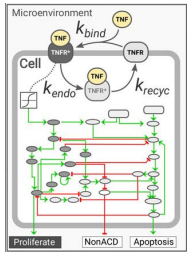
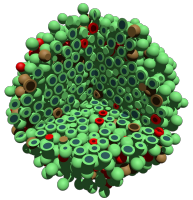
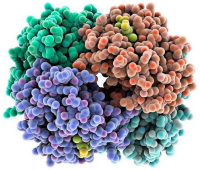
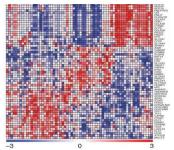




De las redes intracelulares a las simulaciones de sistemas multicelulares





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Tema 3

Fundamentos de teoría de grafos y redes complejas (Parte I)

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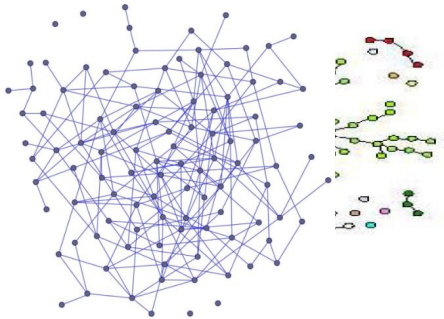
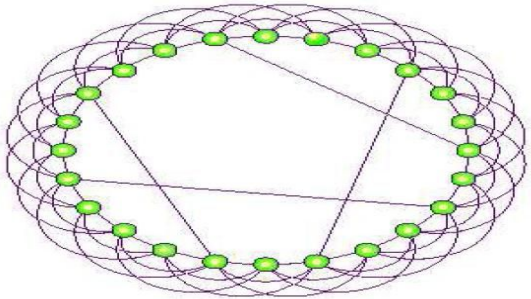
What is a network (graph) model?

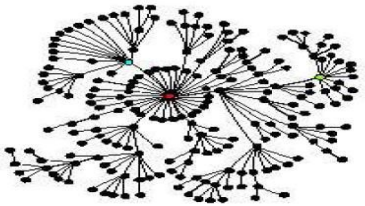
Erdös-Rényi (ER)



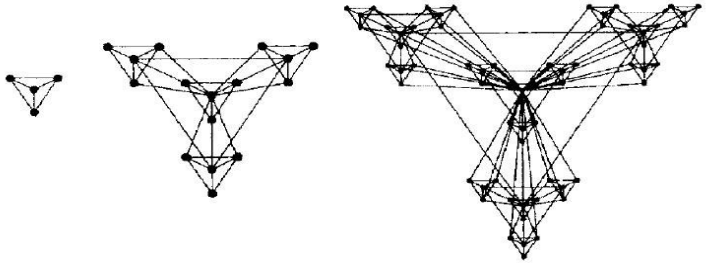
Small-World



Scale-Free (SF)

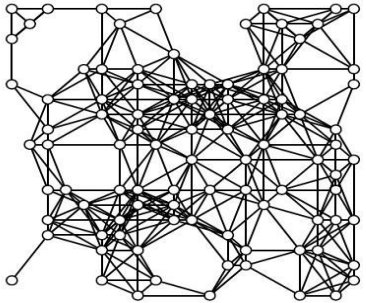


Hierarchical



(a) n=1; N=4 (b) n=2; N=16 (c) n=3; N=64

Geometric (GEO)



Does the model network fit the data?

- Use network properties:
  - Local
  - Global

Why?

- "Hardness" of graph theoretic problems
  - E.g. NP-completeness of subgraph isomorphism
    - Cannot exactly compare/align networks
      - Use heuristics (approximate solutions)
    - Exact comparison inappropriate in biology
      - Due to biological variation
- Noise revise models as data sets evolve

Why model networks?

