Random networks

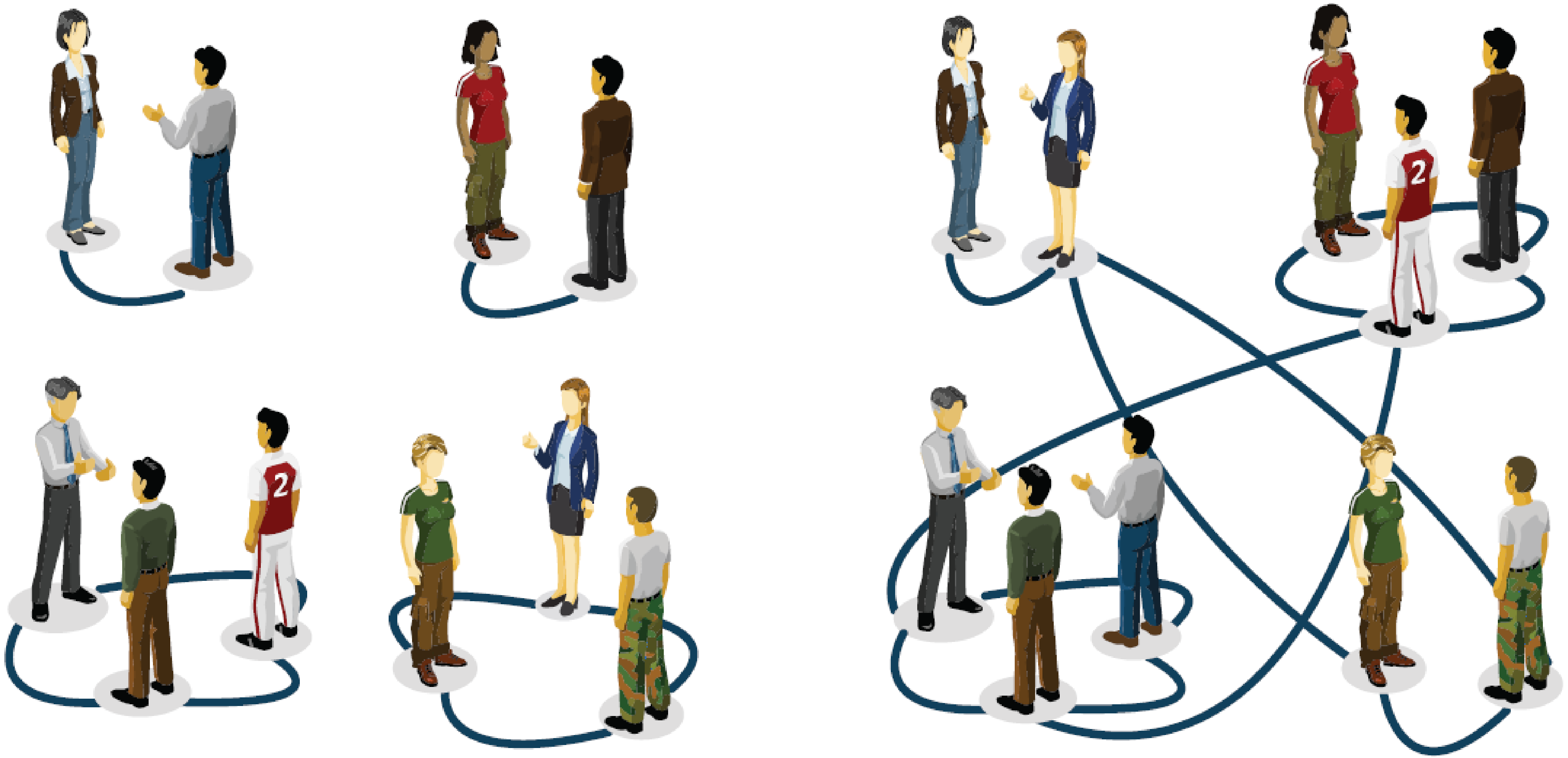


Image 3.1
From a cocktail party to random networks.

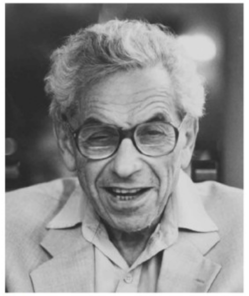


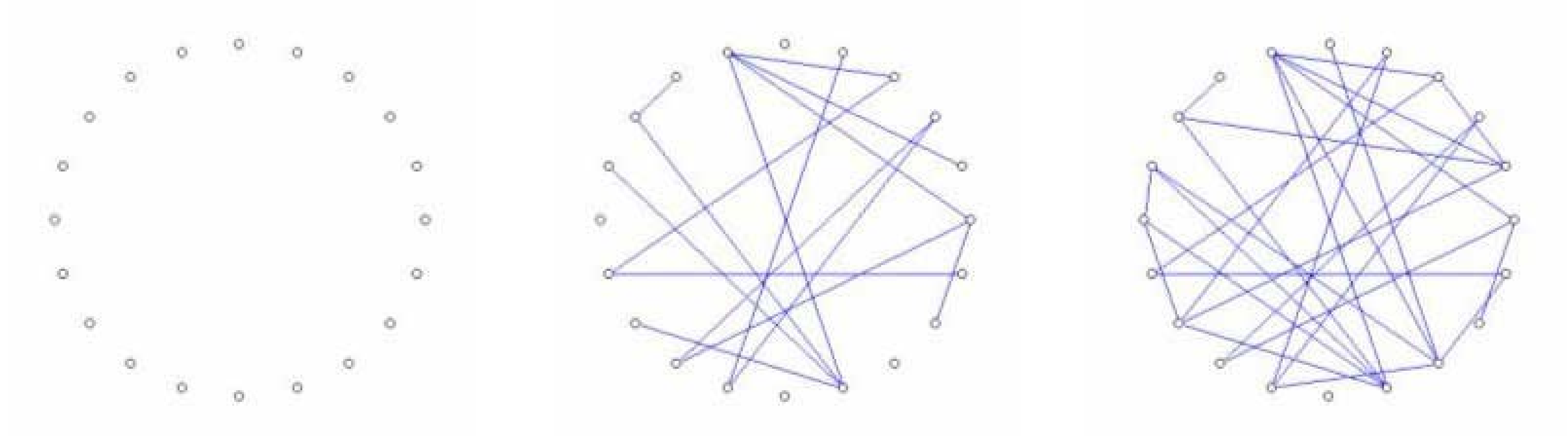
Image 3.2a
Pál Erdős (1913–1996)

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)

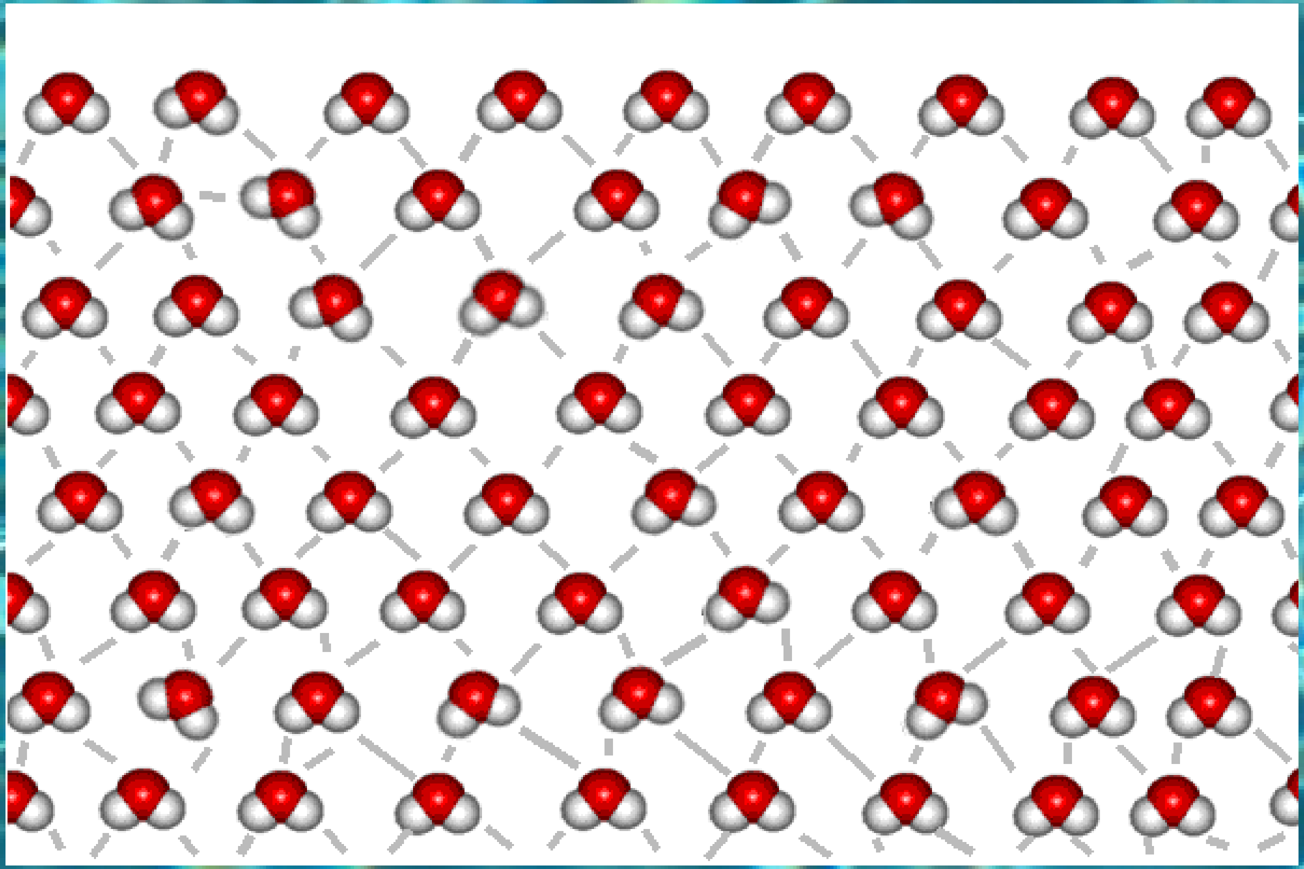
$p = 0.2$
(c)

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



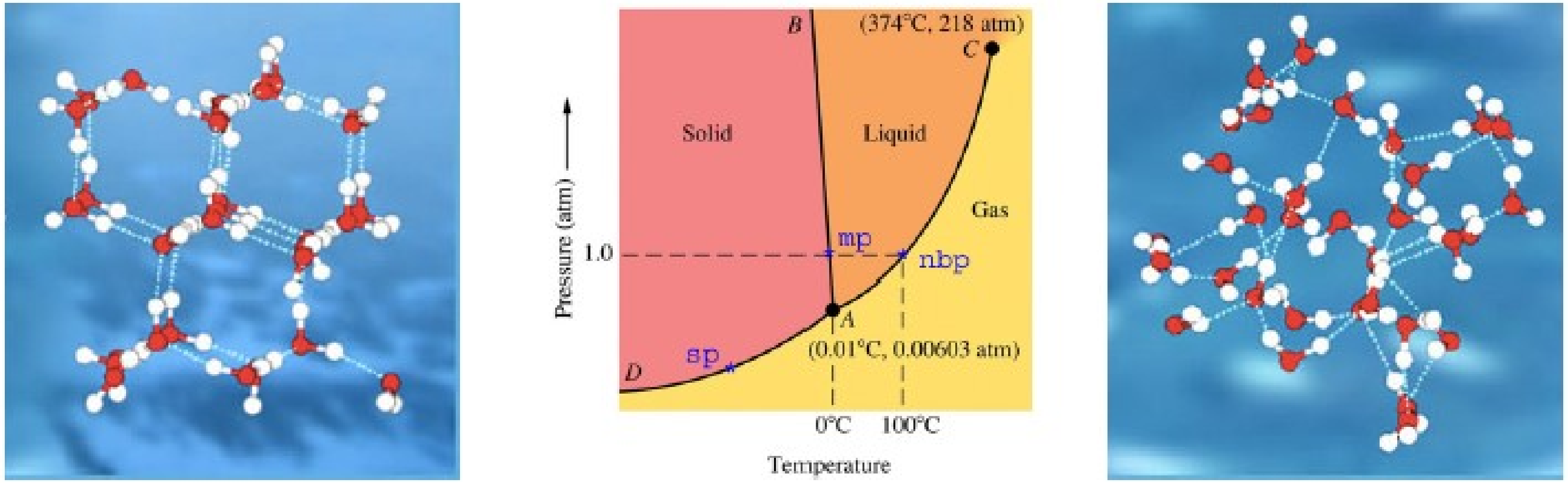


Image 3.22a

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/

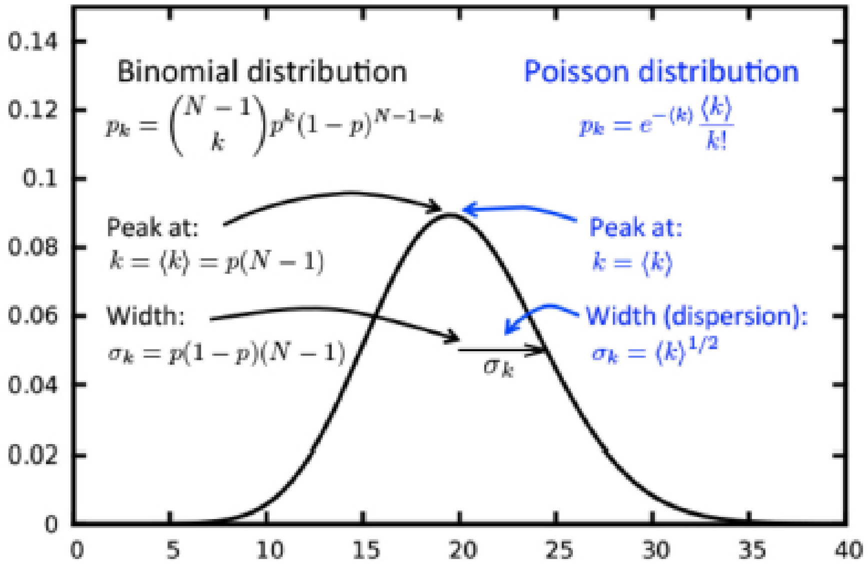


Image 3.4a

Anatomy of a binomial and a Poisson degree distribution.

