Effects of topology on network evolution
Supplementary information

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Boolean Threshold Dynamics The states of the nodes are updated simultaneously at every time step according to the threshold rule depicted in Fig.1C. The state of a given node i at time $t+1$ depends on the state of K_i other nodes at time t, where K_i is the number of inputs for node i. We model the interactions between nodes using the connectivity matrix w_{ij}, in which each coefficient is positive or negative and represents an activating (positive) or inhibiting (negative) interaction between nodes i and j, and $w_{ij}=0$ when there is no interaction. The weights w_{ij} are distributed uniformly in the interval $(-1, 1)$. To determine whether a node is active or inactive (value 1 or 0) we sum all its' interactions and compare them to a given threshold which here is set to 0. Threshold rules (Fig.1C) allow us to implement nodes with large numbers of inputs at relatively low computational cost compared to Boolean Kauffman Networks[1,2]. For reasons explained in Supplementary Information we modify the rules for all $K_i = 1$ nodes as follows to be $\sigma_i (t+1) = \sigma_j (t)$ if $w_{ji} > 0$ and $\sigma_i (t+1) = \neg \sigma_j (t)$ if $w_{ji} < 0$.

Importance of poorly connected nodes ($K_i = 1$) Because nodes with one connection represent a large part of the nodes in scale-free networks (e.g. 83% for $\gamma=3.0$ and 61% for $\gamma=2.0$), poorly connected nodes may play an important role in the dynamics of networks. We find that the updating rules of the $K_i = 1$ nodes is essential in the dynamics of scale-free networks for any value of the exponent γ (see Fig.S3). Similarly, the dynamics of homogeneous random networks with low connectivity $\langle K \rangle$ depend strongly on the updating rules of poorly connected nodes. The threshold rules in Fig.1C for the $K_i = 1$ nodes determine the value of these nodes that are frozen in one state. For example, when a node has the value $\sigma_i (0) = 1$ with a negative weight $w_{ji} < 0$, it then will either take the value 0 from the first step and remain 0 for ever, or it will remain 1 for a few time steps and then take the value 0 thereafter. The fact that the nodes with connectivity $K_i = 1$ create a large set of components that are frozen in one state prevents the networks from exhibiting rich dynamics. We therefore modify the rules for every node with $K_i = 1$ node as follows: ($\sigma_i (t+1) = \sigma_j (t)$ if $w_{ji} > 0$ and $\sigma_i (t+1) = \neg \sigma_j (t)$ if $w_{ji} < 0$).

Advantages of Boolean Threshold Networks In Kauffman networks, each node with K_i inputs is associated with a truth table of size 2^{K_i}. Therefore, such exponential complexity may be a limitation for numerical studies of Kaufmann networks[3,4 5]. As for threshold rules (Fig.1C) the state of a node with K_i inputs is the sum of K_i numbers, and the associated complexity of the calculation grows linearly with K_i. Consequently, BTNs are convenient for simulating numerically (within practical computational times) the dynamics of networks with large connectivity and scale-free distributions.

Generation of directed networks Random networks are generated using the binomial model described in [6]. In our study, scale-free networks have inward and outward connection distributions which are both power-law. In general, in order to generate scale-free networks we implement the configuration model[7,8] (CM). Since the networks are directed, we have to discriminate between networks that have only in- or out- or both degrees scale-free distributed. For networks with only in- or out degree being scale-free, we choose the corresponding degree k_i of every node using a power law random number generator. The connections between nodes are then assigned by picking the k_i connections for every node at random avoiding identical connections (self connections are here allowed because the graph is directed). In the case when both in- and out-degrees are scale-free, we first assign the out-degree k_i^{out} of every node according to the

distribution; then, we assign the in-degree k_i^{in} for every node (such that $\sum_N k_i^{out} = \sum_N k_i^{in}$). The connections are then assigned: for every node from which k_i^{out} connections start (tail of the arrow) we choose the other end of the connection (head) randomly out of the set of nodes that have not yet been assigned all of their inputs. In order to be able to assign all connections without identical arrows, we first assign as inputs the nodes with high k_i^{out}.

The only difference between the CM and the UCM algorithm is a cut-off $k_c = \sqrt{\langle K \rangle \cdot N}$ imposed on the degree of every node[9]. The CM algorithm has a natural cut-off $k_c^{CM} \propto N^{\frac{1}{\gamma-1}}$, given by the fact that we draw N numbers from a power-law distribution. Imposing the cut-off eliminates degree correlations between nodes. We compared the two algorithms (Fig.S12); imposing the new cut-off has small influence on the evolutionary paths of scale-free networks.

Network Size The network size is *500* nodes (*N=500*). The size of the network is large enough in order to clearly distinguish scale-free from random topology. The defining feature of a scale-free network is the existence of nodes with large numbers of connections. However, these connections cannot be observed unless $N>>\langle K \rangle$. When $\langle K \rangle$ and N are comparable the probability of finding a highly connected node is approximately equal for both topologies. Additionally, for random networks with $\langle K \rangle << N$ finite size does not affect the distribution of connections, while for scale free networks the finite size puts a cut-off on the possible number of connections.

$$P_{SF}(k) = \frac{k^{-\gamma}}{\sum_{k=1}^{N} k^{-\gamma}} \qquad for\ N \geq k \geq 1 \qquad \textbf{(1)}$$

