Systems Biology: A Personal View
VI. Networks: Models II

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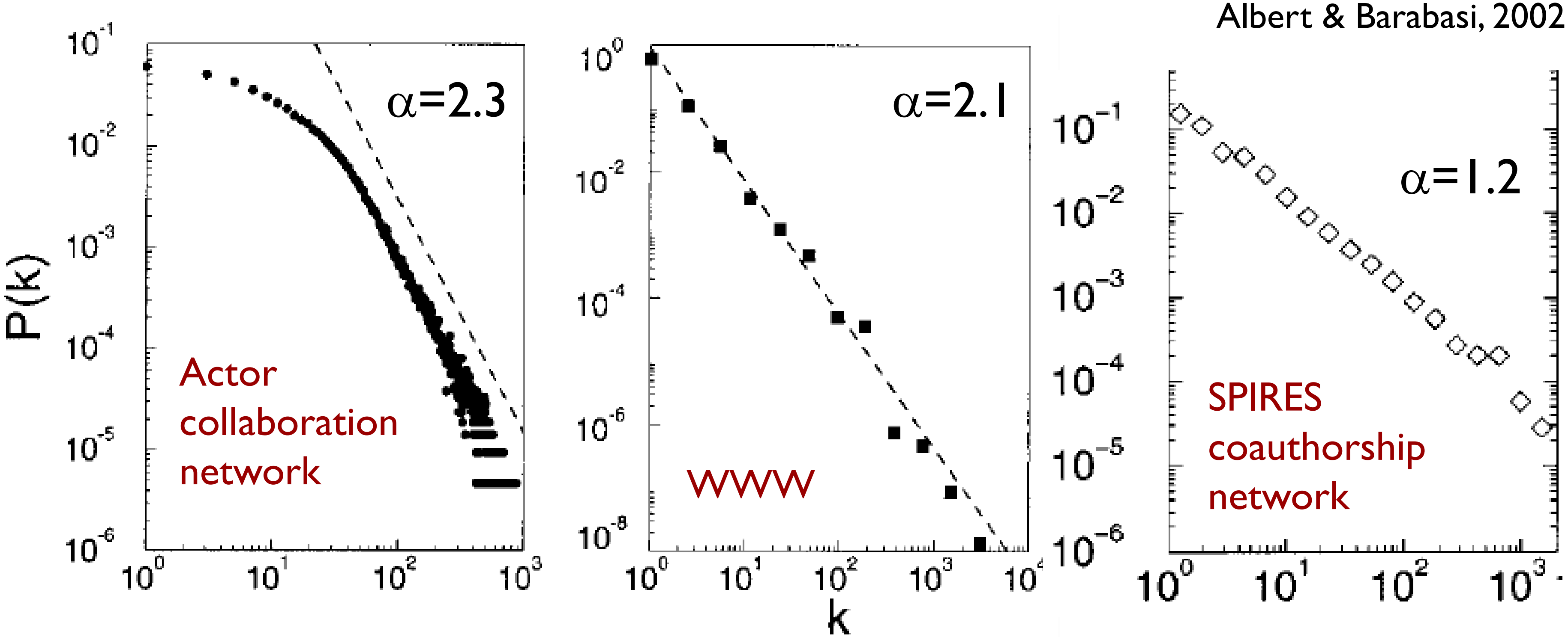
Example: *scale-free* networks

Barabasi and Albert (1999): In many large networks the vertex connectivities follow a scale-free distributions, i.e., the degree distrn has a power law tail: $P(k) \sim k^{-\alpha}$.