- Understand laws reproduction/predictions

- Network models have already been used in biological applications:
  - Network motifs
    (Shen-Orr *et al.,* Nature Genetics 2002, Milo et al., Science 2002)
  - De-noising of PPI network data
    (Kuchaiev *et al.,* PLoS Comp. Biology, 2009)
  - Guiding biological experiments
    (Lappe and Holm, Nature Biotechnology, 2004)
  - Development of computationally easy algorithms for PPI nets that are computationally intensive on graphs in general

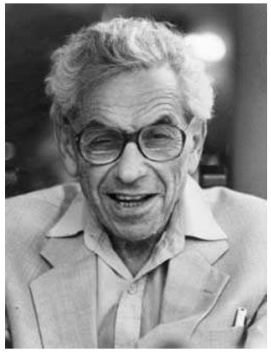
Network models

We will cover the following network models:

I. Erdos–Renyi random graphs
II. Generalized random graphs (with the same degree distribution as the data networks)
III. Small-world networks
IV. Scale-free networks
V. Hierarchical model

Erdos–Renyi random graphs (ER)

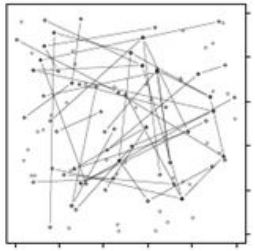
- Model a data network $G(V,E)$ with $|V|=n$ and $|E|=m$
- An ER graph that models G is constructed as follows:
  - It has n nodes
  - Edges are added between pairs of nodes uniformly at random with the same probability p
  - Two (equivalent) methods for constructing ER graphs:
    - $\boldsymbol{G_{n,p}}$: pick p so that the resulting model network has m edges
    - $\boldsymbol{G_{n,m}}$: pick randomly m pairs of nodes and add edges between them with probability 1

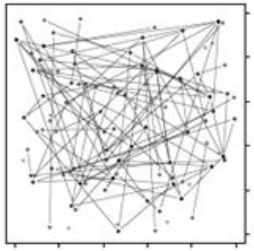


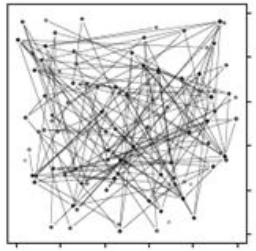
Erdös

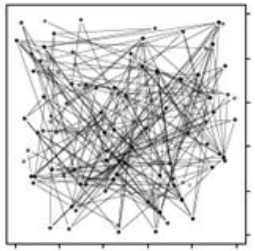
Rényi

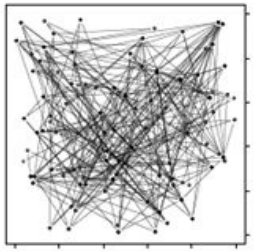
Erdös–Rényi

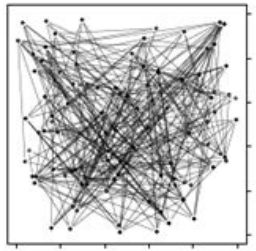












Erdos–Renyi random graphs (ER)

- Number of edges, |E|=m, in $G_{n,p}$ is:

$$|E| = \binom{n}{2} p = \text{pn(n-1)/2}$$

- Average degre

$$z = \frac{2|E|}{n} = \frac{2\binom{n}{2}p}{n} = (n-1)p$$

Erdos–Renyi random graphs (ER)

- Many properties of ER can be proven theoretically
  (See: Bollobas, "Random Graphs," 2002)
- Example:
  - When $m=n/2$, suddenly the giant component emerges, i.e.:
    - One connected component of the network has O(n) nodes
    - The next largest connected component has O(log(n)) nodes

Erdos–Renyi random graphs (ER)

- The **degree distribution** is binomial:

- For large *n,* this can be approximated with Poisson distribution:

$$P(k) = \frac{z^k e^{-z}}{k!}$$

where z is the average degree

- **However**, currently available biological networks have *power-law degree distribution*

Erdos–Renyi random graphs (ER)