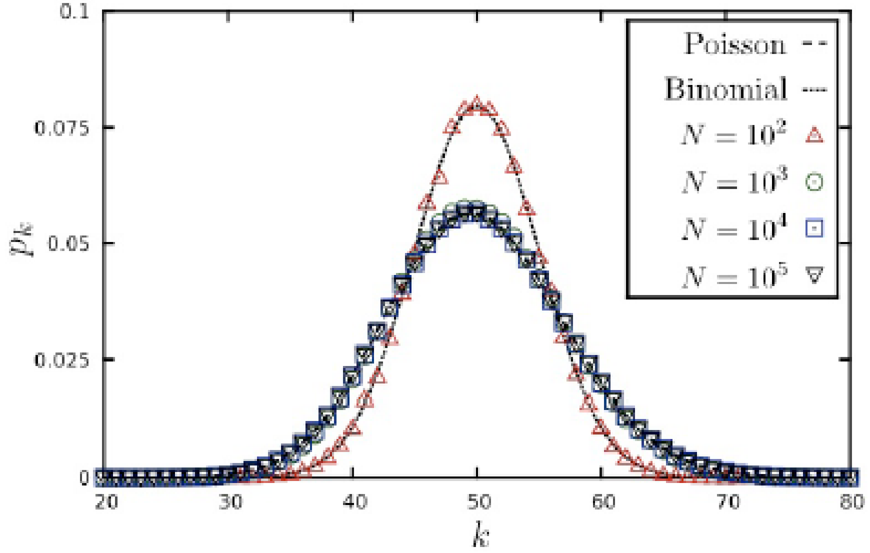


Image 3.4b

Degree distribution is independent of the network size.

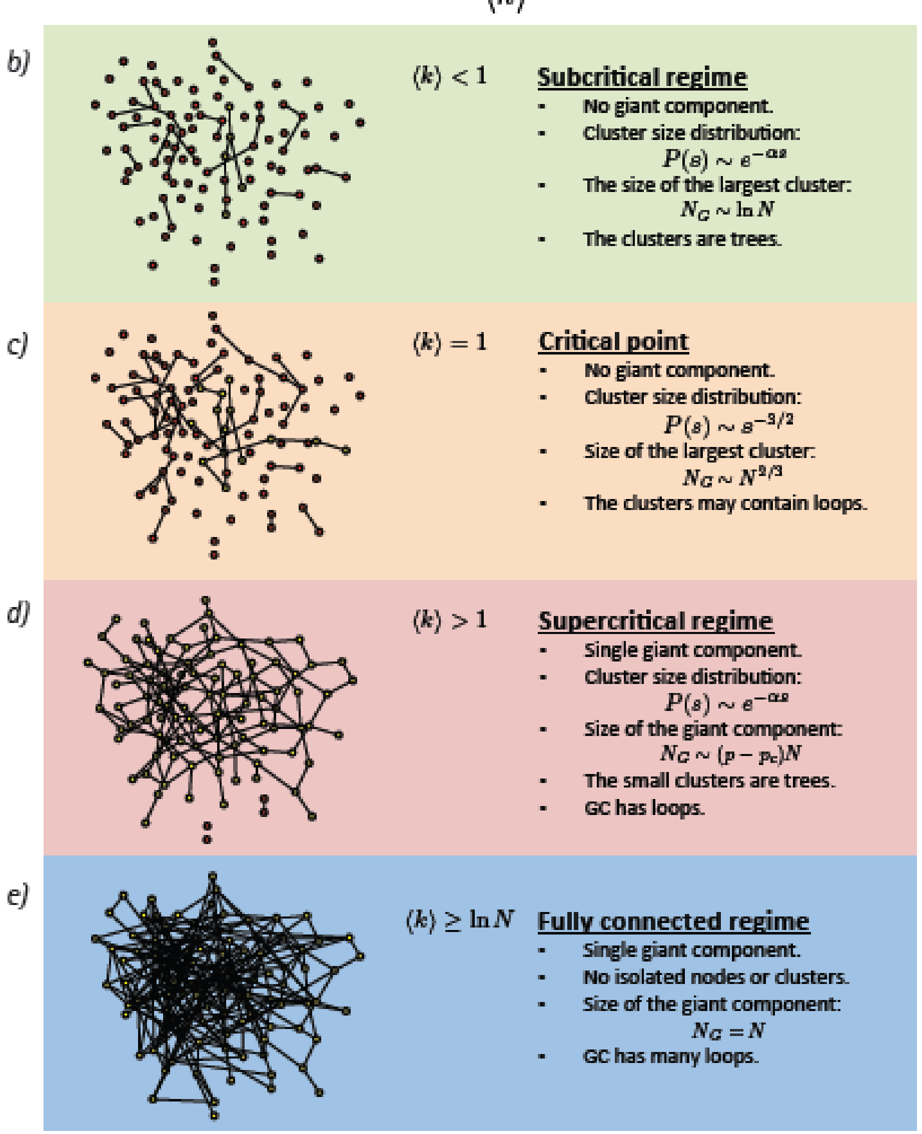


Image 3.6

Evolution of a random network.

(a) The relative size of the giant component in function of the average degree ‹k› 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

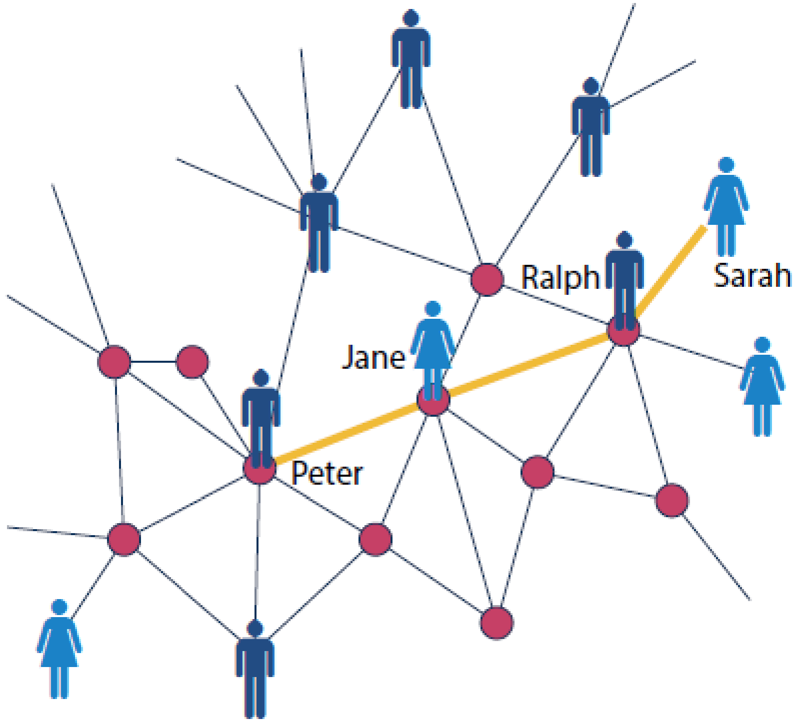


Image 3.9

Six degrees of separation.

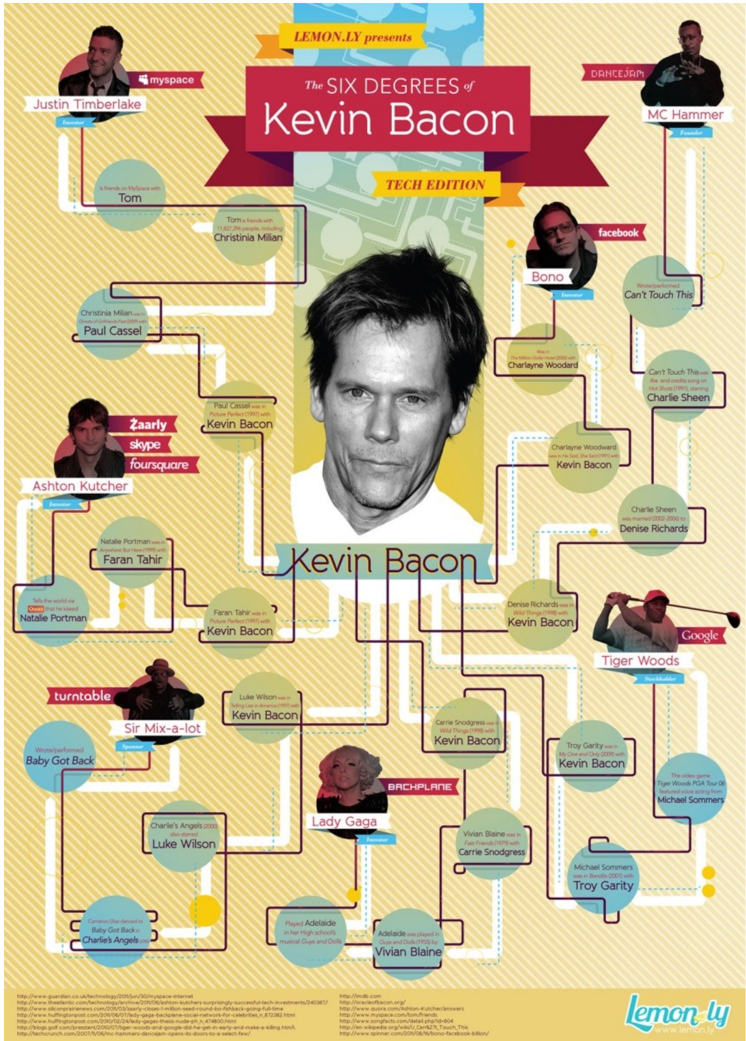
According to six degrees of separation any two individuals, anywhere in the world, can be connected through a chain of six or fewer acquaintances. This means that while Sarah does not know Peter, she knows Ralph, who knows Jane and who in turn knows Peter. Hence Sarah is three degrees from Peter. In 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

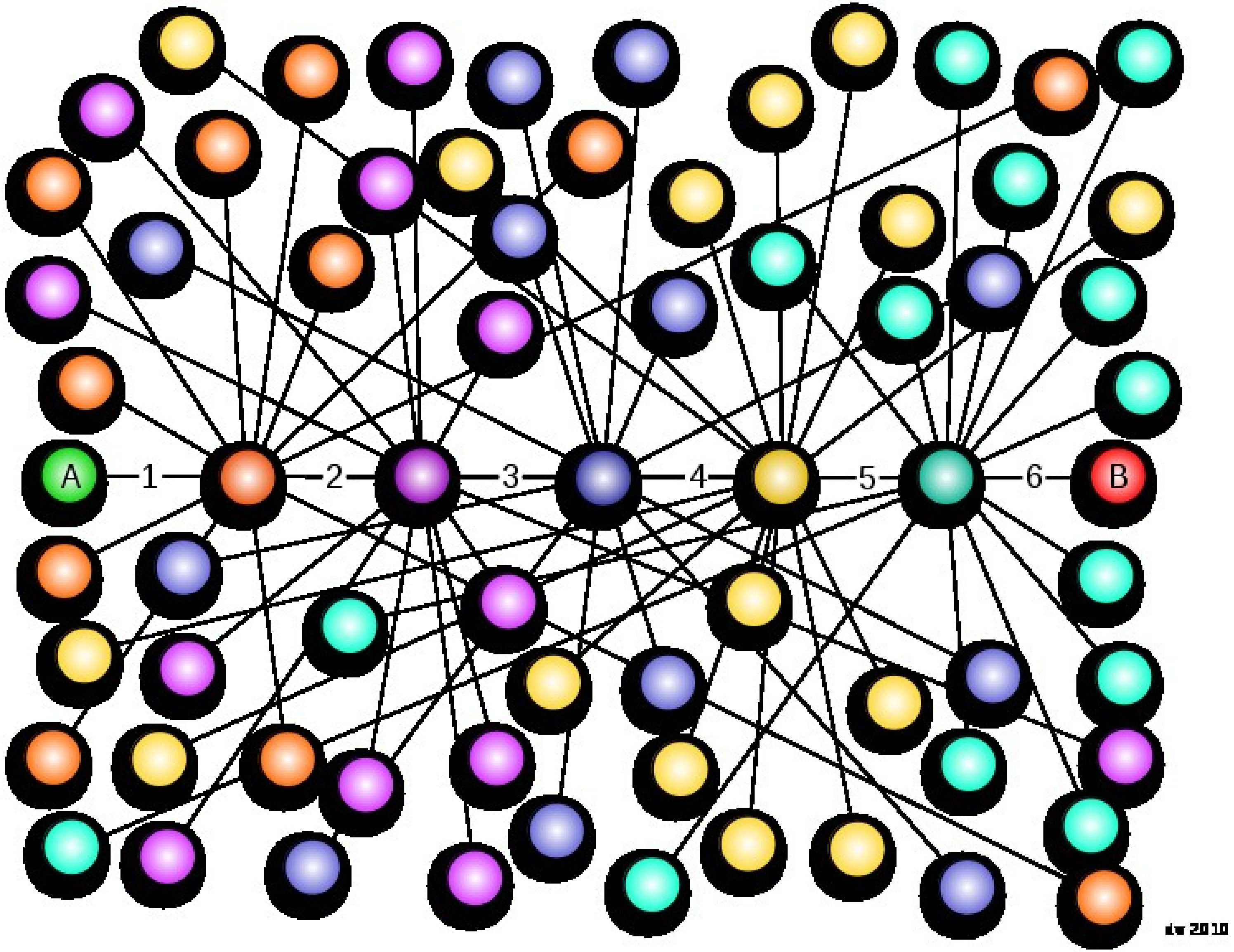
Stanley Milgram (1933–1984)