Albert & Barabasi, 2002



In contrast,

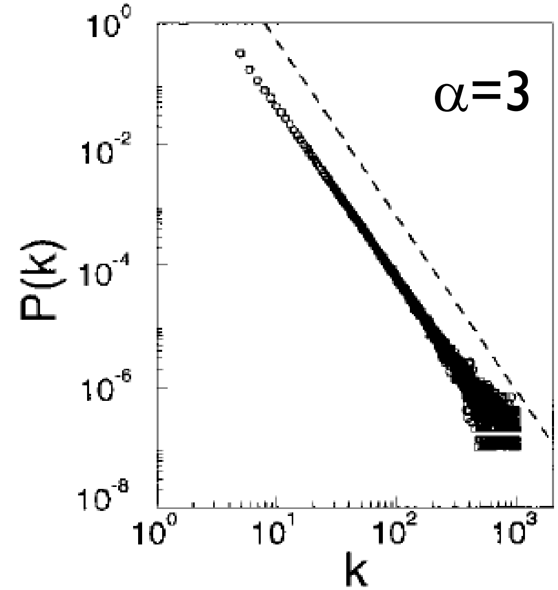
ER random networks (start with *N* nodes and connect each pair with probability *p*) have Poisson degree distrn: $P(k) = e^{-\lambda} (\lambda^k/k!)$

How can *scale-free* networks evolve ?

The Price-Barabasi-Albert preferential attachment scheme:

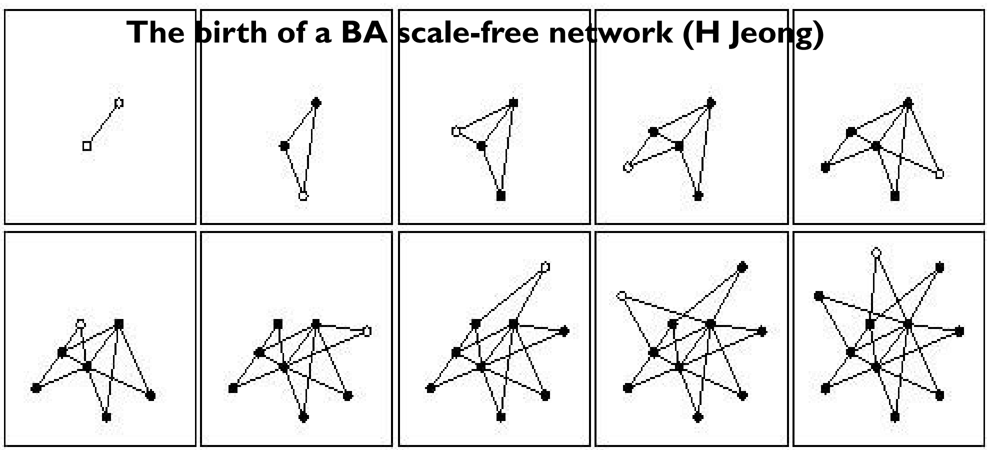
(A) Networks expand continuously by addition of new nodes

(B) New nodes attach preferentially to nodes already well-connected, i.e., probability that a new node is connected to a node of degree k_i is $\Pi(k_i)=k_i/\Sigma_j k_j$ ("*linear*" scheme)

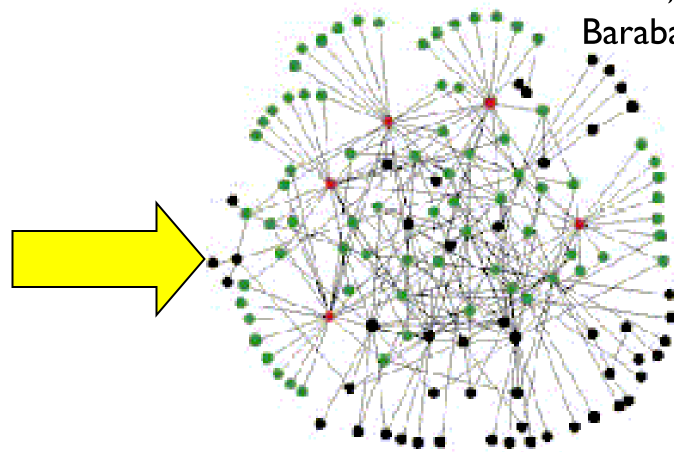


Albert, Jeong & Barabasi, 2000

Resulting network degree distribution: $P(k) \sim k^{-3}$



The birth of a BA scale-free network (H Jeong)



Characterised by highly connected "hubs", which hold the network together

Achilles' heel: Network fragile to directed attack on "hubs"