Phase Transition Calculation

Imagine we choose a network and make two copies with slightly different initial conditions $\{\sigma_i^{(1)}\}$ and $\{\sigma_i^{(2)}\}$. We monitor the propagation of the difference in terms of the hamming distance:

$$d(t) = \frac{1}{N} \sum \left| \sigma_i^{(1)}(t) - \sigma_i^{(2)}(t) \right| \qquad \textbf{(2)}$$

In order to calculate the critical point, we use the annealed approximation introduced by Derrida and Pomeau [10]:

$$M = \left. \frac{\partial d(t+1)}{\partial d(t)} \right|_{d(t)=0} = \sum_{k_i=1}^{\infty} P(k_i) \cdot k_i \cdot p_s(k_i) \qquad \textbf{(3)}$$

The function M is a measure of the noise propagation within the network. If $M > 1$, the network is in the chaotic phase; if $M < 1$, the network is in the frozen phase. $M = 1$ gives the condition for criticality. $p_s(k)$ is the probability that a change of state of one arbitrary input of the node i at time t changes the state of the output of this node i at t+1. This quantity is also known as the local probability of noise propagation [11,12]. In order to determine the critical point for BTNs we need to calculate $p_s(k)$. This calculation depends on the updating rules of the network. Using the threshold rules (Fig.1C) we find [13]:

$$p_s(k_i) \propto k_i^{-0.5} \quad \textbf{(4)}$$

Remarkably, the local probability of noise propagation, $p_s(k_i)$, depends on the connectivity k_i of each node. Consequently, the quantity M in eq.(1) depends not only on $\langle K \rangle$ like in Kauffman networks[14], but on the higher moments of the distribution $P(k)$. As a result, scale-free and homogeneous random networks with the same average connectivity can exhibit different dynamical behavior[11,15]. Random networks exhibit chaotic behavior for $\langle K \rangle$ larger than $K_c = 3.83$ and scale-free networks exhibit chaotic behavior for exponents γ lower than $\gamma_c = 2.42$ for $N \to \infty$ and $\gamma_c = 2.4$ for $N = 500$ [13].

The effect of mutations We want to estimate the probability that a mutation, which changes the dynamics of a random node, affects the dynamics of the output node. This is roughly the probability that this dynamical mutation propagates at distance λ:

$$\langle P \rangle \approx \langle P_{dyn} \rangle^{\lambda} \quad \textbf{(5)}$$

where $\langle P_{dyn} \rangle$ is the probability that a perturbation of the dynamics of a given node affects the dynamics of a directly connected node. To estimate the average distance between nodes in a directed graph with arbitrary degree distribution we use the notation in [16], where

$$x = 1 + \frac{\log(N/z_1)}{\log(z_2/z_1)}$$

for directed graphs with uncorrelated in and out degrees $z_2 = \langle K_{in} K_{out} \rangle = \langle K \rangle^2$ and $z_a = \langle K \rangle$. Hence

$$x = \frac{\log(N)}{\log(\langle K \rangle)} \quad \textbf{(6)}$$

for any degree distribution. For scale-free networks the average connectivity is simply $\langle K \rangle = \sum_{k=1}^{N} k^{-\gamma+1} \Big/ \sum_{k=1}^{N} k^{-\gamma}$. In the previous section we calculated the probability $p_s(k_i)$ that a change in one arbitrary input of a node with k connections changes the state of that node. Let's assume that we mutate a given node i in a way that changes its dynamics (the time series of its status). If there is a connection between the mutated node i and another node j, the average probability that the dynamics of j changes is:

$$\langle P_{dyn} \rangle = \sum_{k=1}^{N} p_s(k_i) P(k_i) \quad \textbf{(7)}$$

which depends on the connectivity distribution. We insert eq.6 and 7 in eq.5 to calculate $\langle P \rangle$ (see Fig.S9). The probability is at least two orders of magnitude smaller for all values of $\langle K \rangle$ and γ that were used.

Computational time A typical evolutionary run ($\langle K \rangle = 2$, $L_c = 10$, $N = 500$) took approximately 1.5hrs on a single 2.4 GHz Pentium Xeon processor. The networks and the evolutionary algorithm were implemented in C programming language.

Comparison of random and scale-free networks with equal connectivity We compared networks with the same average connectivity which is the 'natural' choice, since if we were to rearrange the connections of one network we could construct the other. However, there could be more than one way of comparing networks of different topologies. For example, we can compare networks that have similar dynamical properties as measured by the function M defined in Eq.(3). We could therefore compare networks within the same dynamical phase, i.e. random networks of small connectivity with scale-free networks with large degree exponent γ and vice versa. However, our results show that the convergence of the fitness function of scale-free networks is always superior to that of random networks independent of the values of $\langle K \rangle$ and γ.

Targets of smaller cycle length It is difficult to characterize what the role of the distribution of cycle length is on evolution of networks. It has been demonstrated[17] for Boolean dynamics that random networks with small $\langle K \rangle$ (in the ordered phase) have short cycles while networks with large $\langle K \rangle$ (in the chaotic phase) have a broader distribution of cycles. However, scale-free networks always evolve faster than random networks independent of the specific values of $\langle K \rangle$ and γ. We performed a series evolutionary runs (Fig.S17) where the cycle length of the target function is much shorter ($L_c=2$ and $L_c=3$) than that discussed in main text. For this target function, we find that scale-free networks still perform better.

Dependence of simulations on parameters We have checked our results for various types of target tasks. We varied the length of the target function L_c from 1 to 50, the mutation rate μ from 0.001 to 0.1 and the number of output nodes N_{out} from 1 to 500. We found that the difference between evolutionary paths of the two topologies is suppressed only when the target function is too "hard", namely when N_{out} is more than 50, or when the task is trivial $L_c = 1$.