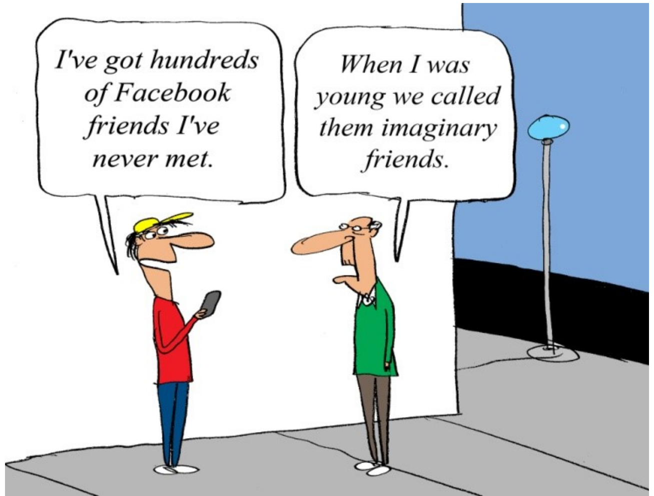
Six degree of separation

Milgram experiment



Small wolrd





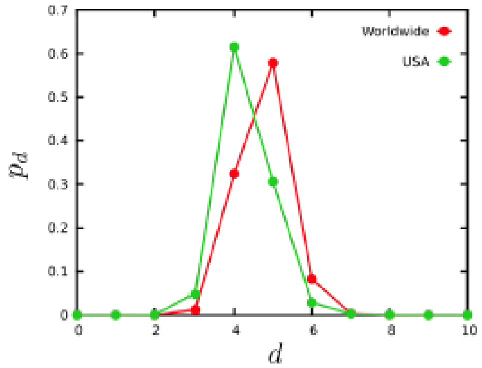
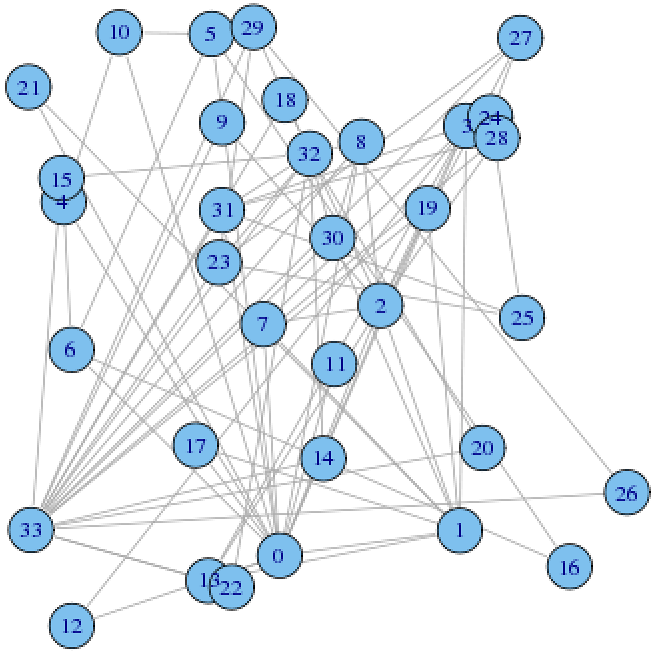


Image 3.11

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

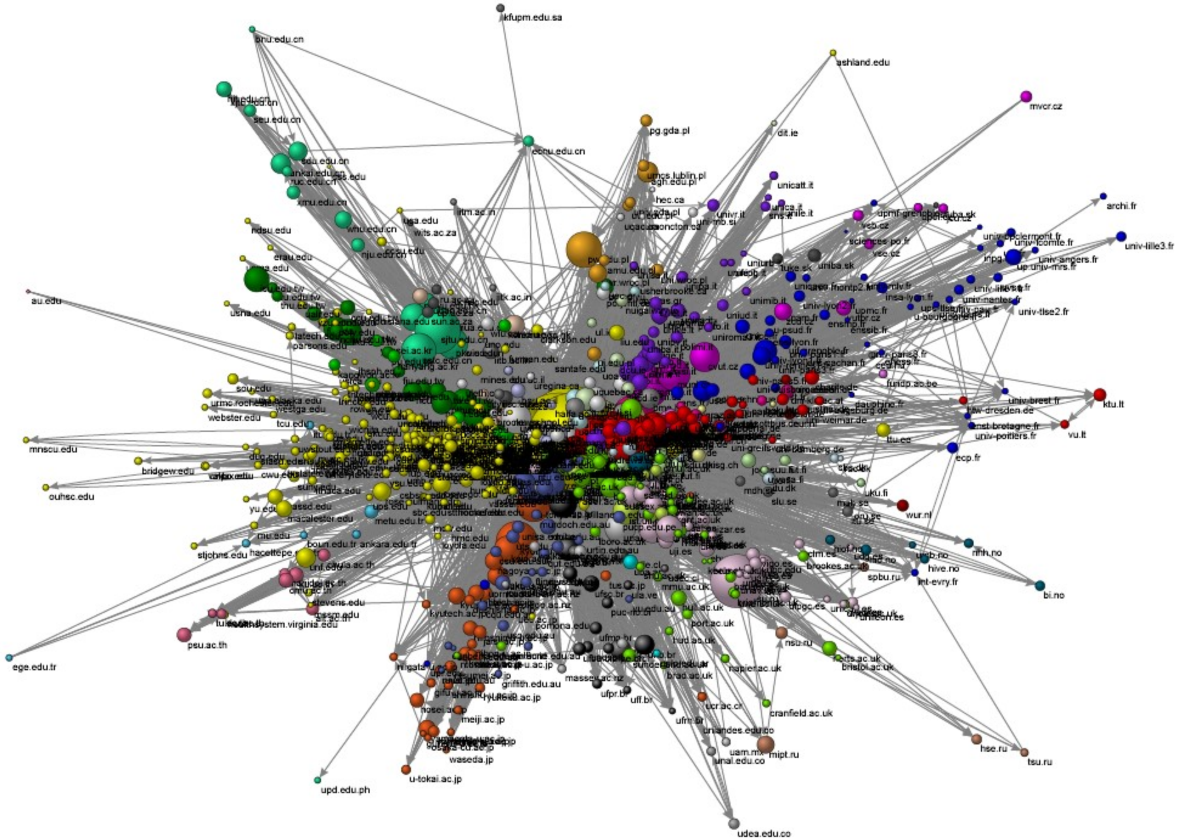
- Specifically, a **small-world network** is defined to be a network where the typical distance *L* between two randomly chosen nodes (the number of steps required) grows proportionally to the logarithm of the number of nodes*N* in the network, that is:[1]

$$L \propto \log N$$

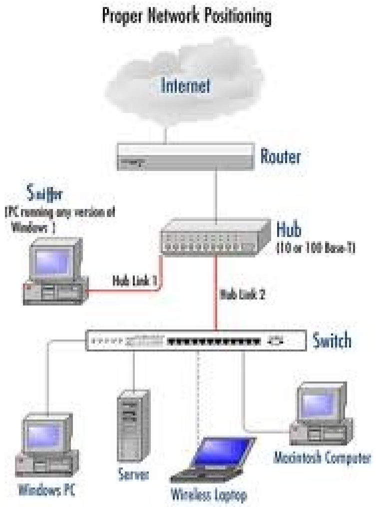
The hubs

Barabasi-Albert model

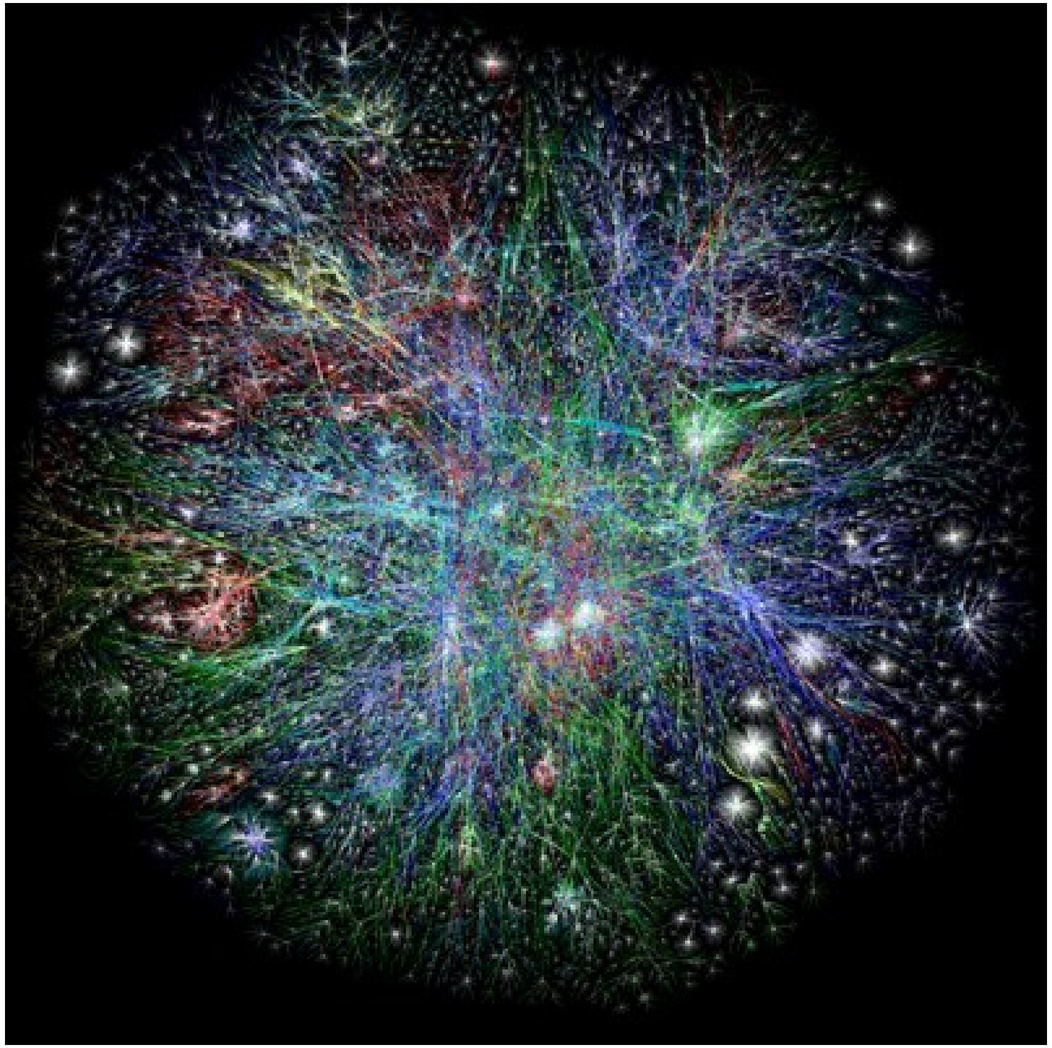
- Node degree: $\mathbf{y} = a\,\mathbf{x}^{-b}$