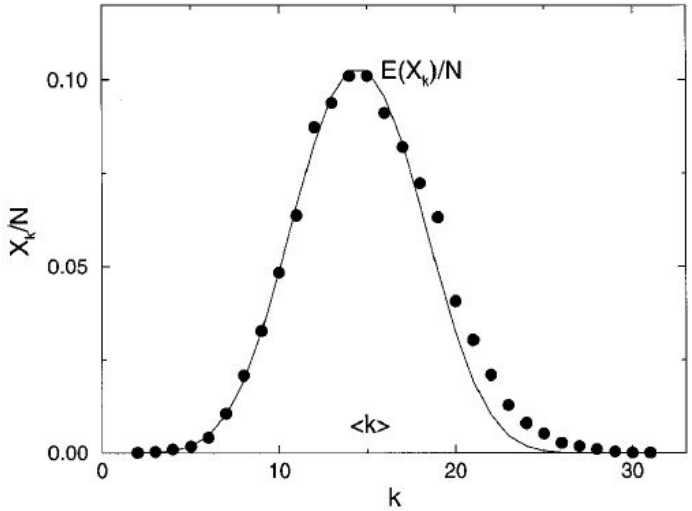


FIG. 7. The degree distribution that results from the numerical simulation of a random graph. We generated a single random graph with $N=10\,000$ nodes and connection probability $p=0.0015$, and calculated the number of nodes with degree k, X_k. The plot compares X_k/N with the expectation value of the Poisson distribution (13), $E(X_k)/N=P(k_i=k)$, and we can see that the deviation is small.

Erdos–Renyi random graphs (ER)

- **Clustering coefficient**, *C*, of ER is low (for low *p)*
- *C=p,* since probability *p* of connecting any two nodes in an ER graph is the same, regardless of whether the nodes are neighbors
- **However**, biological networks have *high clustering coefficients*

Erdos–Renyi random graphs (ER)

- **Average diameter** of ER graphs is small
  - It is equal to 
- Biological networks **also** have *small average diameters*
- **Summary**

	Deg. Distr.	Clust. Coef.	Avg. Diam.
Real Networks	Power-law	High	Small
ER	Poison	Low	Small
	✗	✗	✓

Generalized random graphs (ER-DD)

- Preserve the degree distribution of data ("ER-DD")
- Constructed as follows:
  - An ER-DD network has *n* nodes (so does the data)
  - Edges are added between pairs of nodes using the "stubs method"

Generalized random graphs (ER-DD)

- The “stubs method” for constructing ER-DD graphs:
  - The number of “stubs” (to be filled by edges) is assigned to each node in the model network according to the degree distribution of the real network to be modeled
  - Edges are created between pairs of nodes with “available” stubs picked at random
  - After an edge is created, the number of stubs left available at the corresponding “end nodes” of the edges is decreased by one
  - Multiple edges between the same pair of nodes are not allowed

Generalized random graphs (ER-DD)

- **Summary**

	Deg. Dist.	Clust. Coef.	Avg.Diam.
Real Networks	Power-law	High	Small
ER-DD	Power-law	Low	Small



- 2 global network properties are matched by ER-DD
- How about local network properties (**graphlet frequencies**)?
  - Low-density graphlets are over-represented in ER and ER-DD
  - **However**, data have lots of *dense graphlets*, since they have high clustering coefficients

Small-world networks (SW)

letters to nature

typically slower than ~1 km s^{-1}) might differ significantly from what is assumed by current modelling efforts[27]. The expected equation-of-state differences among small bodies (ice versus rock, for instance) presents another dimension of study; having recently adapted our code for massively parallel architectures (K. M. Olson and E. A, manuscript in preparation), we are now ready to perform a more comprehensive analysis.

The exploratory simulations presented here suggest that when a young, non-porous asteroid (if such exist) suffers extensive impact damage, the resulting fracture pattern largely defines the asteroid's response to future impacts. The stochastic nature of collisions implies that small asteroid interiors may be as diverse as their shapes and spin states. Detailed numerical simulations of impacts, using accurate shape models and rheologies, could shed light on how asteroid collisional response depends on internal configuration and shape, and hence on how planetesimals evolve. Detailed simulations are also required before one can predict the quantitative effects of nuclear explosions on Earth-crossing comets and asteroids, either for hazard mitigation[28] through disruption and deflection, or for resource exploitation[29]. Such predictions would require detailed reconnaissance concerning the composition and internal structure of the targeted object. □

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11. Hudson, R. S. & Ostro, S. J. Shape of asteroid 4769 Castalia (1989 PB) from inversion of radar images.