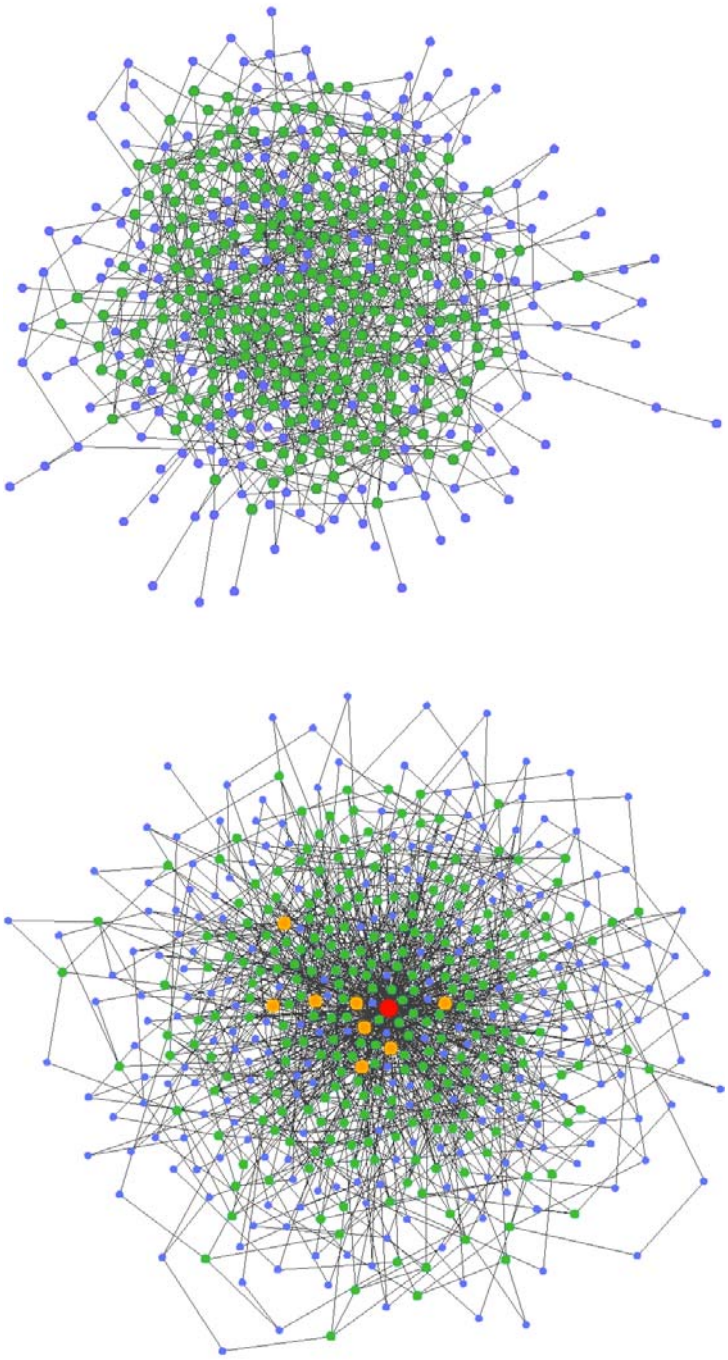
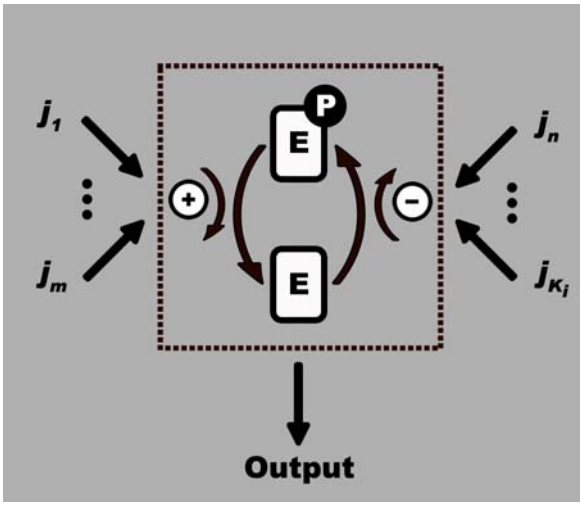


Figure S1: Heterogeneous versus homogeneous topology – Random networks (A) and scale-free networks (B). Networks are represented as undirected graphs for simplicity. Each network has *500* nodes. Nodes are colour coded according to their connectivity: (blue) 1-3 connections; (green) 4-10; (orange) 11-100; (red) over 100.

A.



B.