Why the degree distribution is *scale-free*

From

Statistical mechanics of complex networks

Reka Albert and Albert-Laszlo´Barabasi

Rev Mod Phys 74 (2002) 47-97

Continuum theory: The continuum approach introduced by Barabási and Albert (1999) and Barabási, Albert, and Jeong (1999) calculates the time dependence of the degree k_i of a given node i. This degree will increase every time a new node enters the system and links to node i, the probability of this process being $\Pi(k_i)$. Assuming that k_i is a continuous real variable, the rate at which k_i changes is expected to be proportional to $\Pi(k_i)$. Consequently k_i satisfies the dynamical equation

$$\frac{\partial k_i}{\partial t} = m\Pi(k_i) = m\frac{k_i}{\sum_{j=1}^{N-1} k_j}. \quad (79)$$

The sum in the denominator goes over all nodes in the system except the newly introduced one; thus its value is $\Sigma_j k_j = 2mt - m$, leading to

$$\frac{\partial k_i}{\partial t} = \frac{k_i}{2t}. \quad (80)$$

The solution of this equation, with the initial condition that every node i at its introduction has $k_i(t_i) = m$, is

$$k_i(t) = m\left(\frac{t}{t_i}\right)^{\beta} \quad \text{with} \quad \beta = \frac{1}{2}. \quad (81)$$

Equation (81) indicates that the degree of all nodes evolves the same way, following a power law, the only difference being the intercept of the power law.

Using Eq. (81), one can write the probability that a node has a degree $k_i(t)$ smaller than k, $P[k_i(t) < k]$, as

$$P[k_i(t) < k] = P\left(t_i > \frac{m^{1/\beta}t}{k^{1/\beta}}\right). \quad (82)$$

Assuming that we add the nodes at equal time intervals to the network, the t_i values have a constant probability density

$$P(t_i) = \frac{1}{m_0 + t}. \quad (83)$$

Substituting this into Eq. (82) we obtain

$$P\left(t_i > \frac{m^{1/\beta}t}{k^{1/\beta}}\right) = 1 - \frac{m^{1/\beta}t}{k^{1/\beta}(t + m_0)}. \quad (84)$$

The degree distribution $P(k)$ can be obtained using

$$P(k) = \frac{\partial P[k_i(t) < k]}{\partial k} = \frac{2m^{1/\beta}t}{m_0 + t}\frac{1}{k^{1/\beta + 1}}, \quad (85)$$

predicting that asymptotically $(t \to \infty)$

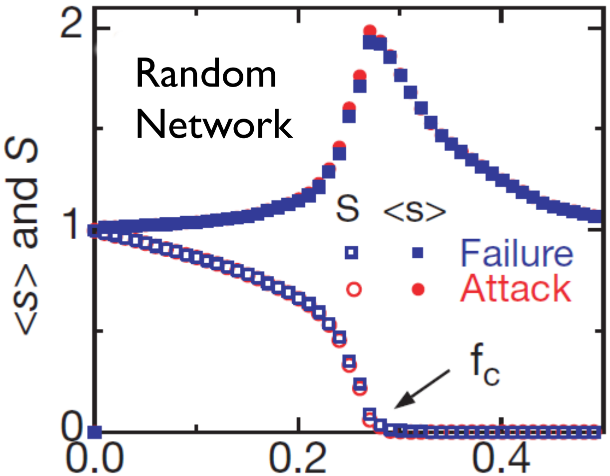
$$P(k) \sim 2m^{1/\beta}k^{-\gamma} \quad \text{with} \quad \gamma = \frac{1}{\beta} + 1 = 3 \quad (86)$$

