutorial](#) | [JavaDoc](#) | [Contact](#)

**FluxViz-v0.12**  
Plugin for visualisation of flux distributions.

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Flux distributions

Name	Min	...

Settings

Load val  Fil

Load sim

Export SVG

Data Panel

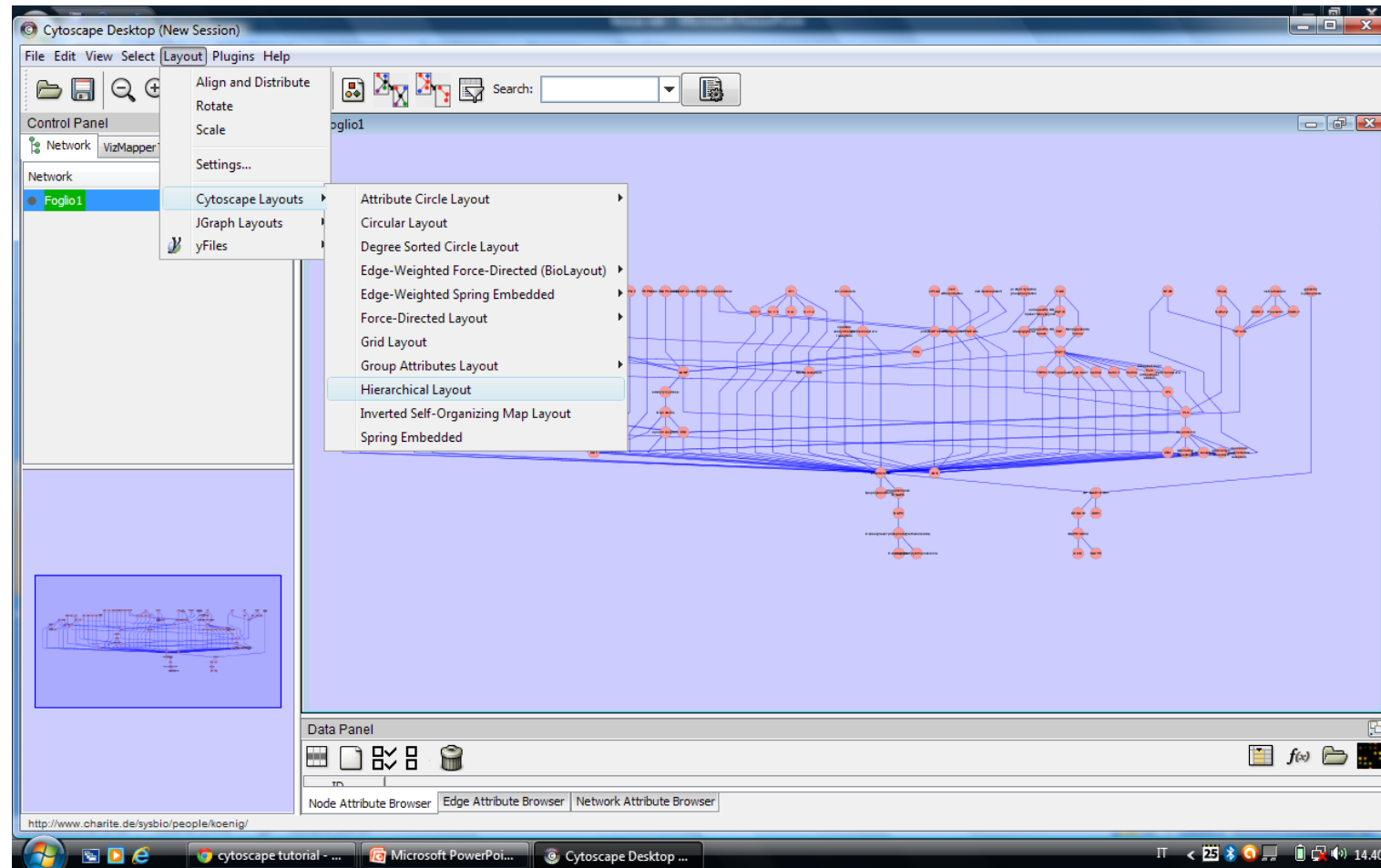
Node Attribute Browser Edge Attribute Browser Network Attribute Browser

Windows taskbar: cytoscape tutorial - ... Microsoft PowerPoi... Cytoscape Desktop ... IT < 25 14:39