Collective dynamics of 'small-world' networks

Duncan J. Watts* & Steven H. Strogatz

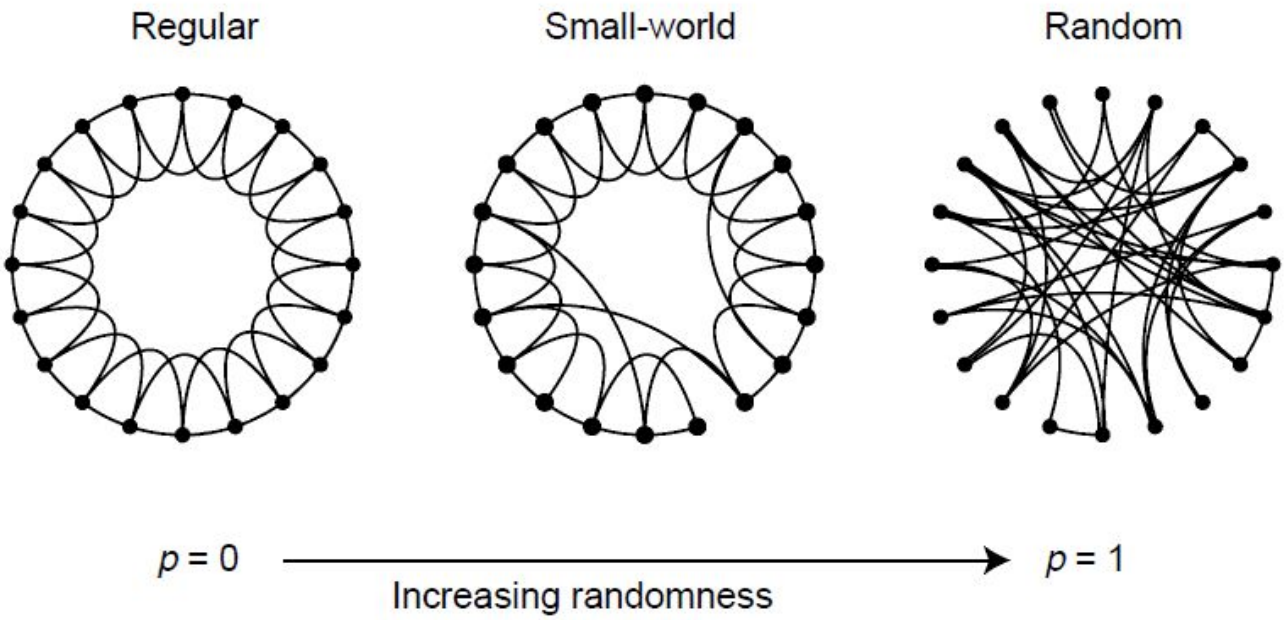
Department of Theoretical and Applied Mechanics, Kimball Hall, Cornell University, Ithaca, New York 14853, USA

Networks of coupled dynamical systems have been used to model biological oscillators[1–4], Josephson junction arrays[5,6], excitable media[7], neural networks[8–10], spatial games[11], genetic control networks[12] and many other self-organizing systems. Ordinarily, the connection topology is assumed to be either completely regular or completely random. But many biological, technological and social networks lie somewhere between these two extremes. Here we explore simple models of networks that can be tuned through this middle ground: regular networks 'rewired' to introduce increasing amounts of disorder. We find that these systems can be highly clustered, like regular lattices, yet have small characteristic path lengths, like random graphs. We call them 'small-world' networks, by analogy with the small-world phenomenon[13,14] (popularly known as six degrees of separation[15]). The neural network of the worm *Caenorhabditis elegans*, the power grid of the western United States, and the collaboration graph of film actors are shown to be small-world networks. Models of dynamical systems with small-world coupling display enhanced signal-propagation speed, computational power, and synchronizability. In particular, infectious diseases spread more easily in small-world networks than in regular lattices.

To interpolate between regular and random networks, we consider the following random rewiring procedure (Fig. 1). Starting from a ring lattice with n vertices and k edges per vertex, we rewire each edge at random with probability p. This construction allows us to 'tune' the graph between regularity ($p = 0$) and disorder ($p = 1$), and thereby to probe the intermediate region $0 < p < 1$, about which little is known.