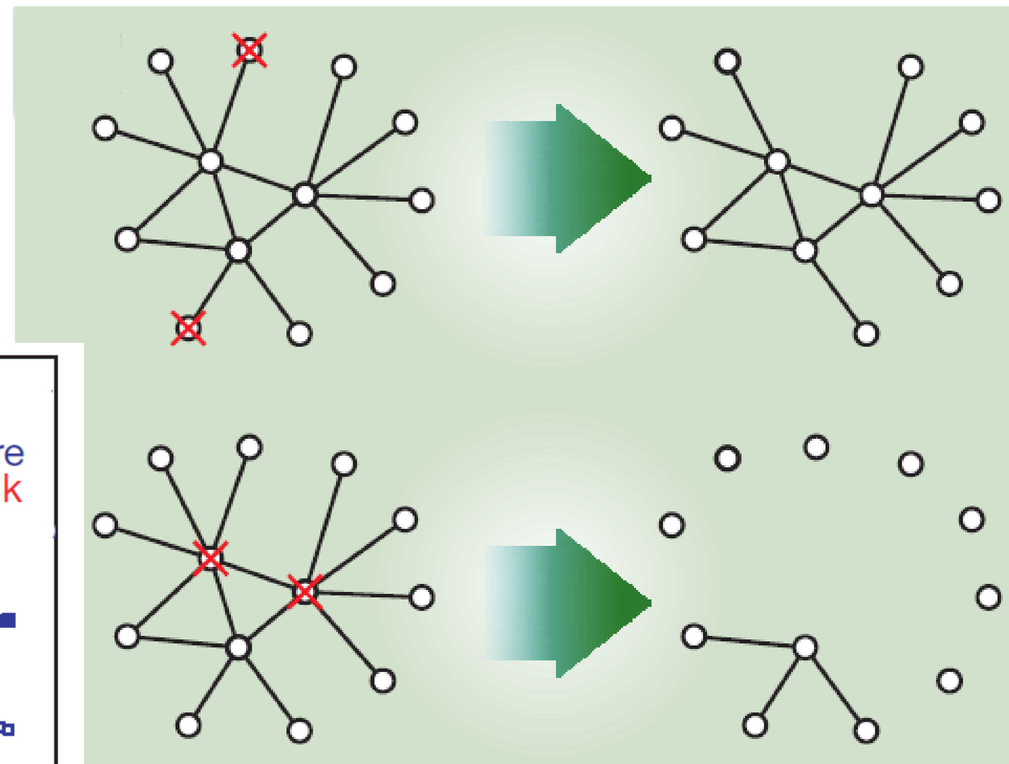
being independent of m, in agreement with the numerical results.

Importance of "hubs"

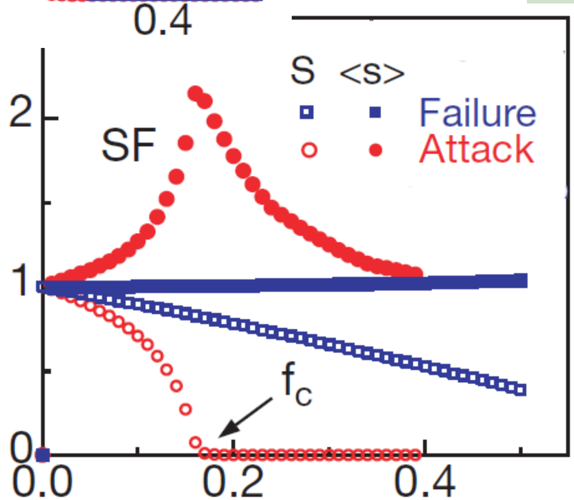
Random failure of nodes typically has little effect on scale-free network as most nodes connect only to a few other nodes: *Robustness to random node removal*

Newman 2008





S: relative size of largest cluster, and <s> : average size of the isolated clusters, shown as a function of the fraction of removed nodes



However targeting the highest-degree nodes (hubs) has devastating effect on the network – most nodes become isolated on removing a few hubs: *Vulnerability to targeted removal of hubs*

No threshold for epidemics in *scale-free networks*

Networks of sexual relations have been claimed to be scale-free !
A few highly promiscuous individuals act as "hub" nodes
May play a crucial role in spreading sexually transmitted diseases !

If the contact structure of a disease is network with inhomogeneous degree distribution, the condition for occurrence of an epidemic is:

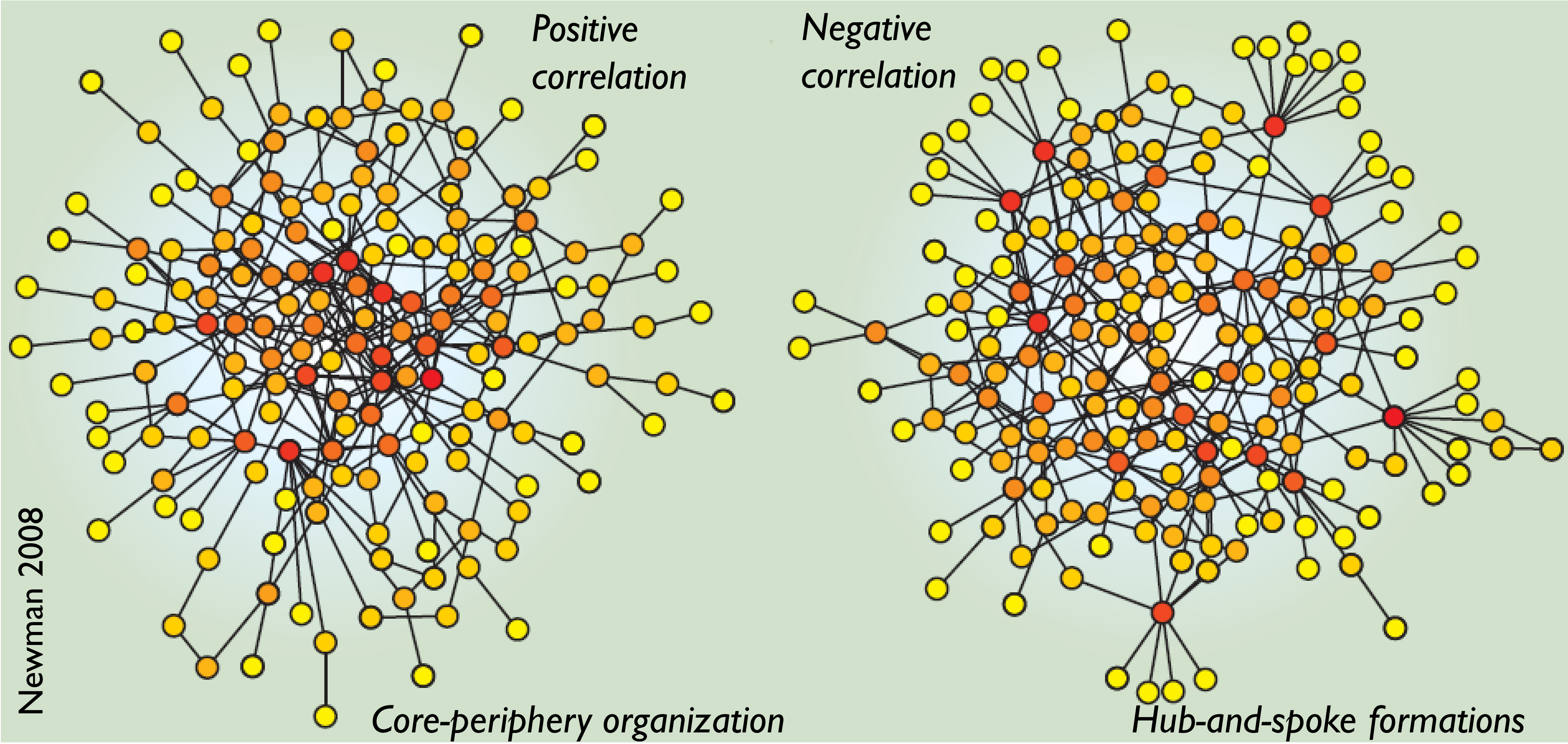
$$R = bN/g \quad > \quad \langle k \rangle / \langle k^2 \rangle$$

b: rate of infection spreading, g: recovery rate (=1/period of infection)
Initial popn of susceptibles, $S(t = 0) = N$, the total population

For a scale-free network having degree exponent $2 < \alpha \leq 3$, $\langle k^2 \rangle \to \infty$
$\Rightarrow$ There is no epidemic threshold !