# Layout II

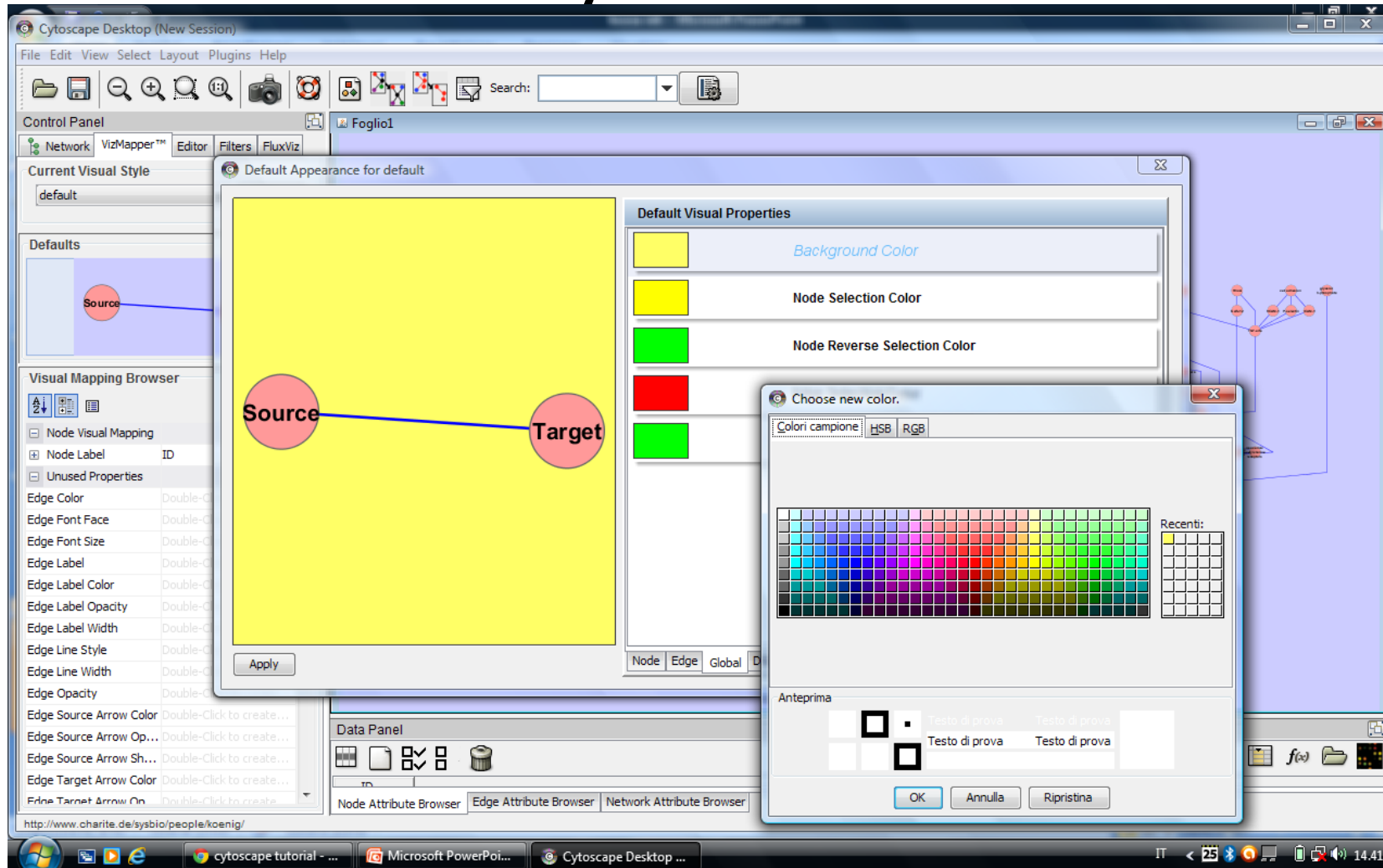
The screenshot displays the Cytoscape Desktop interface with a network graph and an open layout menu. The menu lists various layout algorithms, with 'Force-Directed Layout (unweighted)' selected. The network graph shows a central node 'CDK2' connected to numerous other nodes, including 'CDK1', 'CDK5', 'CDK7', 'CDK8', 'CDK9', 'CDK10', 'CDK11', 'CDK12', 'CDK13', 'CDK14', 'CDK15', 'CDK16', 'CDK17', 'CDK18', 'CDK19', 'CDK20', 'CDK21', 'CDK22', 'CDK23', 'CDK24', 'CDK25', 'CDK26', 'CDK27', 'CDK28', 'CDK29', 'CDK30', 'CDK31', 'CDK32', 'CDK33', 'CDK34', 'CDK35', 'CDK36', 'CDK37', 'CDK38', 'CDK39', 'CDK40', 'CDK41', 'CDK42', 'CDK43', 'CDK44', 'CDK45', 'CDK46', 'CDK47', 'CDK48', 'CDK49', 'CDK50', 'CDK51', 'CDK52', 'CDK53', 'CDK54', 'CDK55', 'CDK56', 'CDK57', 'CDK58', 'CDK59', 'CDK60', 'CDK61', 'CDK62', 'CDK63', 'CDK64', 'CDK65', 'CDK66', 'CDK67', 'CDK68', 'CDK69', 'CDK70', 'CDK71', 'CDK72', 'CDK73', 'CDK74', 'CDK75', 'CDK76', 'CDK77', 'CDK78', 'CDK79', 'CDK80', 'CDK81', 'CDK82', 'CDK83', 'CDK84', 'CDK85', 'CDK86', 'CDK87', 'CDK88', 'CDK89', 'CDK90', 'CDK91', 'CDK92', 'CDK93', 'CDK94', 'CDK95', 'CDK96', 'CDK97', 'CDK98', 'CDK99', 'CDK100'. The interface includes a menu bar (File, Edit, View, Select, Layout, Plugins, Help), a Control Panel (Network, VizMapper), a Data Panel (Node Attribute Browser, Edge Attribute Browser, Network Attribute Browser), and a status bar (http://www.charite.de/sysbio/people/koenig/).