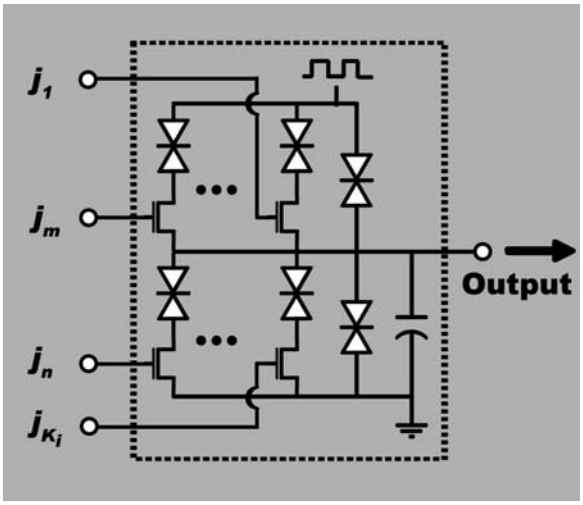
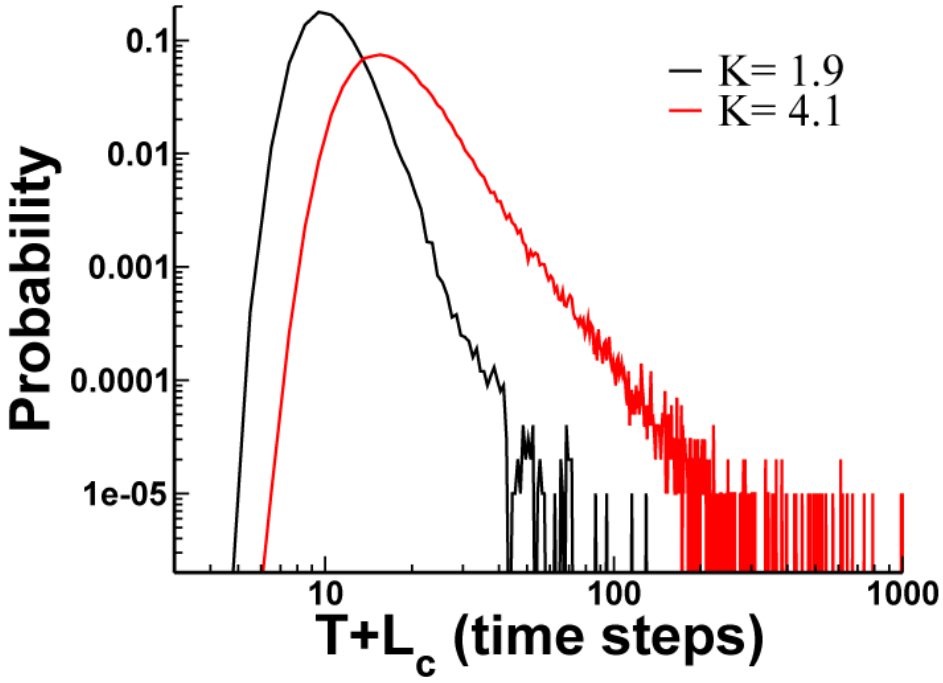


Figure S2: Boolean threshold rules **(A)** Example of a covalent modification reaction of an enzyme that exhibits a switch-like behaviour between two states, phosphorylated (active state) or unphosphorylated (inactive state). The forward and backward reaction rates are controlled by catalyst proteins represented by positive or negative inputs. **(B)** Electronic implementation of the threshold rule. A threshold gate with an arbitrary number of inputs is implemented using nano-electronic devices[18] (Monostable Bistable Logic Element). These devices are built from RTDs (resonant tunneling devices) and HFETs (hetero junction field-effect transistors). The circuit represents a node where positive (negative) weight inputs correspond to the upper (lower) half of the circuit.

A.


Probability
0.1
0.01
0.001
0.0001
1e-05
10
100
1000
T+L_c (time steps)
K= 1.9
K= 4.1

B.

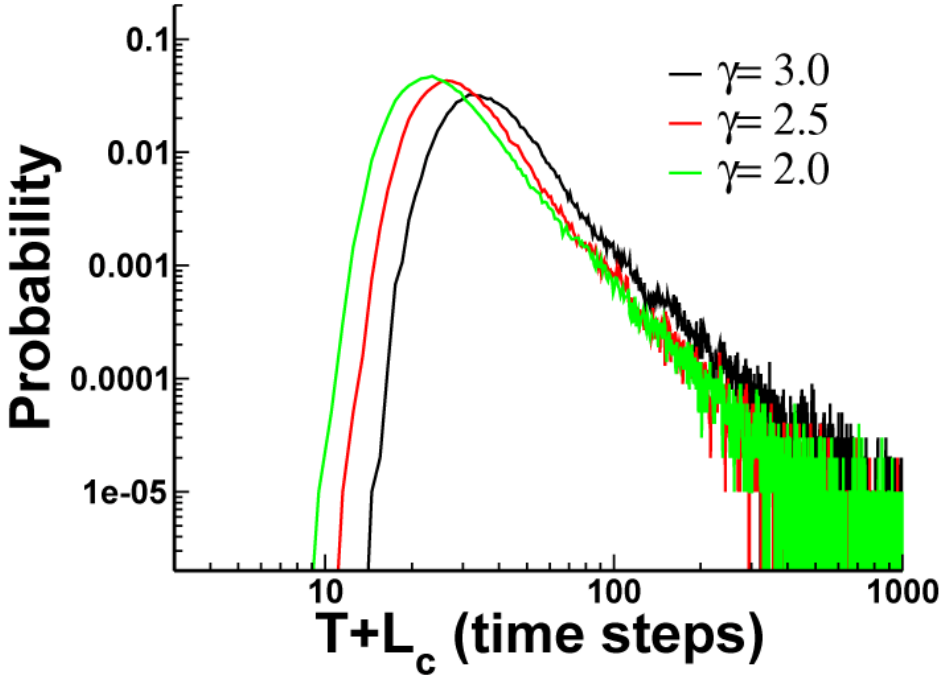

Probability
0.1
0.01
0.001
0.0001
1e-05
10
100
1000
T+L_c (time steps)
γ= 3.0
γ= 2.5
γ= 2.0

Figure S3: Probability distributions of the number of time steps $T+L_c$ needed for a network to complete its first cycle, where T is the transient time and L_c is the length of the cycle. We found that in all categories of networks plotted at least 99% of sampled networks had $T+L_c<t_{max}=350$ where t_{max} is the cut-off used in the calculation of the fitness (see Methods). The distribution is calculated from a sample of *10000* randomly generated networks. We chose an upper limit of number of time steps $(T+L_c)_{max}=2000$. **(A)** Distribution of Random homogeneous networks with $\langle K\rangle = 1.9$ and $\langle K\rangle=4.1$; for chaotic networks $T+L_c$ was above $(T+L_c)_{max}$. **(B)** Distribution of scale-free networks with $\gamma=3.0$, $\gamma=2.5$, and $\gamma=2.0$.