Even diseases with extremely low transmission probabilities are likely to cause a major outbreak involving a signficant fraction of population

Nodes may prefer to connect to nodes with similar or dissimilar connectivity



Two networks may have the same degree distribution but different connectivity patterns overall because high-degree nodes may prefer to connect to other high-degree nodes (positive degree correlation) or may want to avoid them (negative degree correlation)

Measuring degree correlations

Random networks (e.g., random Price-Barabasi-Albert networks) do not exhibit any correlations between the degrees of connected nodes, i.e., The probability a link connects nodes of degrees k & k' is

$P(k,k') = k\,P(k)\,k'\,P(k') / \langle k \rangle^2$ (degree-uncorrelated network)

Most real-life networks exhibit degree correlations measured by

Assortativity, r

$$r = \frac{\frac{1}{L}\left(\sum_{i=1}^{L} j_i k_i\right) - \left(\frac{1}{L}\sum_{i=1}^{L} \frac{1}{2}(j_i + k_i)\right)^2}{\frac{1}{L}\left(\sum_{i=1}^{L} \frac{1}{2}(j_i^2 + k_i^2)\right) - \left(\frac{1}{L}\left(\sum_{i=1}^{L} \frac{1}{2}(j_i + k_i)\right)\right)^2}$$

(Newman, 2002)

j_i, k_i: degrees of vertices at ends of the i-th edge   L: total number of links

r < 0: disassortative mixing

Nodes of high degree mostly have nearest nbrs of low degree
E.g.,most biological & technolgical networks

r > 0: assortative mixing

Nodes of high degree mostly have nearest nbrs of high degree
E.g., social networks

Macroscopic properties of networks

Newman, *SIAM Review*, 2003

	network	type	# nodes n	# links m	avg degree z	avg path length ℓ	degree distrn exponent α	clustering coefficient $C^{(1)}$	clustering coefficient $C^{(2)}$	degree correln r
social	film actors	undirected	449 913	25 516 482	113.43	3.48	2.3	0.20	0.78	0.208
	company directors	undirected	7 673	55 392	14.44	4.60	–	0.59	0.88	0.276
	math coauthorship	undirected	253 339	496 489	3.92	7.57	–	0.15	0.34	0.120
	physics coauthorship	undirected	52 909	245 300	9.27	6.19	–	0.45	0.56	0.363
	biology coauthorship	undirected	1 520 251	11 803 064	15.53	4.92	–	0.088	0.60	0.127
	telephone call graph	undirected	47 000 000	80 000 000	3.16		2.1			
	email messages	directed	59 912	86 300	1.44	4.95	1.5/2.0		0.16	
	email address books	directed	16 881	57 029	3.38	5.22	–	0.17	0.13	0.092
	student relationships	undirected	573	477	1.66	16.01	–	0.005	0.001	−0.029
	sexual contacts	undirected	2 810				3.2			
information	WWW `nd.edu`	directed	269 504	1 497 135	5.55	11.27	2.1/2.4	0.11	0.29	−0.067
	WWW Altavista	directed	203 549 046	2 130 000 000	10.46	16.18	2.1/2.7			
	citation network	directed	783 339	6 716 198	8.57		3.0/–			
	Roget's Thesaurus	directed	1 022	5 103	4.99	4.87	–	0.13	0.15	0.157
	word co-occurrence	undirected	460 902	17 000 000	70.13		2.7		0.44	
technological	Internet	undirected	10 697	31 992	5.98	3.31	2.5	0.035	0.39	−0.189
	power grid	undirected	4 941	6 594	2.67	18.99	–	0.10	0.080	−0.003
	train routes	undirected	587	19 603	66.79	2.16	–		0.69	−0.033
	software packages	directed	1 439	1 723	1.20	2.42	1.6/1.4	0.070	0.082	−0.016
	software classes	directed	1 377	2 213	1.61	1.51	–	0.033	0.012	−0.119
	electronic circuits	undirected	24 097	53 248	4.34	11.05	3.0	0.010	0.030	−0.154
	peer-to-peer network	undirected	880	1 296	1.47	4.28	2.1	0.012	0.011	−0.366
biological	metabolic network	undirected	765	3 686	9.64	2.56	2.2	0.090	0.67	−0.240
	protein interactions	undirected	2 115	2 240	2.12	6.80	2.4	0.072	0.071	−0.156
	marine food web	directed	135	598	4.43	2.05	–	0.16	0.23	−0.263
	freshwater food web	directed	92	997	10.84	1.90	–	0.20	0.087	−0.326
	neural network	directed	307	2 359	7.68	3.97	–	0.18	0.28	−0.226