# Layout III





# Layout IV



# Analysis

The screenshot displays the Cytoscape Desktop interface with a network graph. The 'Network Analysis' menu is open, showing options such as 'Analyze Network', 'Analyze Subset of Nodes', 'Batch Analysis', 'Load Network Statistics', 'Plot Parameters', 'Visualize Parameters', 'NetworkAnalyzer Settings', and 'About NetworkAnalyzer'. The graph consists of numerous red nodes connected by blue edges. The interface includes a menu bar (File, Edit, View, Select, Layout, Plugins, Help), a Control Panel, a Visual Mapping Browser, and a Data Panel. The Visual Mapping Browser shows a list of properties for nodes and edges, such as 'Node Label', 'Edge Color', and 'Edge Font Size'. The Data Panel at the bottom shows 'Node Attribute Browser', 'Edge Attribute Browser', and 'Network Attribute Browser'. The Windows taskbar at the bottom shows the system clock at 14:43 and several open applications.

Cytoscape Desktop (New Session)

File Edit View Select Layout Plugins Help

Control Panel

Network VizMapper™ Editor

Current Visual Style

default

Defaults

Source Target

Visual Mapping Browser

Node Visual Mapping

Node Label ID

Unused Properties

Edge Color Double-Click to create...

Edge Font Face Double-Click to create...

Edge Font Size Double-Click to create...

Edge Label Double-Click to create...

Edge Label Color Double-Click to create...

Edge Label Opacity Double-Click to create...

Edge Label Width Double-Click to create...

Edge Line Style Double-Click to create...

Edge Line Width Double-Click to create...

Edge Opacity Double-Click to create...

Edge Source Arrow Color Double-Click to create...

Edge Source Arrow Op... Double-Click to create...

Edge Source Arrow Sh... Double-Click to create...

Edge Target Arrow Color Double-Click to create...

Edge Target Arrow Op... Double-Click to create...

Data Panel

Node Attribute Browser Edge Attribute Browser Network Attribute Browser

http://www.charite.de/sysbio/people/koenig/

cytoscape tutorial - ... Microsoft PowerPoi... Cytoscape Desktop ...

14.43

# Analysis

The screenshot displays the Cytoscape Desktop interface with a network analysis window open. The network is visualized on a yellow background. The analysis window, titled "Network Analysis of Foglio1 (undirected)", provides the following statistics:

Betweenness Centrality		Closeness Centrality		Stress Centrality Distribution	
Shortest Path Length Distribution	Shared Neighbors Distribution	Neighborhood Connectivity Distribution			
Simple Parameters	Node Degree Distribution	Avg. Clustering Coefficient Distribution		Topological Coefficients	
Clustering coefficient : <b>0.024</b>	Number of nodes : <b>94</b>				
Connected components : <b>1</b>	Network density : <b>0.033</b>				
Network diameter : <b>10</b>	Network heterogeneity : <b>1.245</b>				
Network radius : <b>6</b>	Isolated nodes : <b>0</b>				
Network centralization : <b>0.329</b>	Number of self-loops : <b>0</b>				
Shortest paths : <b>8742 (100%)</b>	Multi-edge node pairs : <b>0</b>				
Characteristic path length : <b>3.939</b>	Analysis time (sec) : <b>0.254</b>				
Avg. number of neighbors : <b>3.064</b>					

The interface also includes a Control Panel on the left with options for Network, VizMapper™, Editor, Filters, and FluxViz. A Visual Mapping Browser is visible below the Control Panel. The Data Panel at the bottom shows Node, Edge, and Network attribute browsers. The Windows taskbar at the bottom indicates the system time is 14:43.