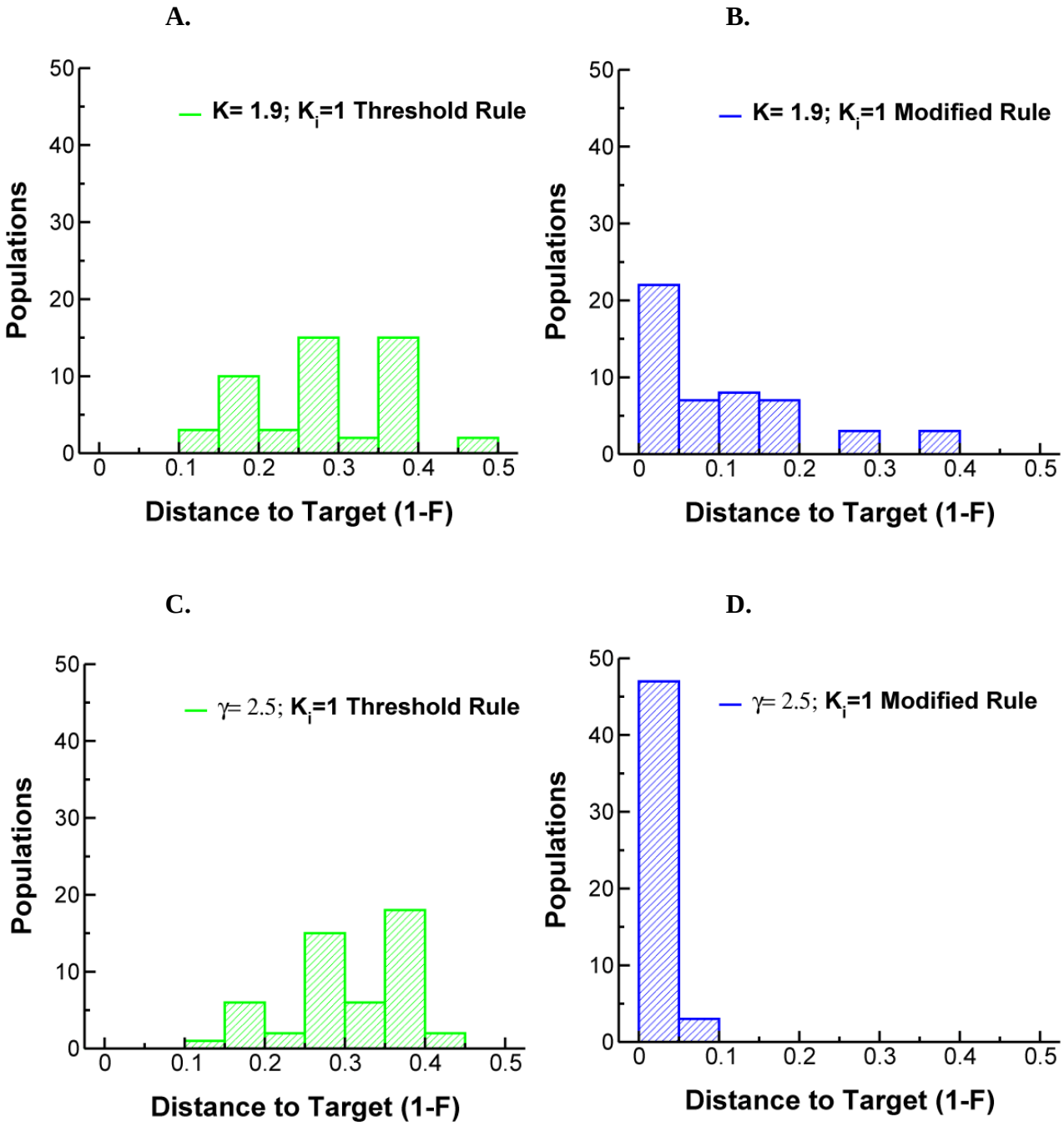


Figure S4: Importance of the dynamics of $K_i = 1$ rules. Despite the heterogeneity of scale-free networks it seems that poorly connected nodes are crucial to perform any interesting dynamics. The same is true for sparsely connected random networks. **(A), (C)**: Distribution of final value of the fitness for networks that have $K_i = 1$ nodes following the threshold rule (and become eventually frozen). **(B), (D)**: $K_i = 1$ rules are modified to either follow or negate the input of the node (final fitness of *50* runs for each case). The network output is chosen to be a highly connected node for the scale-free networks and $K^{out}_i \neq 1$ for random topology. After *10000* generations networks with the modified rules are able to evolve towards the target much better than for the networks with the $K_i = 1$ nodes following the threshold rule. We obtain similar behavior when the states of the $K_i = 1$ nodes are randomly updated.