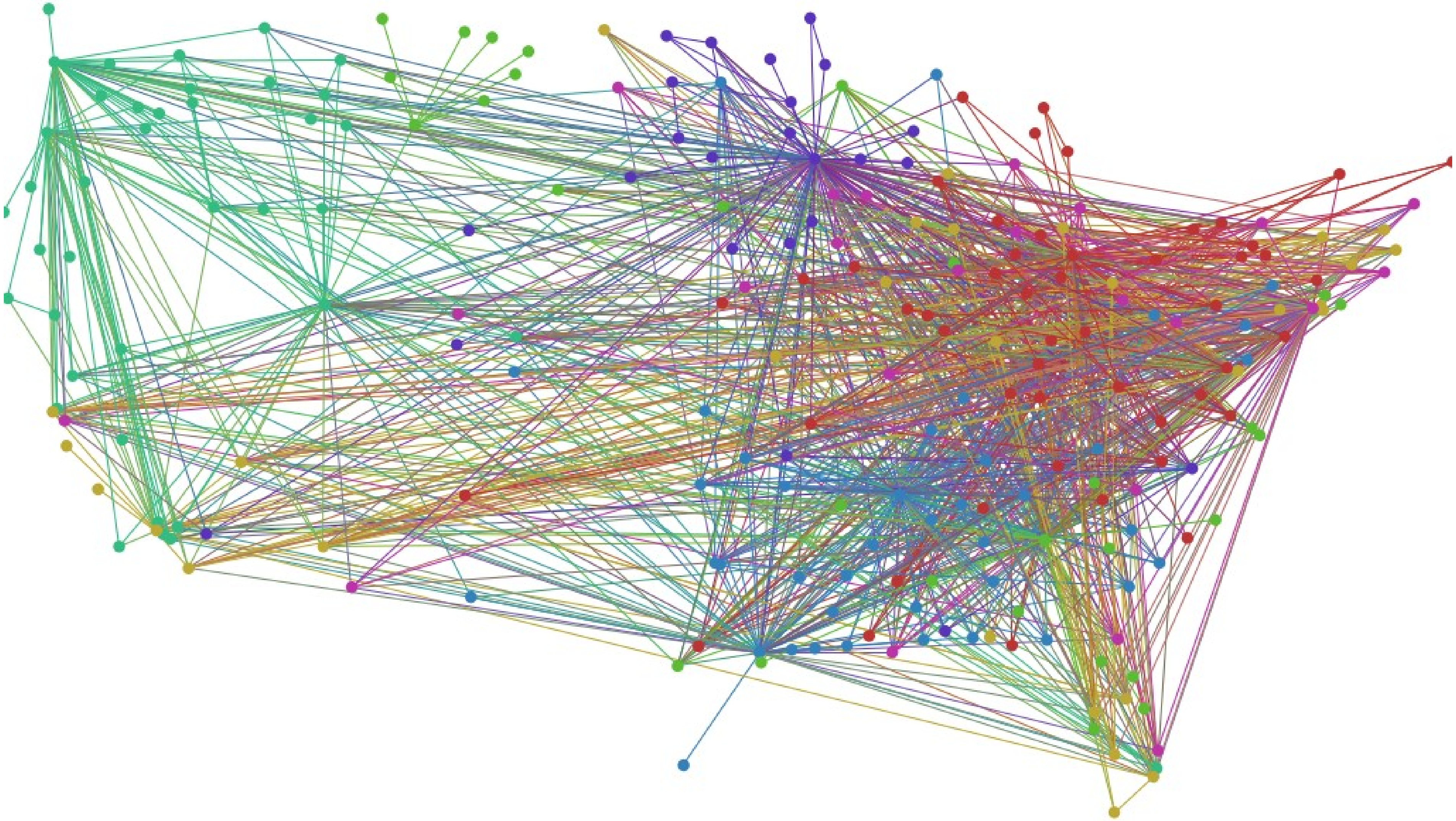
WWW



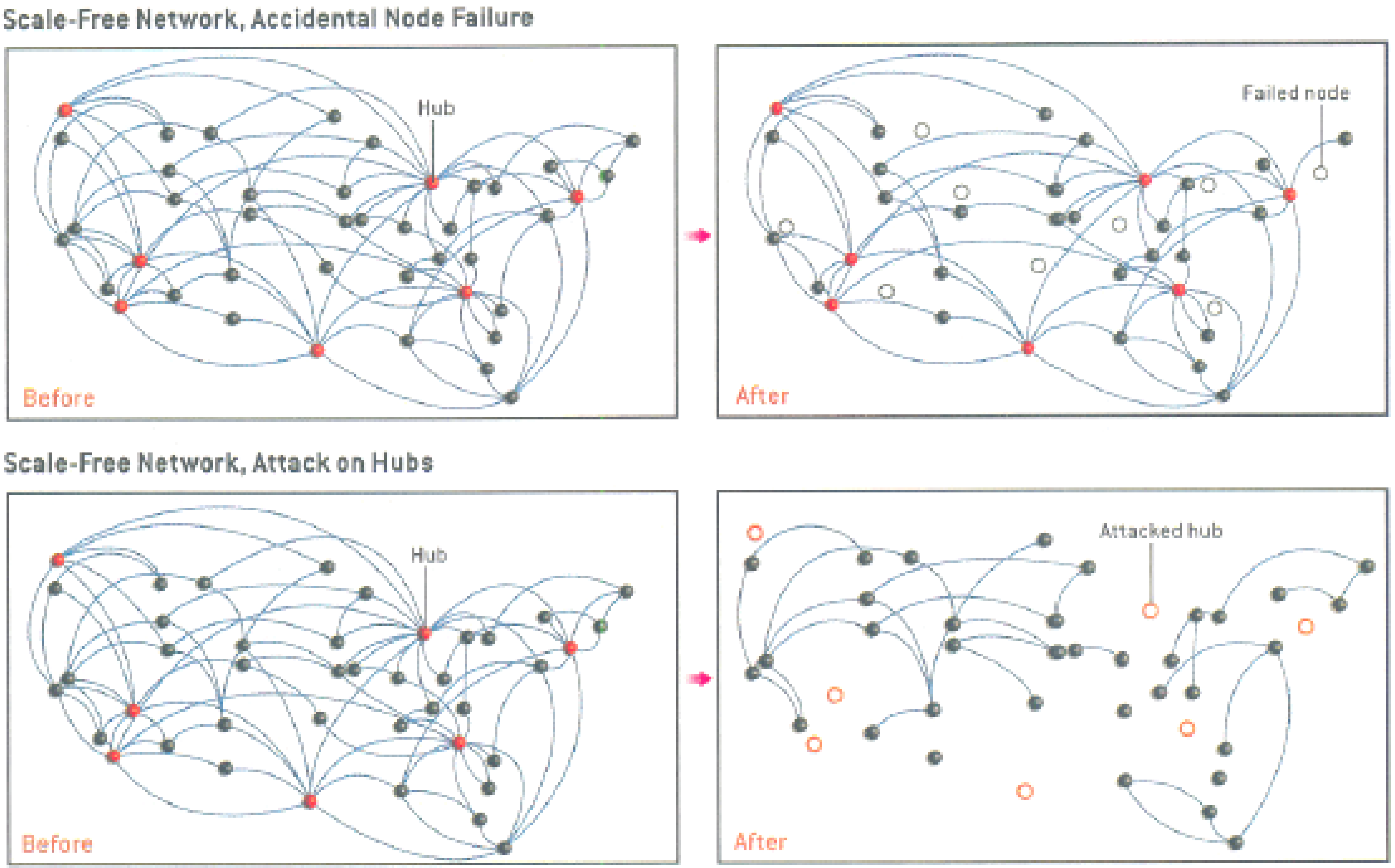
Proper Network Positioning
Internet
Router
Sniffer
(PC running any version of Windows)
Hub
(10 or 100 Base-T)
Hub Link 1
Hub Link 2
Switch
Windows PC
Server
Wireless Laptop
Macintosh Computer