Watts & Strogatz (1998) Nature

Small-world networks (SW)



Watts & Strogatz (1998) Nature

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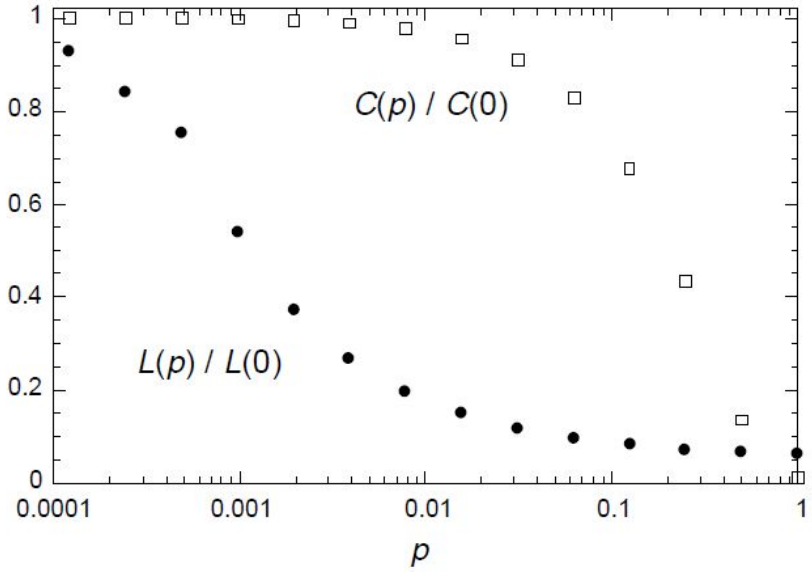
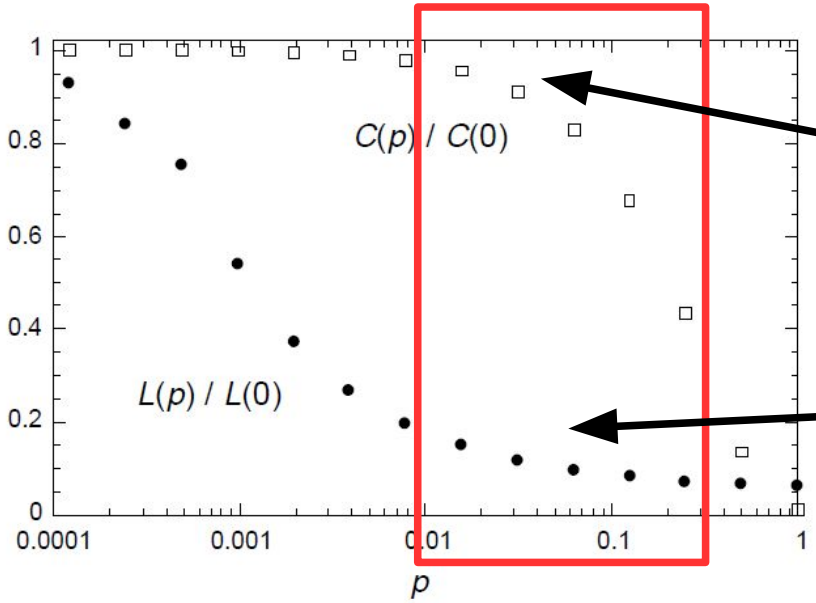


Table 1 Empirical examples of small-world networks

	L_{actual}	L_{random}	C_{actual}	C_{random}
Film actors	3.65	2.99	0.79	0.00027
Power grid	18.7	12.4	0.080	0.005
C. elegans	2.65	2.25	0.28	0.05

Watts & Strogatz (1998) Nature

Small-world networks (SW)



Clustering

Diameter

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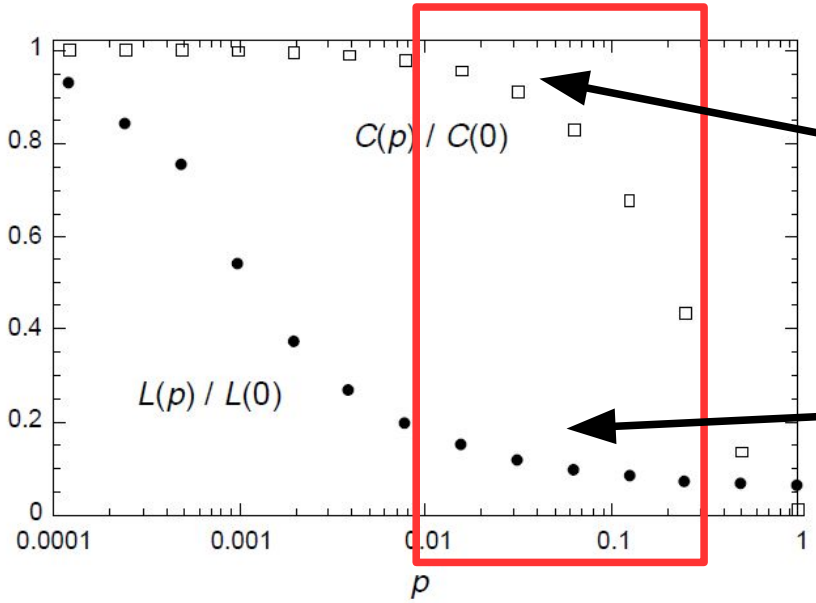