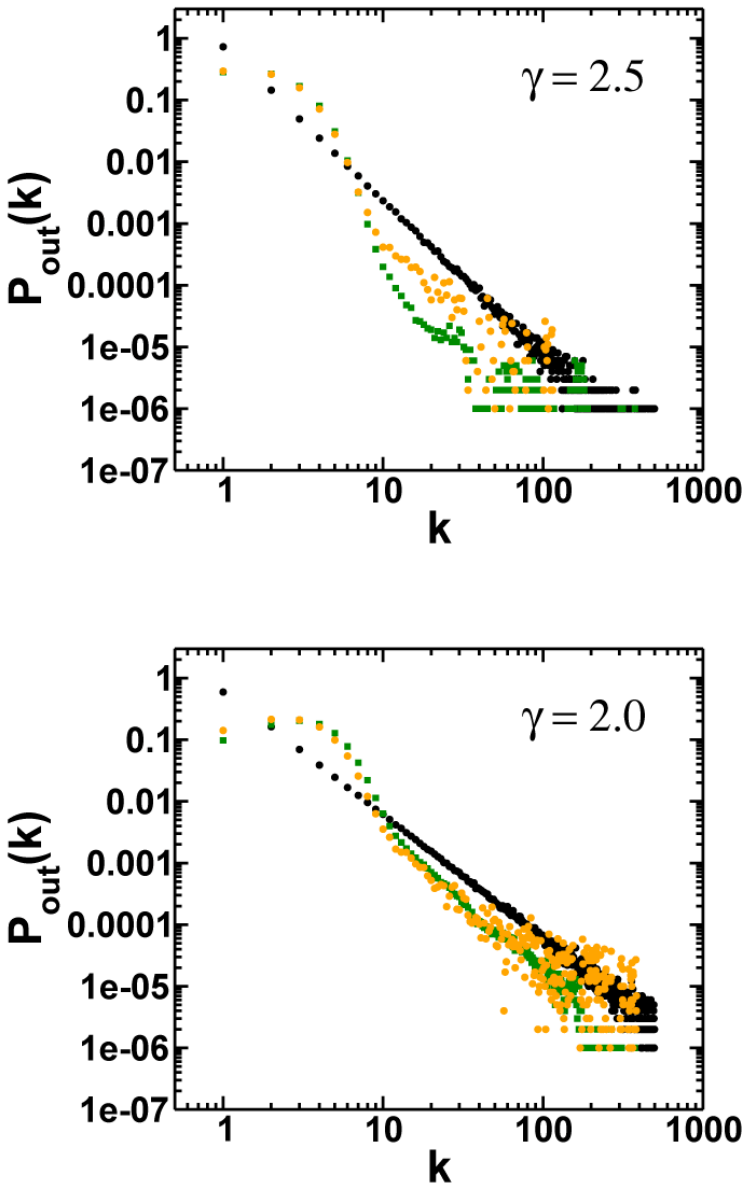


Figure S5: Distribution of out-going connections $P_{out}(k)$ in an initial population of scale-free networks (black), in an evolved population after *10000* generations (orange), and in a randomly mutated population without selection (green). Due to the nature of the mutations described in Methods (see main text), the in-coming distribution of connections remains scale-free while the out-going distribution can change. In this graph we see that $P_{out}(k)$ evolves as if there was no particular selection (orange and green distributions look similar).