transportation

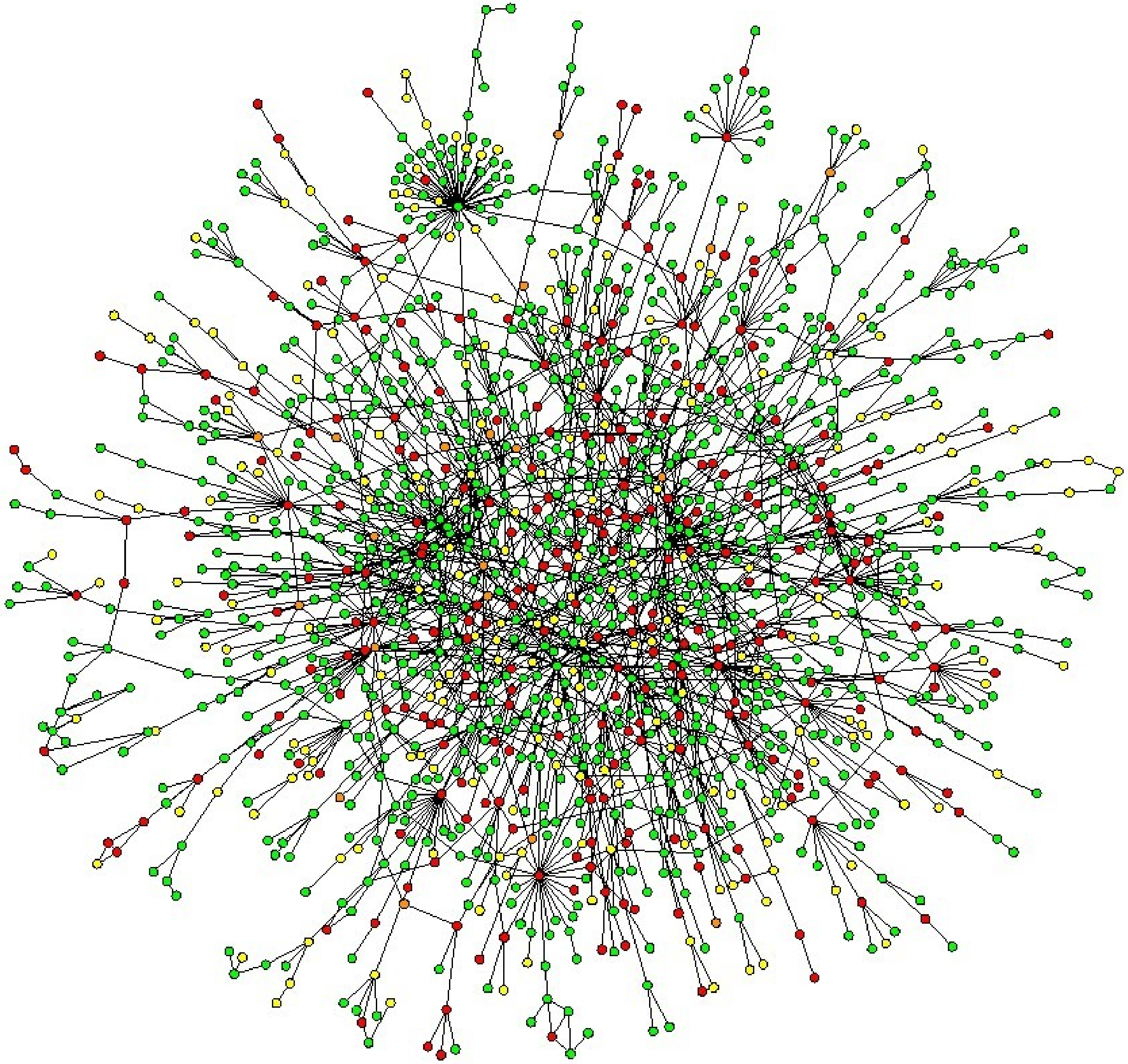


Robustness against random attacks

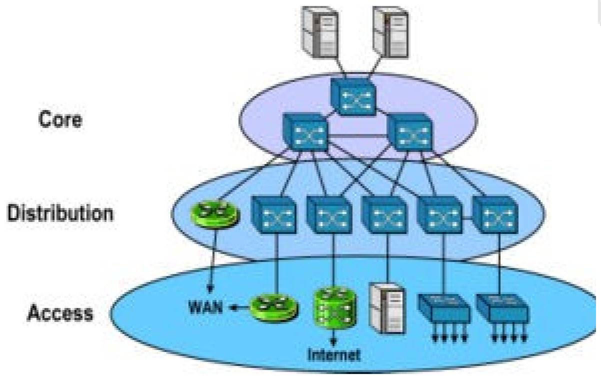


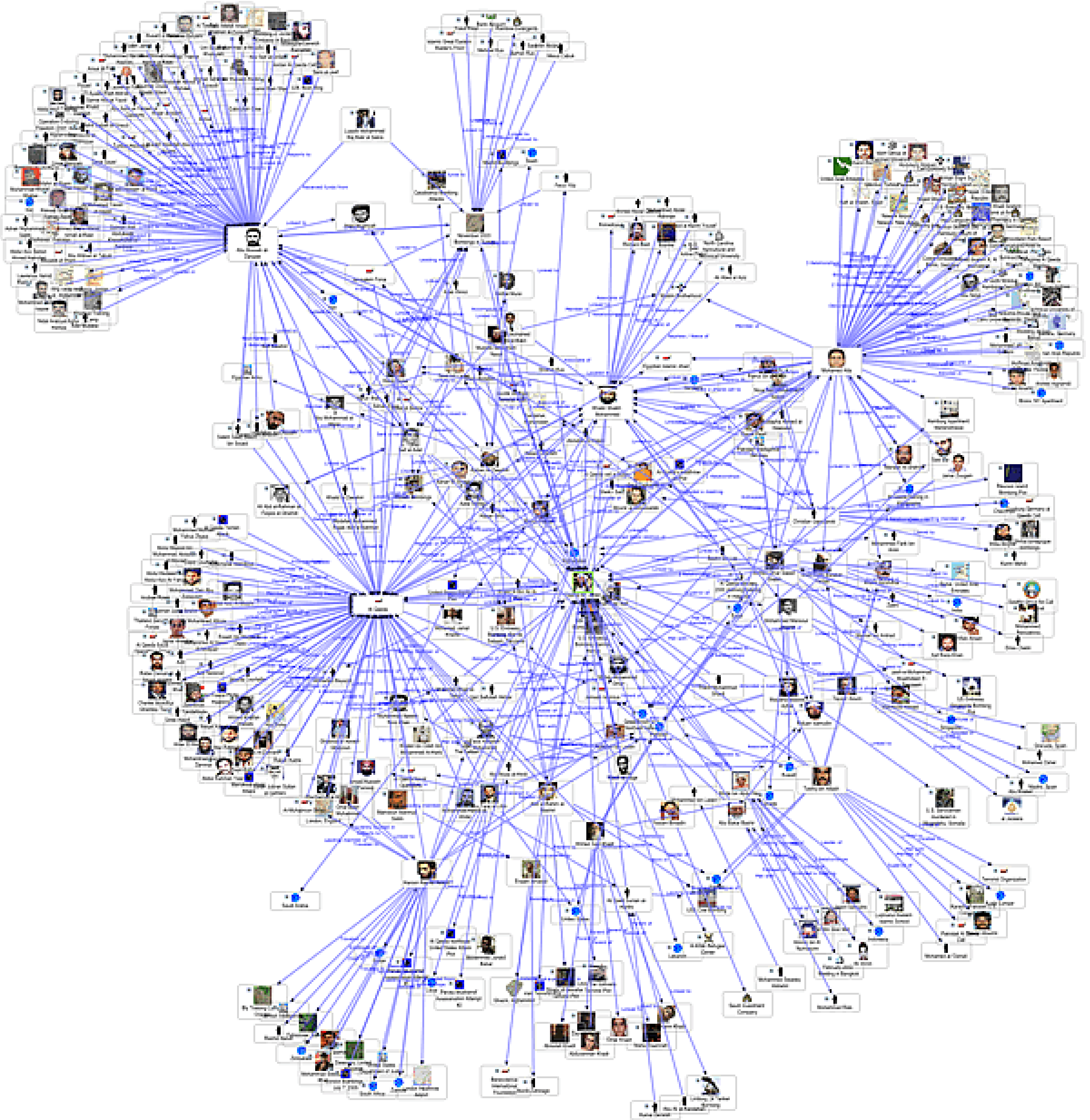
Targeted attaks

A biological example…

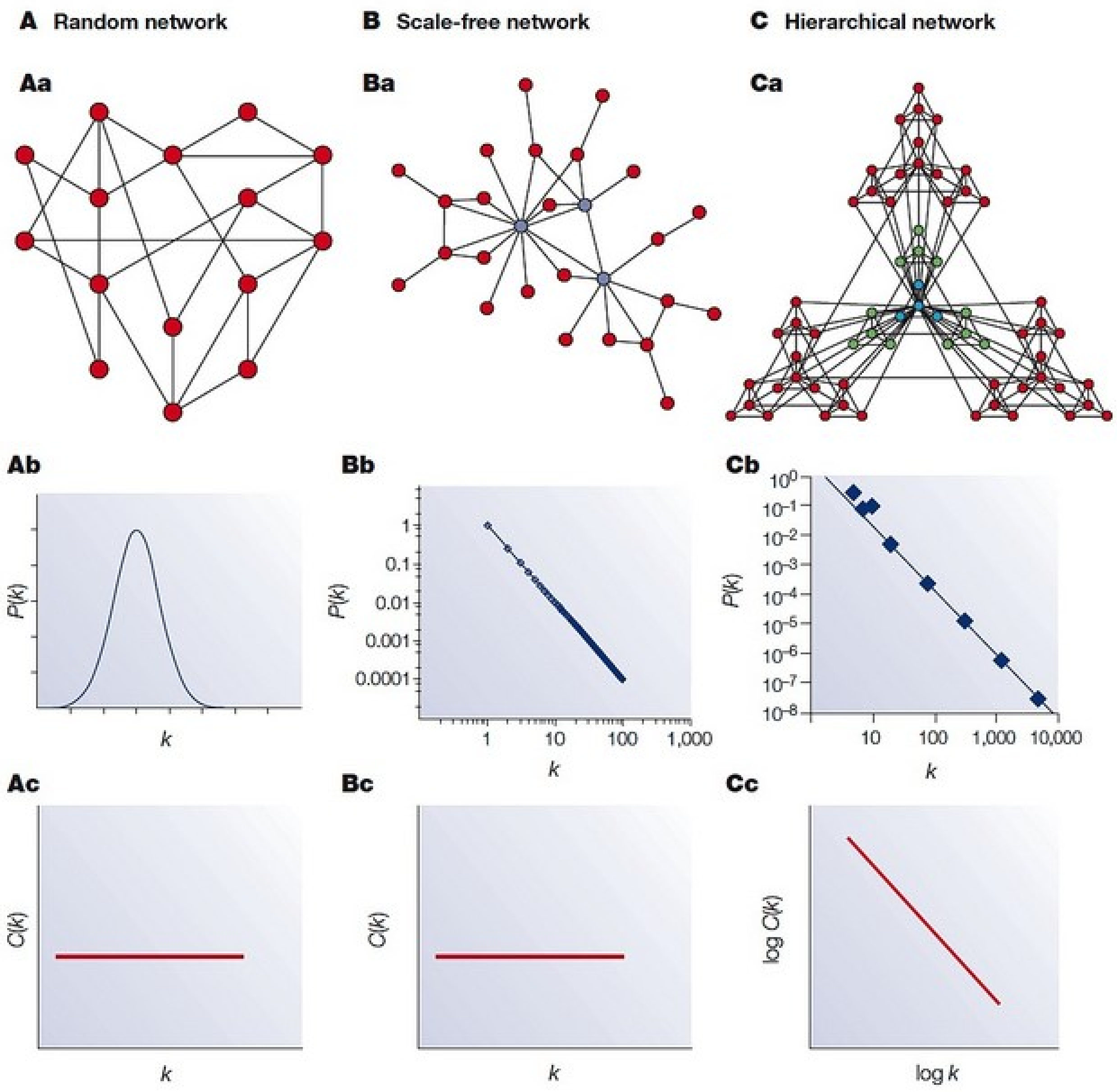


Hierarchical networks





… in conclusion



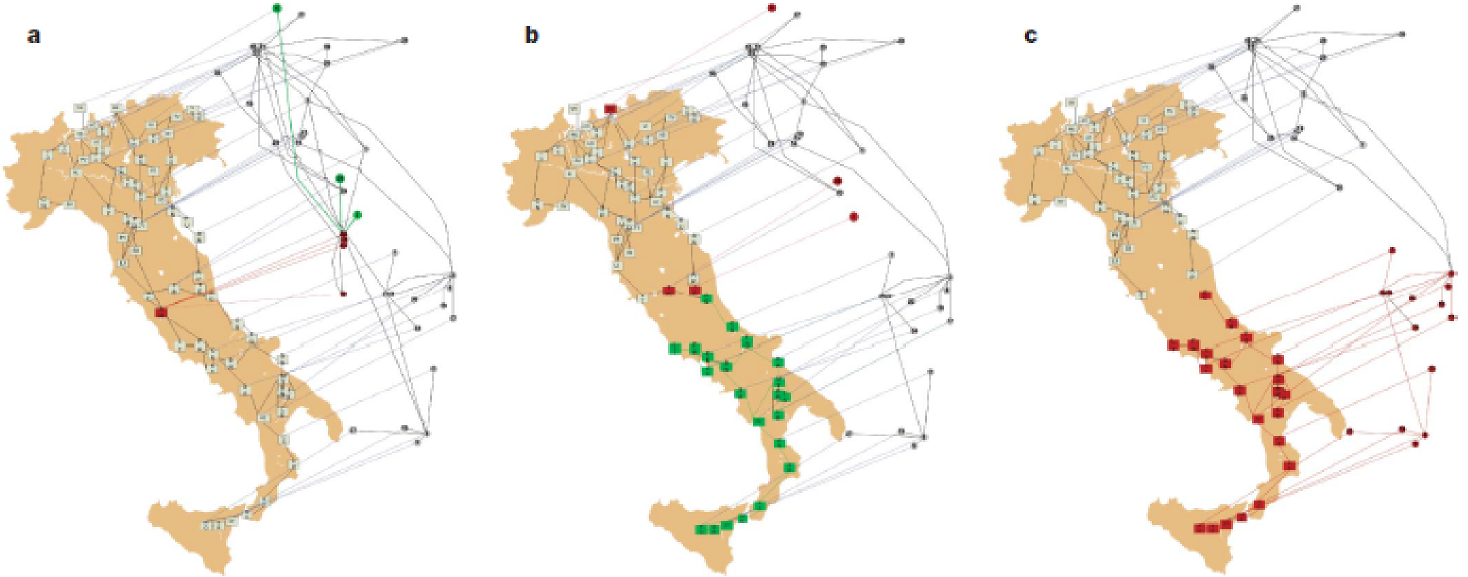


Figure 1 | Modelling a blackout in Italy. Illustration of an iterative process of a cascade of failures using real-world data from a power network (located on the map of Italy) and an Internet network (shifted above the map) that were implicated in an electrical blackout that occurred in Italy in September 2003[20]. 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…

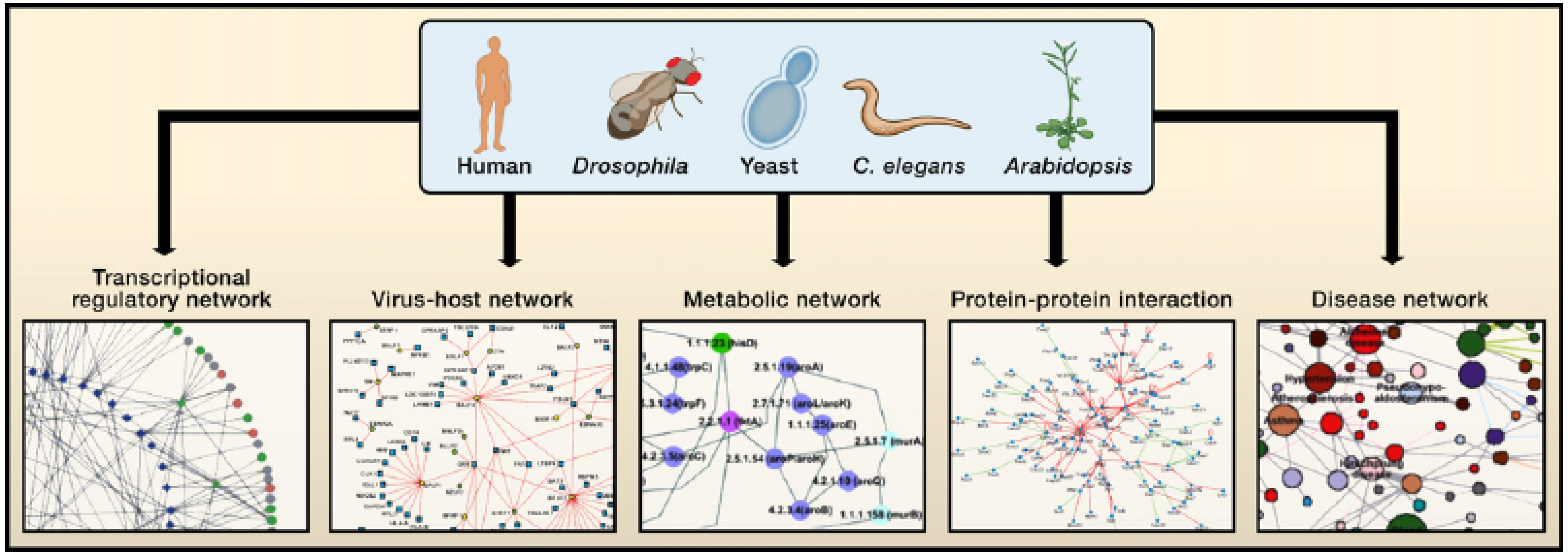


Figure 2. Networks in Cellular Systems

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

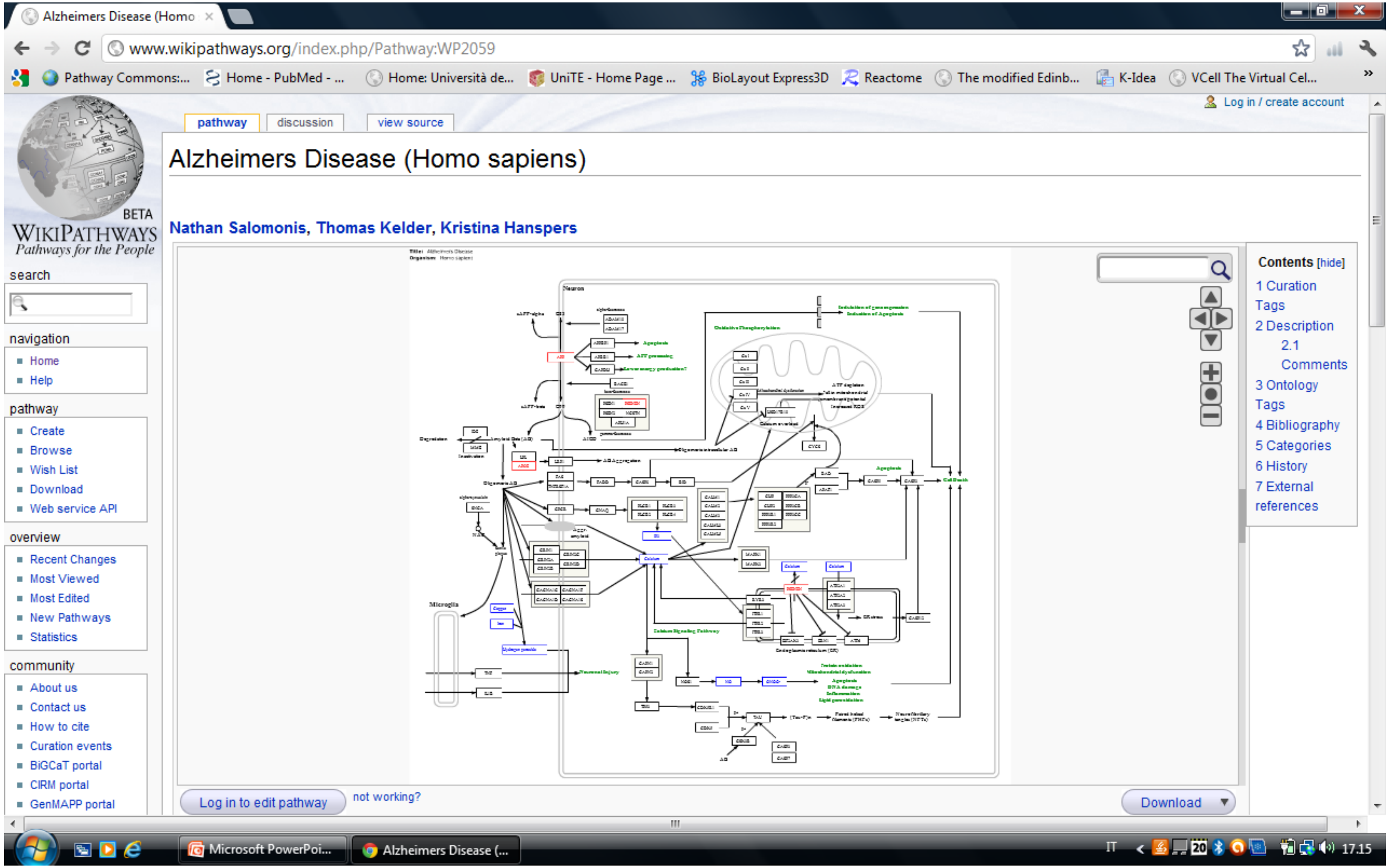
PC Pathway Commons

KEGG Kyoto Encyclopedia of Genes and Genomes

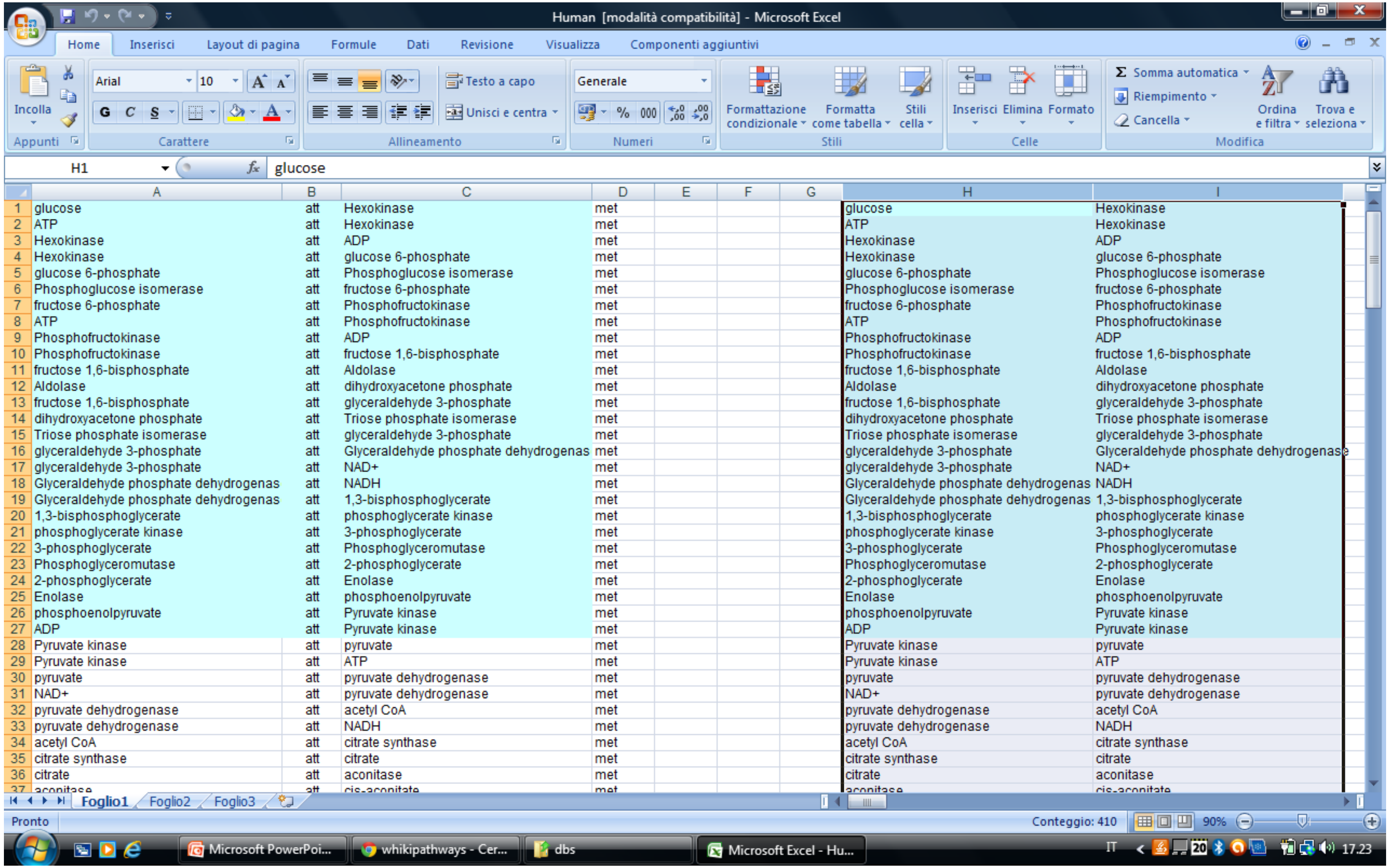
REACTOME

WIKIPATHWAYS
Pathways for the People

For instance…



or… .xls o .xlsx



	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 dehydrogenase
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