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Watts & Strogatz (1998) Nature

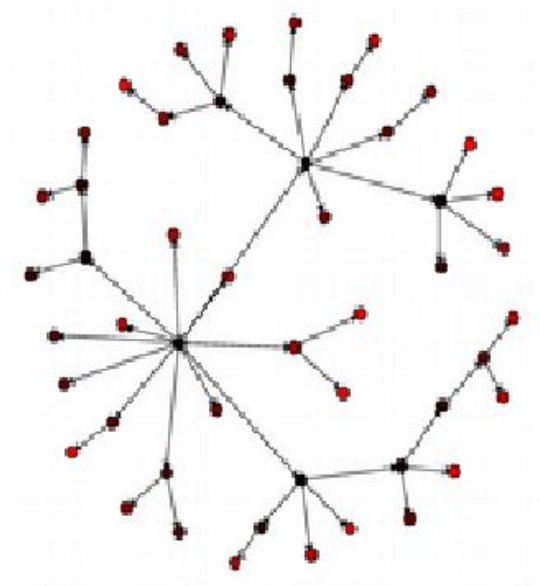
Small-world networks (SW)

- SW networks have:
- High clustering coefficients – introduced by “ring regularity”
- Large average diameters of regular lattices – fixed by randomly re-wiring a small percentage of edges
- Summary

	Deg. Dist.	Clust. Coef.	Avg.Diam.
Real Networks	Power-law	High	Small
SW	Poisson?	High	Small

Scale-free networks (SF)

- Power-law degree distributions: $P(k) = k^{-\gamma}$
  - $\gamma > 0; 2 < \gamma < 3$