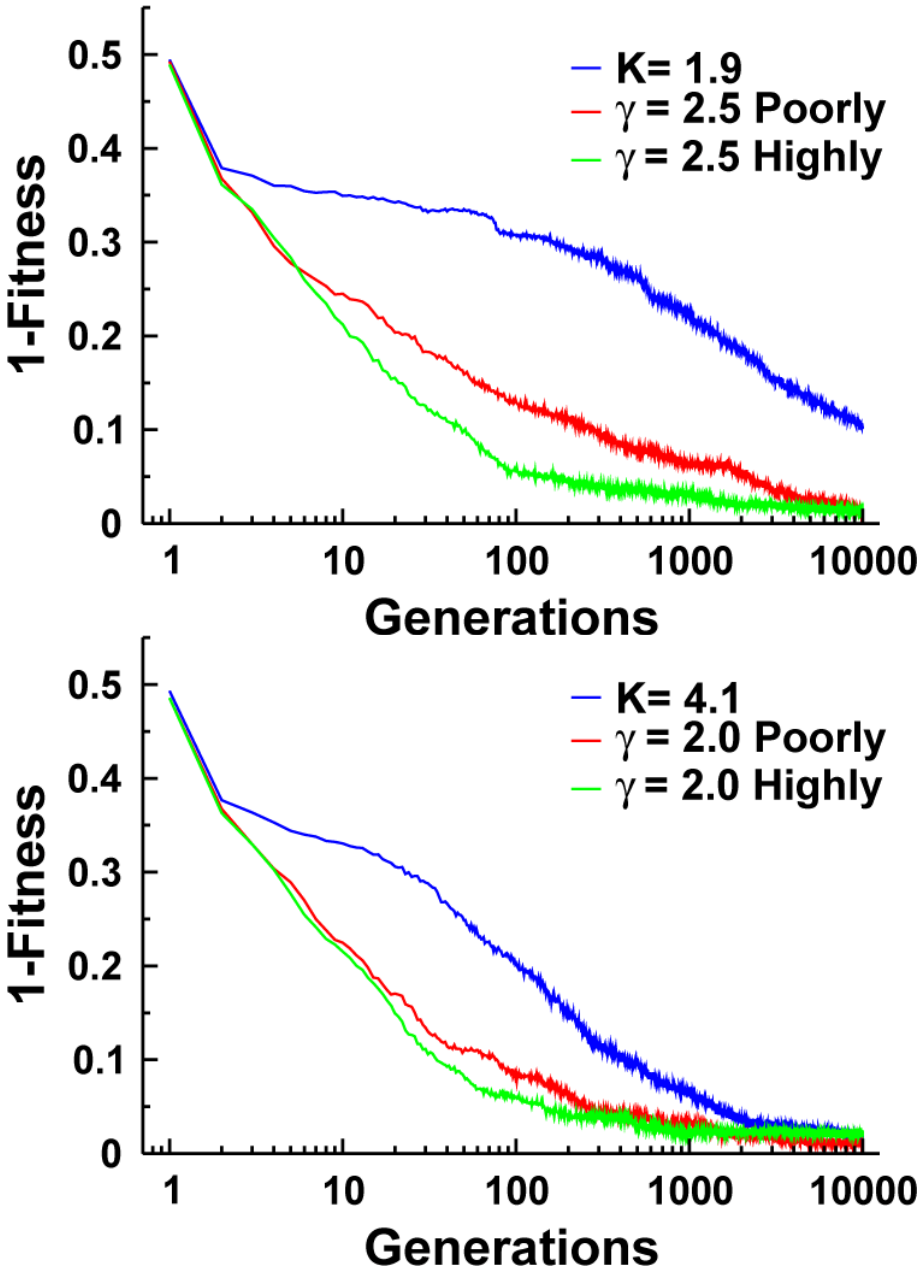


Figure S6: Average evolution for networks of random and scale free topology. Average fitness of *50* independent evolutionary paths *(N_{pop}= 50, N= 500, L_c = 10* and *μ = 0.02)*. We compare random and scale-free networks with the same connectivity *‹K›;* (A): *γ = 2.5 - ‹K›= 1.9*; (B): γ = 2.0 - *‹K›= 4.1*. The fitness of scale-free networks with poorly-connected output nodes has the same qualitative behaviour as the one of scale-free networks with highly-connected output nodes. However, for all exponents *γ*, the fitness function associated with a highly connected output node (many inputs) converges faster than that of a poorly connected node. This indicates that the computation is made at the highly connected nodes and then distributed to the rest of the network.

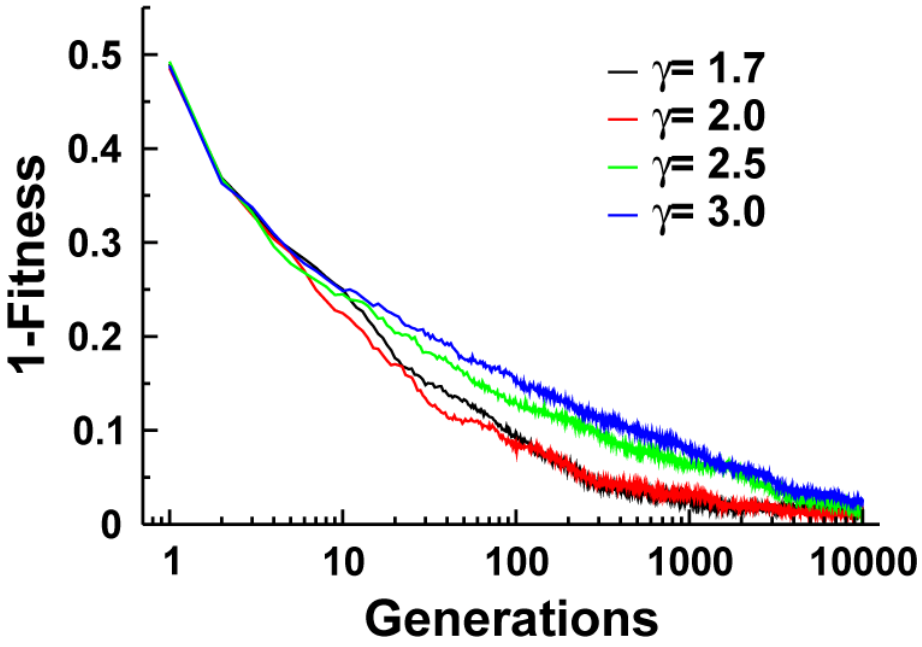


Figure S7: Mean evolutionary path for scale-free networks in which the output node is poorly connected ($K_i = 1$). The plot shows the average fitness of *50* independent evolutionary paths ($N_{pop}= 50$, $N= 500$, $L_c = 10$ and $\mu = 0.02$). The fitness of scale-free networks with poorly-connected output nodes have the same qualitative behaviour as scale-free networks with highly-connected output nodes.