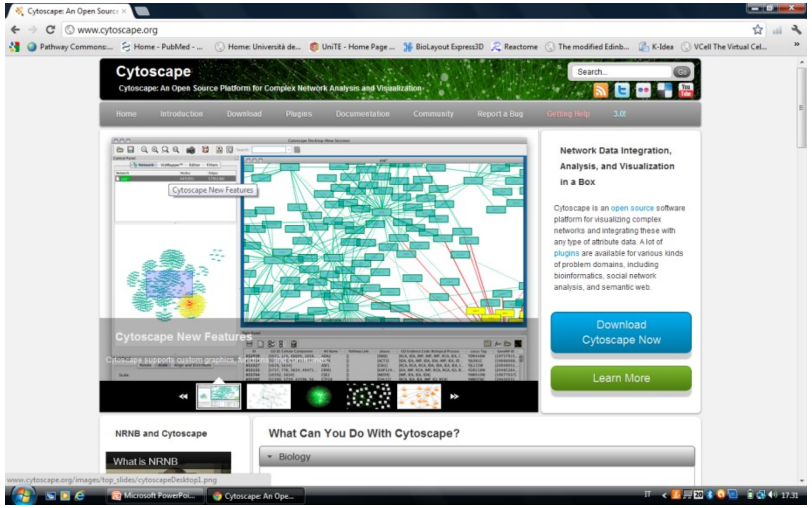
Or .txt

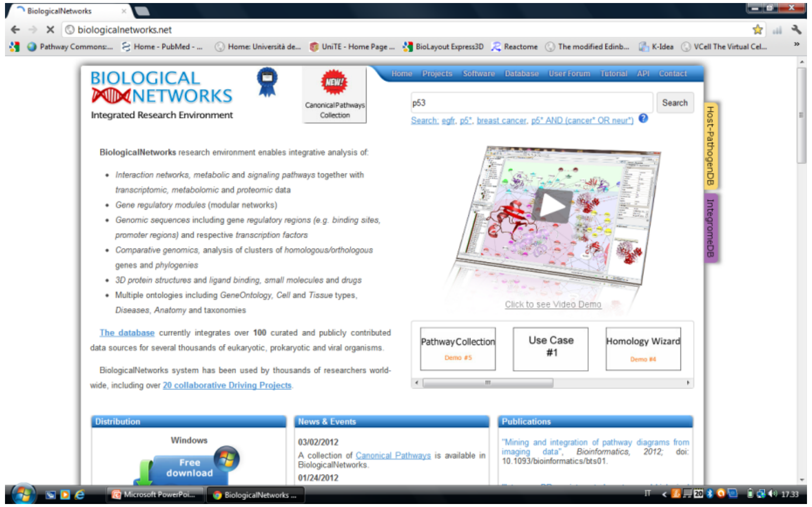
uomo - Blocco note

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	Phosphofructokinase
ATP	Phosphofructokinase
Phosphofructokinase	ADP
Phosphofructokinase	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



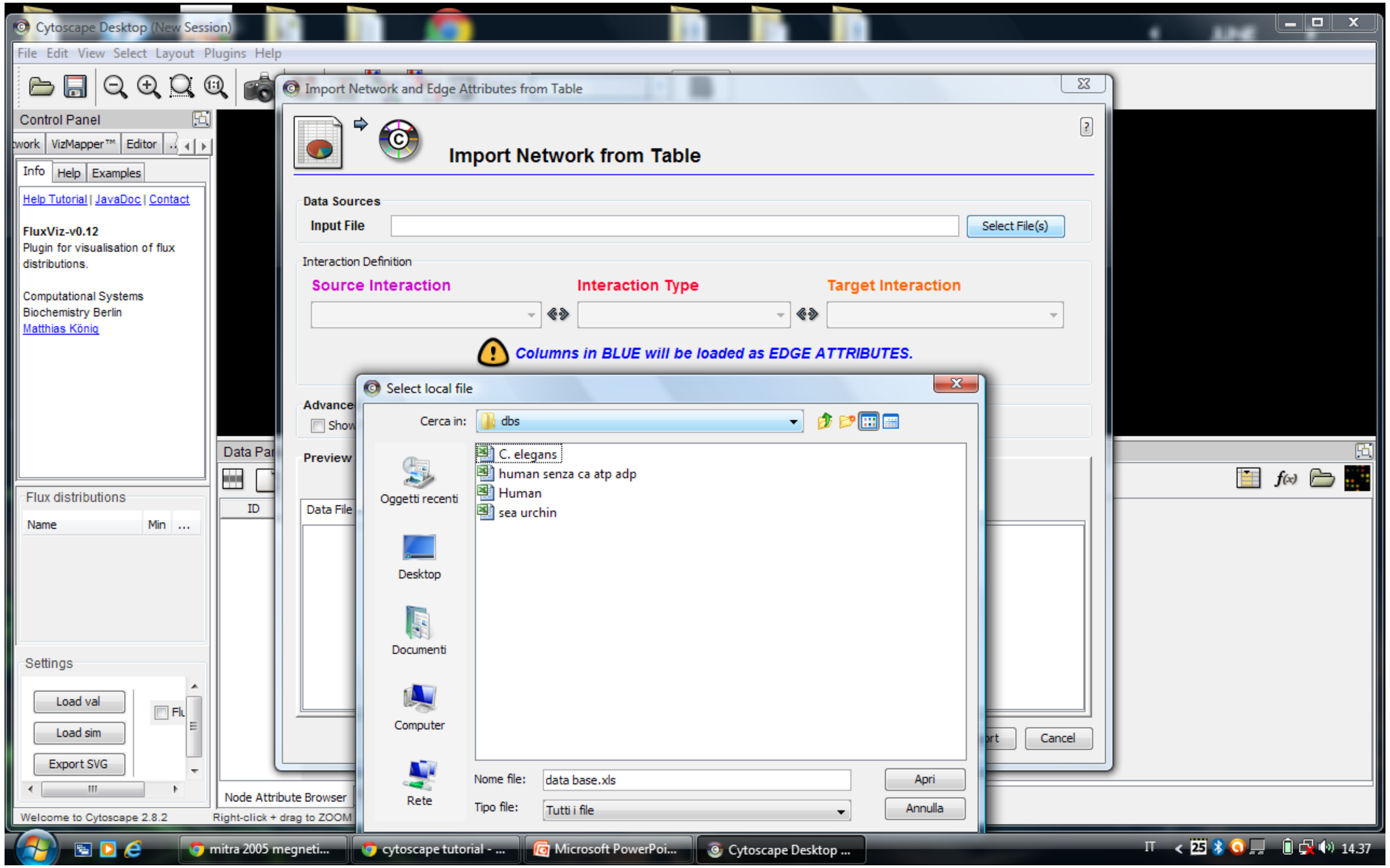


Cytoscape

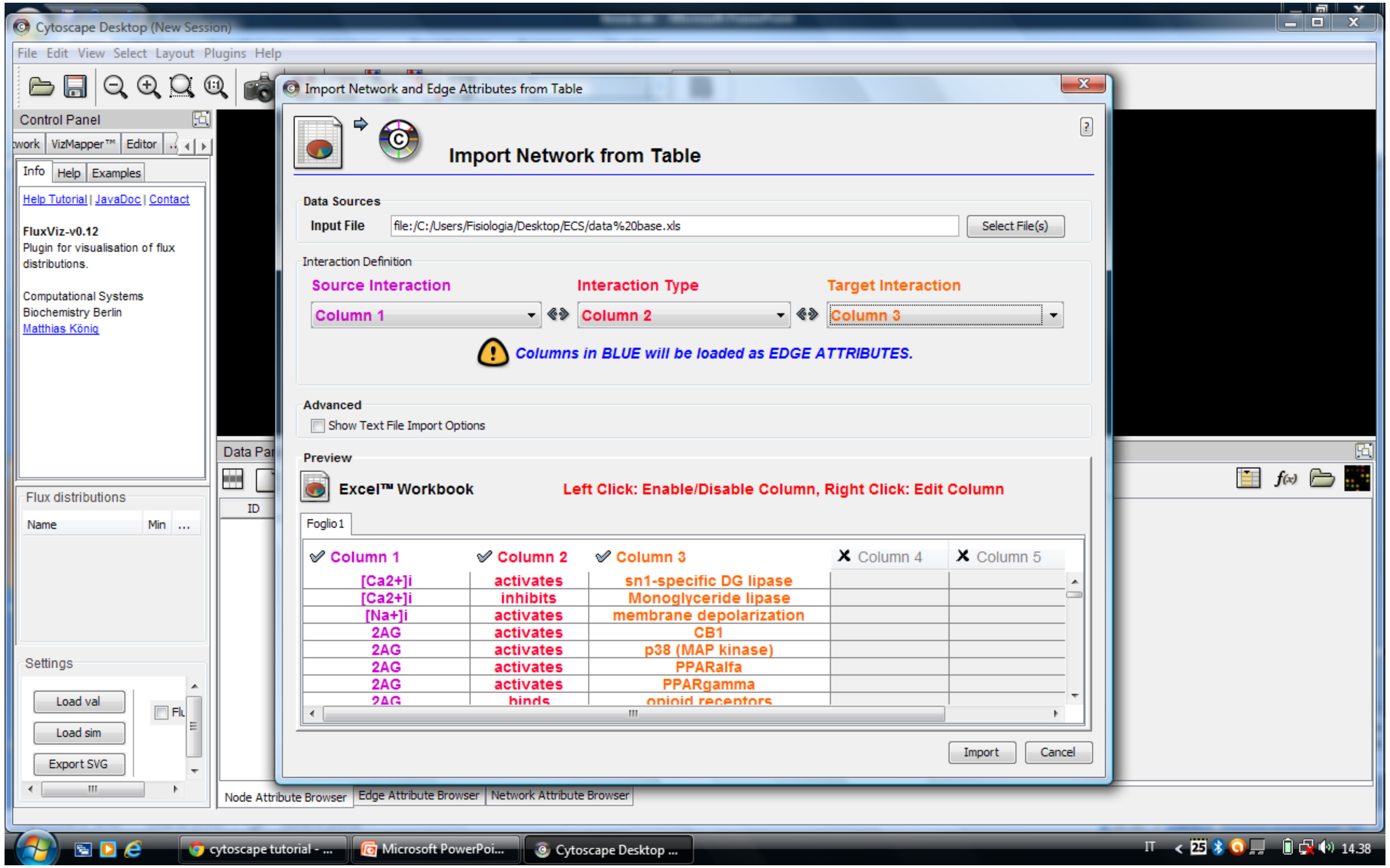
File formats

- 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)