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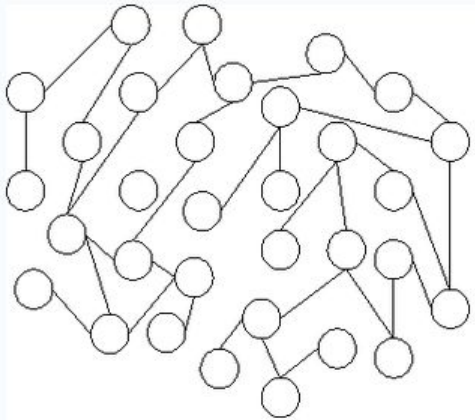
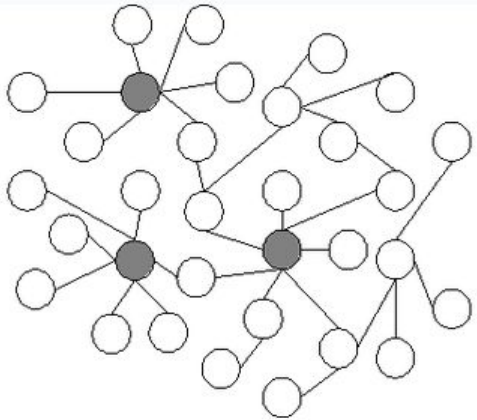
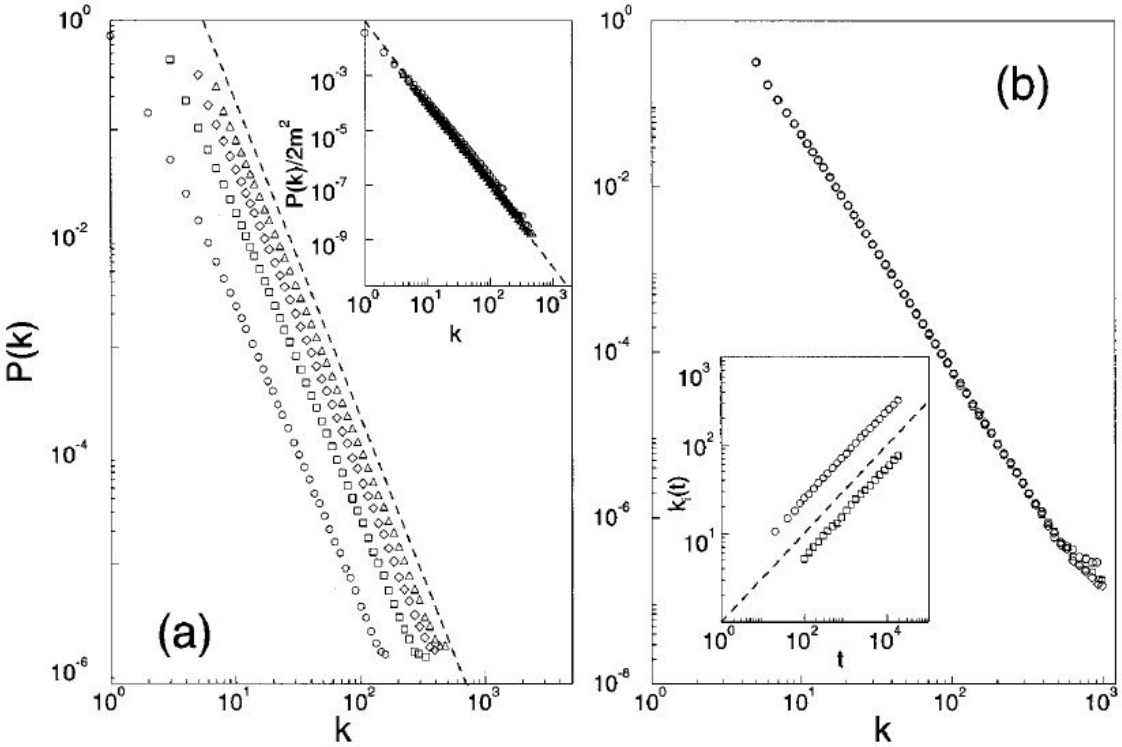


Random network



Scale-free network


(a)
P(k)
k
P(k)/2m²
k
(b)
k
k_i(t)
t

Scale-free networks (SF)

- Different models exist, e.g.:
  - Preferential Attachment Model (SF-BA) (Barabasi-Albert, 1999)
  - Gene Duplication and Mutation Model (SF-GD) (Vazquez *et al.*, 2003)

Scale-free networks (SF)

- Preferential Attachment Model (SF-BA)
  - "Growth" model: nodes are added to an existing network
  - New nodes preferentially attach to existing nodes with probability proportional to the degrees of the existing nodes; e.g.:

  - This is repeated until the size of SF network matches the size of the data
  - "Rich getting richer"
  - The starting network strongly influences the properties

Scale-free networks (SF)

- Gene Duplication and Mutation Model (SF-GD)
  - Biologically motivated
  - Attempts to mimic gene duplication and mutation processes

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Scale-free networks (SF)

- Gene Duplication and Mutation Model (SF-GD)
- At each time step, a node is added to the network as follows:

1. Start with a small, connected network.
2. Duplication:
   (a) Select node i at random.
   (b) A new node, i' is added and linked to all nodes that i is linked to; as such, the neighbourhoods of the two nodes are the same, i.e., $N(i) = N(i')$.
   (c) With probability p, add an edge between i and i'.
3. Divergence/mutation:
   (a) For each node j linked to nodes i and i' described above, choose one of the two links randomly and remove it with probability q.
4. Repeat steps 2 and 3 until the number of of nodes is similar to that of empirical network to be modeled.

The parameters of this gene duplication & mutation model are p and q.

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Scale-free networks (SF)

- **Summary**

	Deg. Dist.	Clust. Coef.	Avg.Diam.
Real Networks	Power-law	High	Small
SF	Power-law	Low	Small

Hierarchical model

- Preserves network “modularity” via a fractal-like generation of the network