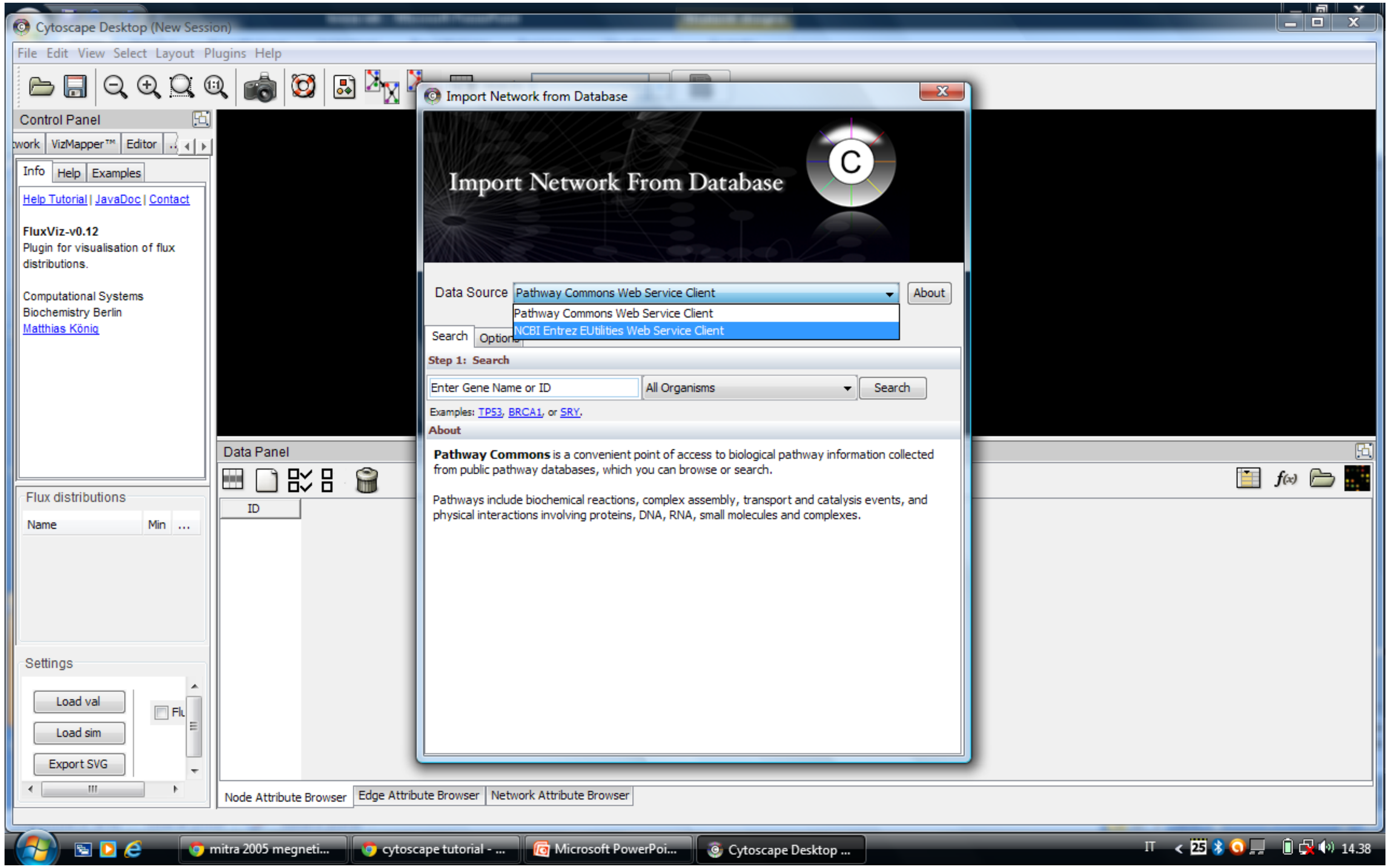
Network realization I



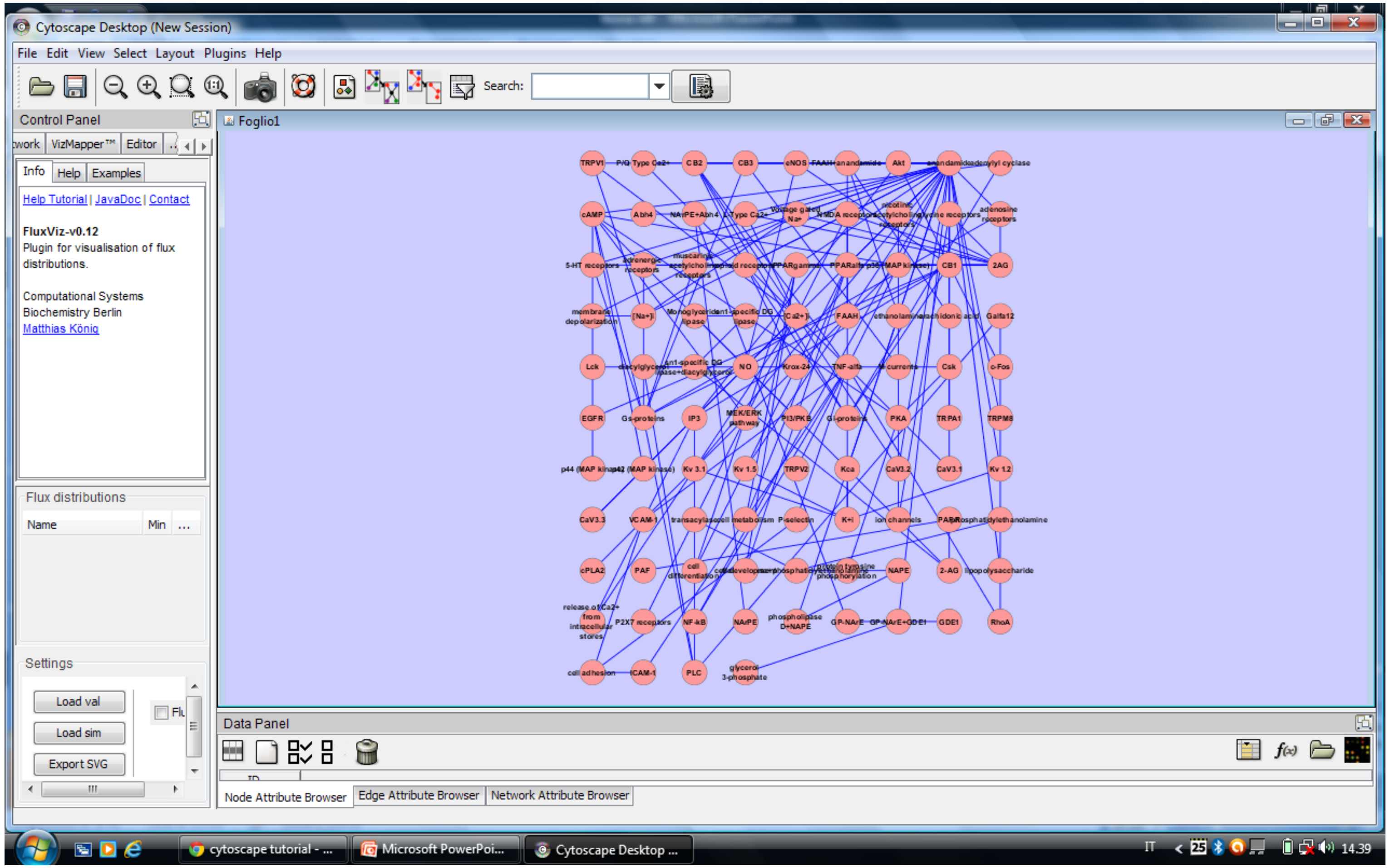
Network realization II



Network realization III



Layout



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FluxViz-v0.12
Plugin for visualisation of flux distributions.
Computational Systems Biochemistry Berlin
Matthias König
Flux distributions
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Settings
Load val
Load sim
Export SVG
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Edge Attribute Browser
Network Attribute Browser
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Microsoft PowerPoi...
Cytoscape Desktop ...
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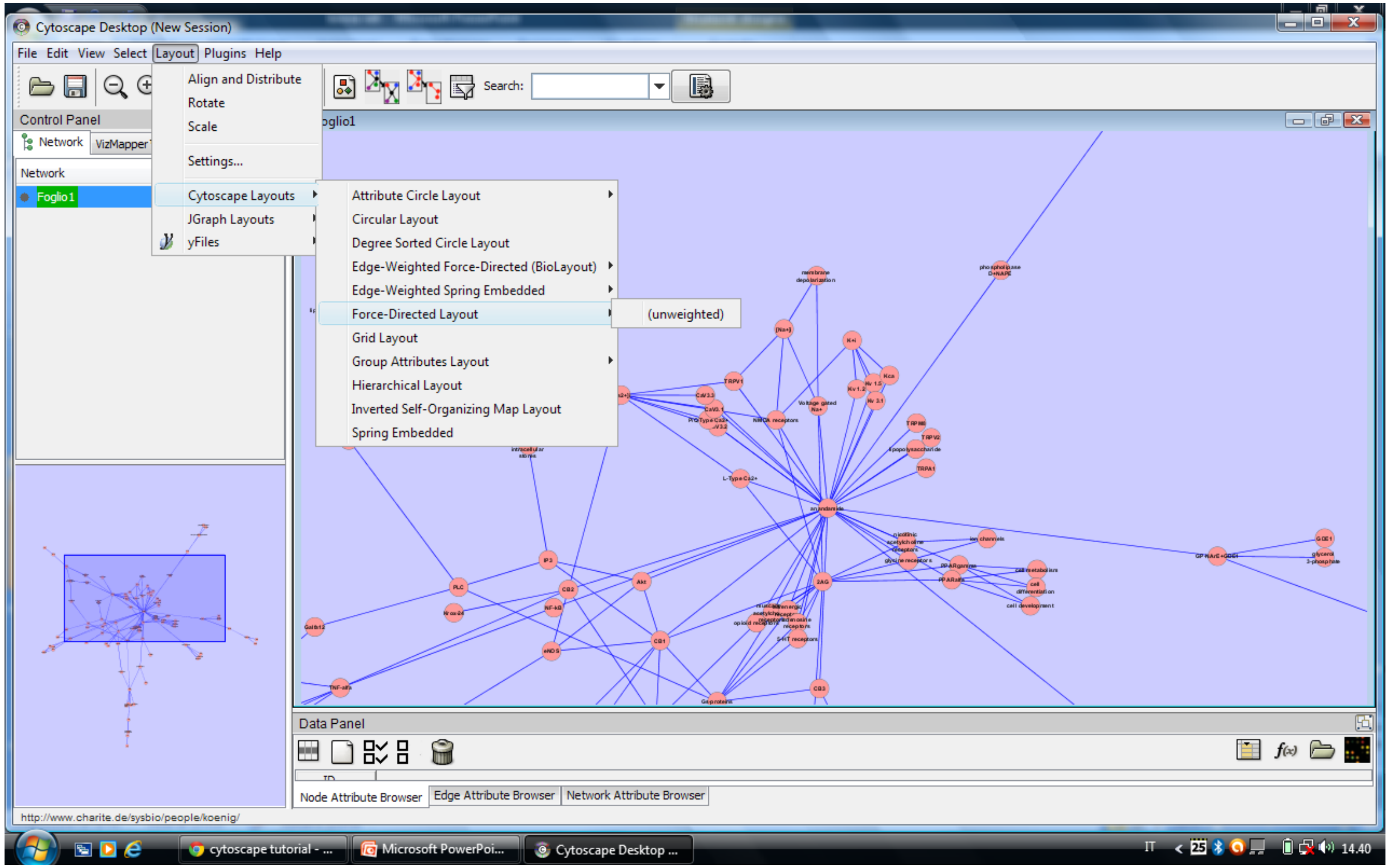
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Circular Layout
Degree Sorted Circle Layout
Edge-Weighted Force-Directed (BioLayout)
Edge-Weighted Spring Embedded
Force-Directed Layout
(unweighted)
Grid Layout
Group Attributes Layout
Hierarchical Layout
Inverted Self-Organizing Map Layout
Spring Embedded
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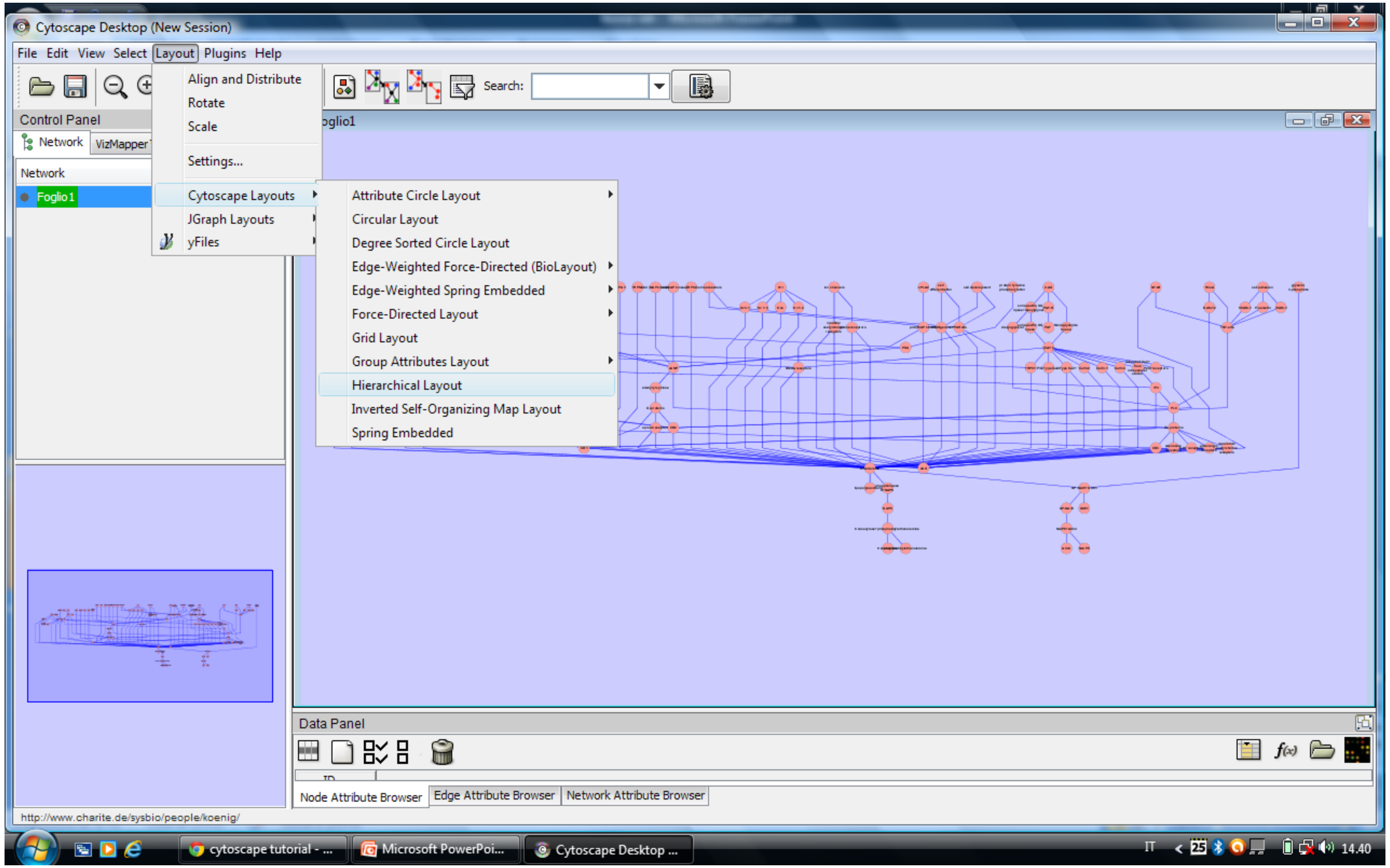
Network Attribute Browser
http://www.charite.de/sysbio/people/koenig/

Layout III



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Network
Foglio1
Align and Distribute
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Cytoscape Layouts
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Attribute Circle Layout
Circular Layout
Degree Sorted Circle Layout
Edge-Weighted Force-Directed (BioLayout)
Edge-Weighted Spring Embedded
Force-Directed Layout
Grid Layout
Group Attributes Layout
Hierarchical Layout
Inverted Self-Organizing Map Layout
Spring Embedded
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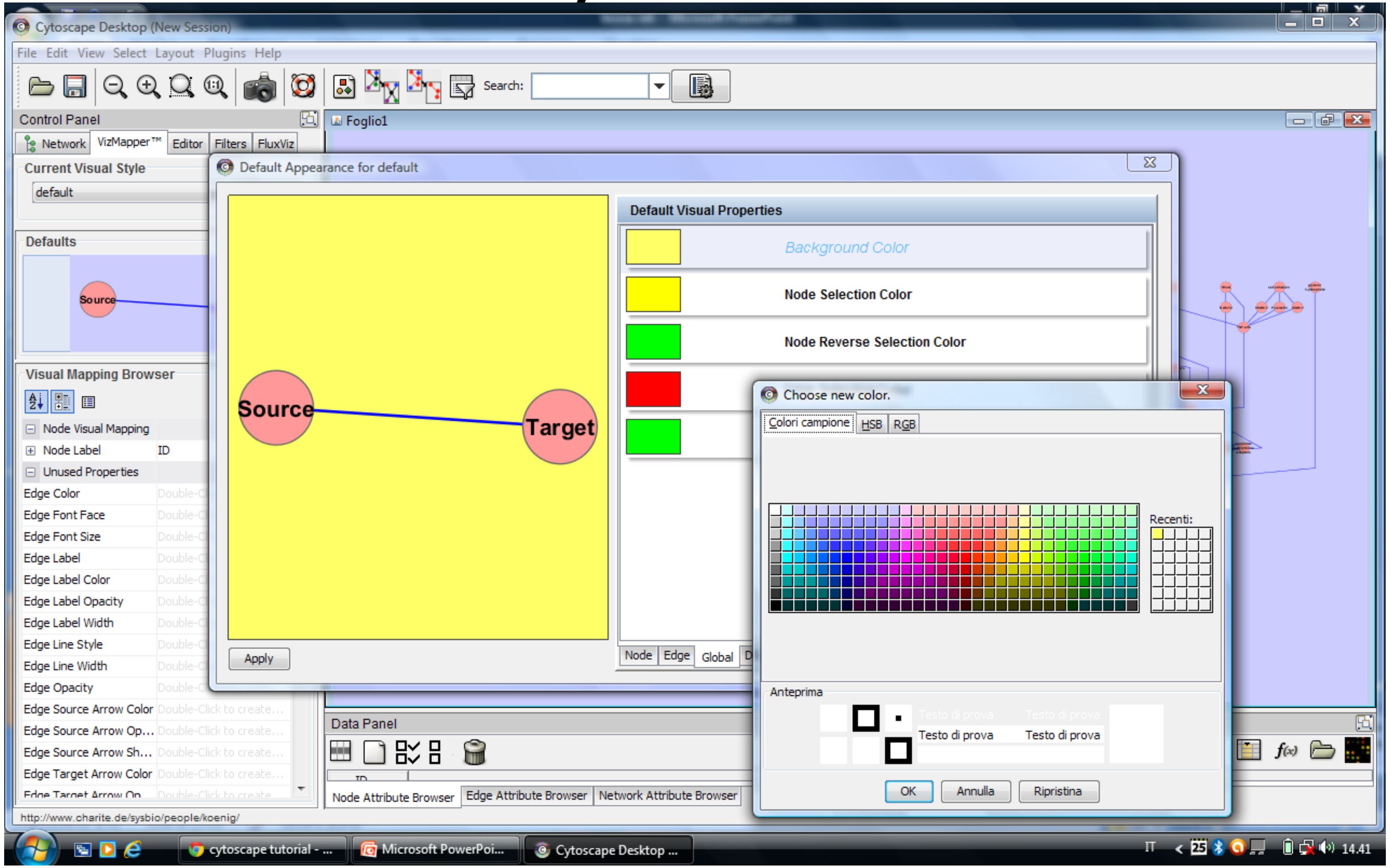
Layout IV



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Edge Color
Edge Font Face
Edge Font Size
Edge Label
Edge Label Color
Edge Label Opacity
Edge Label Width
Edge Line Style
Edge Line Width
Edge Opacity
Edge Source Arrow Color
Edge Source Arrow Op...
Edge Source Arrow Sh...
Edge Target Arrow Color
Foglio1
Default Appearance for default
Source
Target
Apply
Default Visual Properties
Background Color
Node Selection Color
Node Reverse Selection Color
Node Edge Global
Choose new color.
Colori campione HSB RGB
Recenti:
Anteprima
Testo di prova
Testo di prova
OK Annulla Ripristina
Data Panel
Node Attribute Browser Edge Attribute Browser Network Attribute Browser
http://www.charite.de/sysbio/people/koenig/
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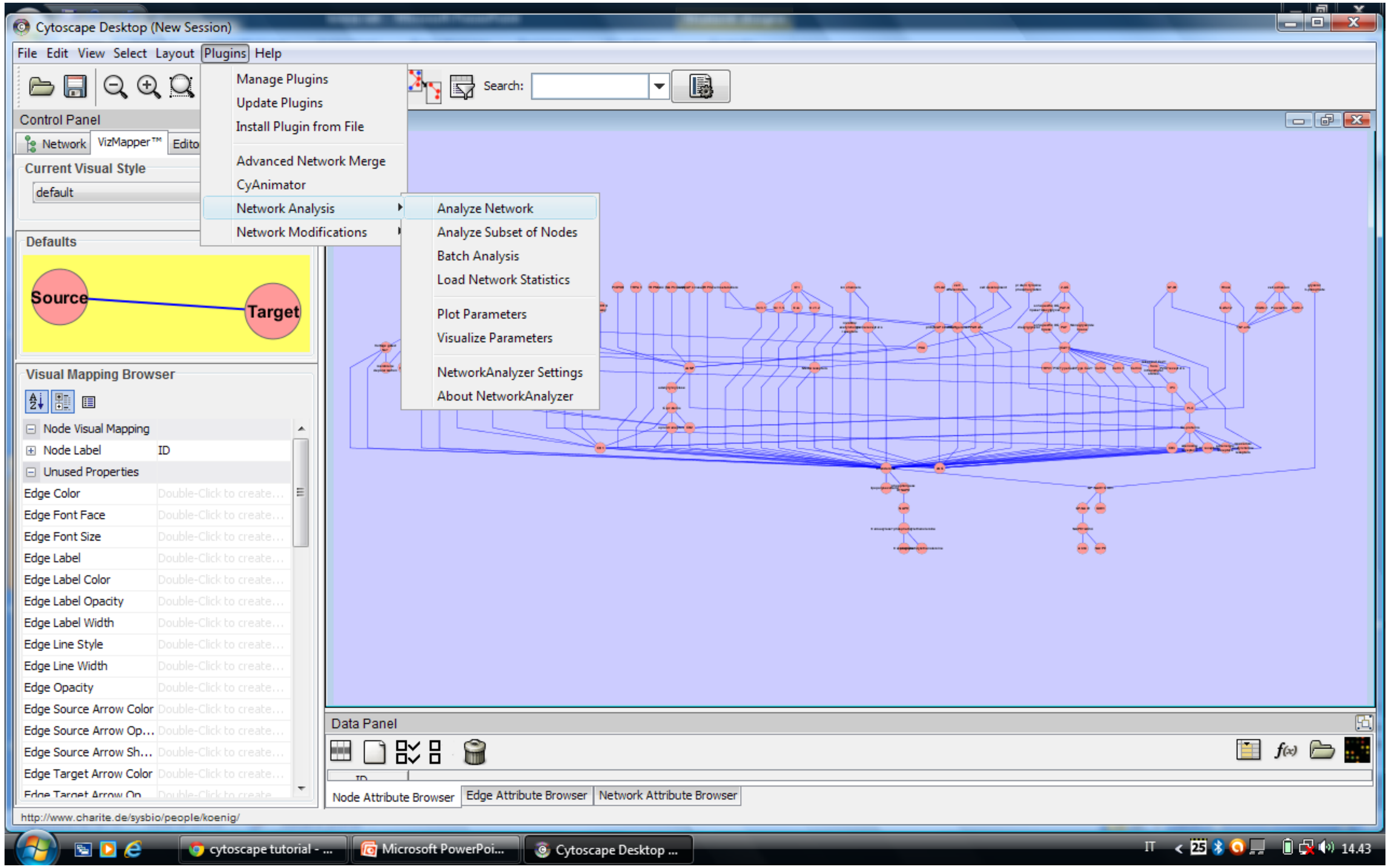
Analysis



Cytoscape Desktop (New Session)
File Edit View Select Layout Plugins Help
Manage Plugins
Update Plugins
Install Plugin from File
Advanced Network Merge
CyAnimator
Network Analysis
Network Modifications
Analyze Network
Analyze Subset of Nodes
Batch Analysis
Load Network Statistics
Plot Parameters
Visualize Parameters
NetworkAnalyzer Settings
About NetworkAnalyzer
Search:
Control Panel
Network
VizMapper™
Current Visual Style
default
Defaults
Source
Target
Visual Mapping Browser
Node Visual Mapping
Node Label
ID
Unused Properties
Edge Color
Edge Font Face
Edge Font Size
Edge Label
Edge Label Color
Edge Label Opacity
Edge Label Width
Edge Line Style
Edge Line Width
Edge Opacity
Edge Source Arrow Color
Edge Target Arrow Color
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Network Attribute Browser
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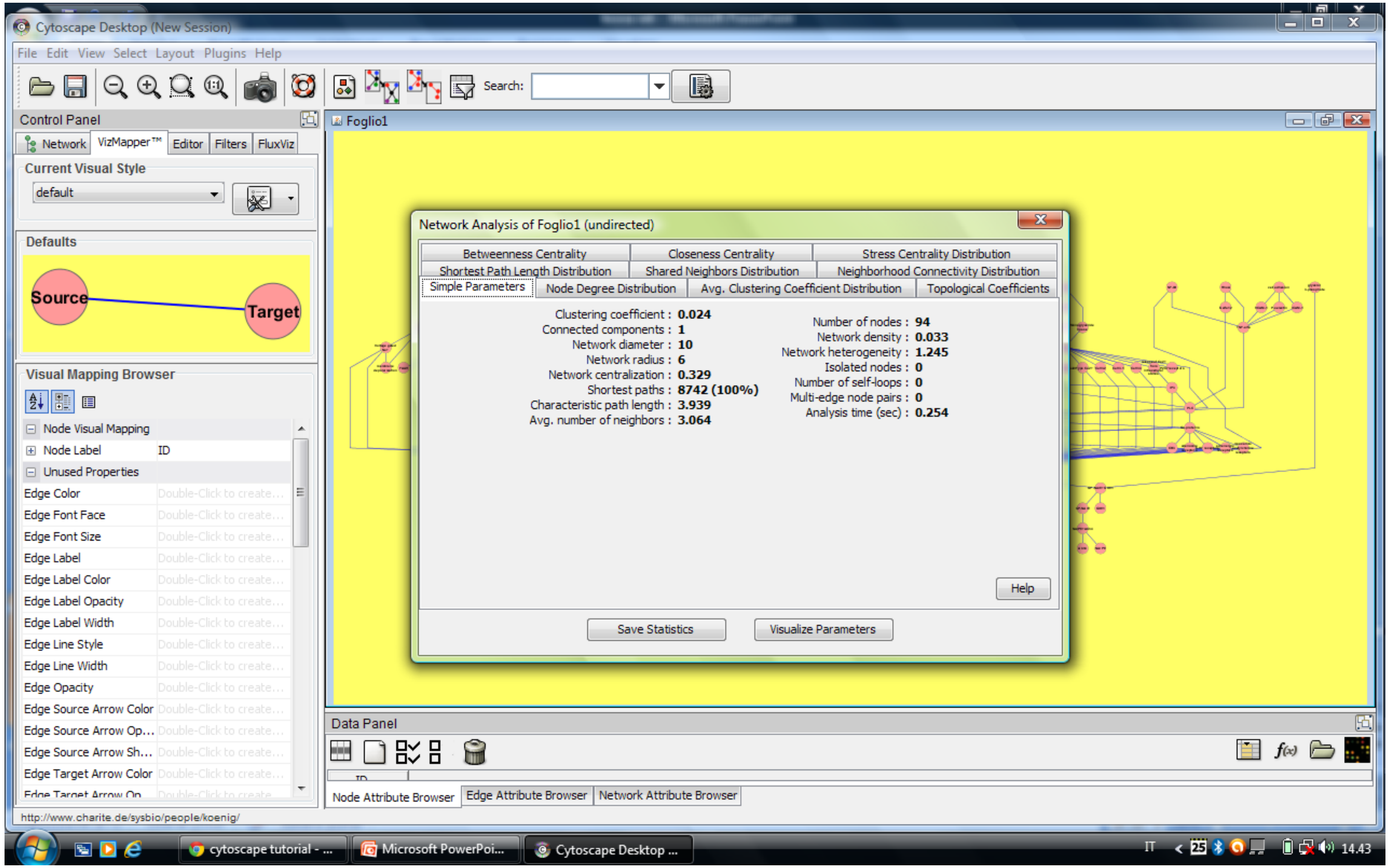
Analysis


Cytoscape Desktop (New Session)
File Edit View Select Layout Plugins Help
Search:
Control Panel
Network VizMapper™ Editor Filters FluxViz
Current Visual Style
default
Defaults
Source
Target
Visual Mapping Browser
Node Visual Mapping
Node Label ID
Unused Properties
Edge Color
Edge Font Face
Edge Font Size
Edge Label
Edge Label Color
Edge Label Opacity
Edge Label Width
Edge Line Style
Edge Line Width
Edge Opacity
Edge Source Arrow Color
Edge Source Arrow Op...
Edge Source Arrow Sh...
Edge Target Arrow Color
Foglio1
Network Analysis of Foglio1 (undirected)
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 : 0.024
Connected components : 1
Network diameter : 10
Network radius : 6
Network centralization : 0.329
Shortest paths : 8742 (100%)
Characteristic path length : 3.939
Avg. number of neighbors : 3.064
Number of nodes : 94
Network density : 0.033
Network heterogeneity : 1.245
Isolated nodes : 0
Number of self-loops : 0
Multi-edge node pairs : 0
Analysis time (sec) : 0.254
Help
Save Statistics
Visualize Parameters
Data Panel
Node Attribute Browser
Edge Attribute Browser
Network Attribute Browser
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