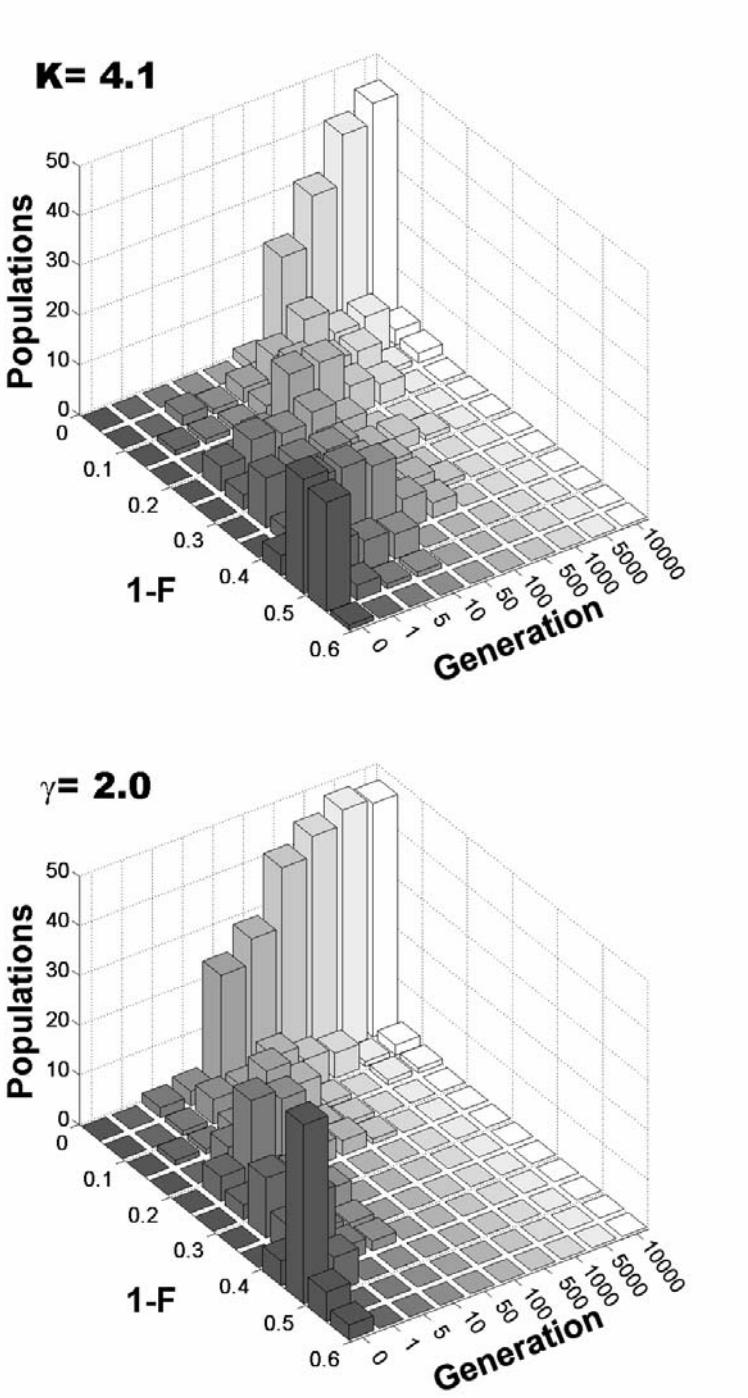


Figure S8: Distribution of the fitness of 50 populations as a function of generation time. **(A)** $\langle K \rangle = 4.1$ random homogeneous networks. The length of the plateaus becomes smaller for larger values of $\langle K \rangle$ and the transitions can be either gradual or punctuated. However, we still observe waiting periods interrupted by transitions from one level of fitness to another.and **(B)** Scale-free networks with $\gamma = 2.0$. Similar to Fig.3B in main text.

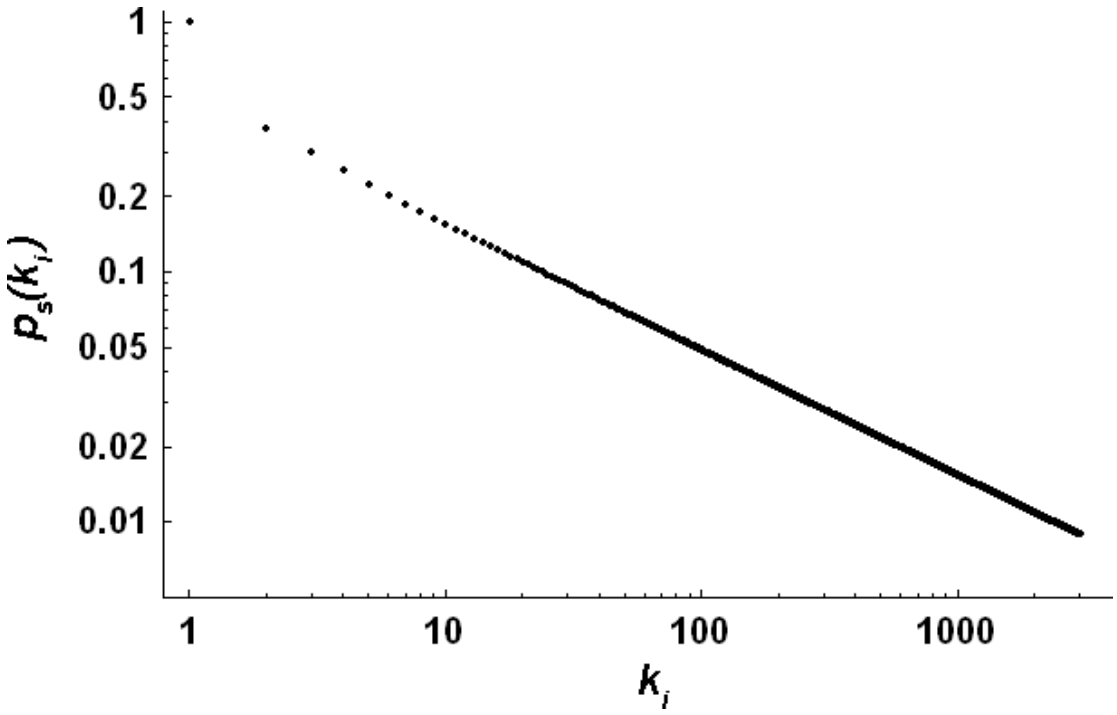


Figure S9: The probability $p_s(k_i)$ that the output of a function is altered if we change one of the inputs.

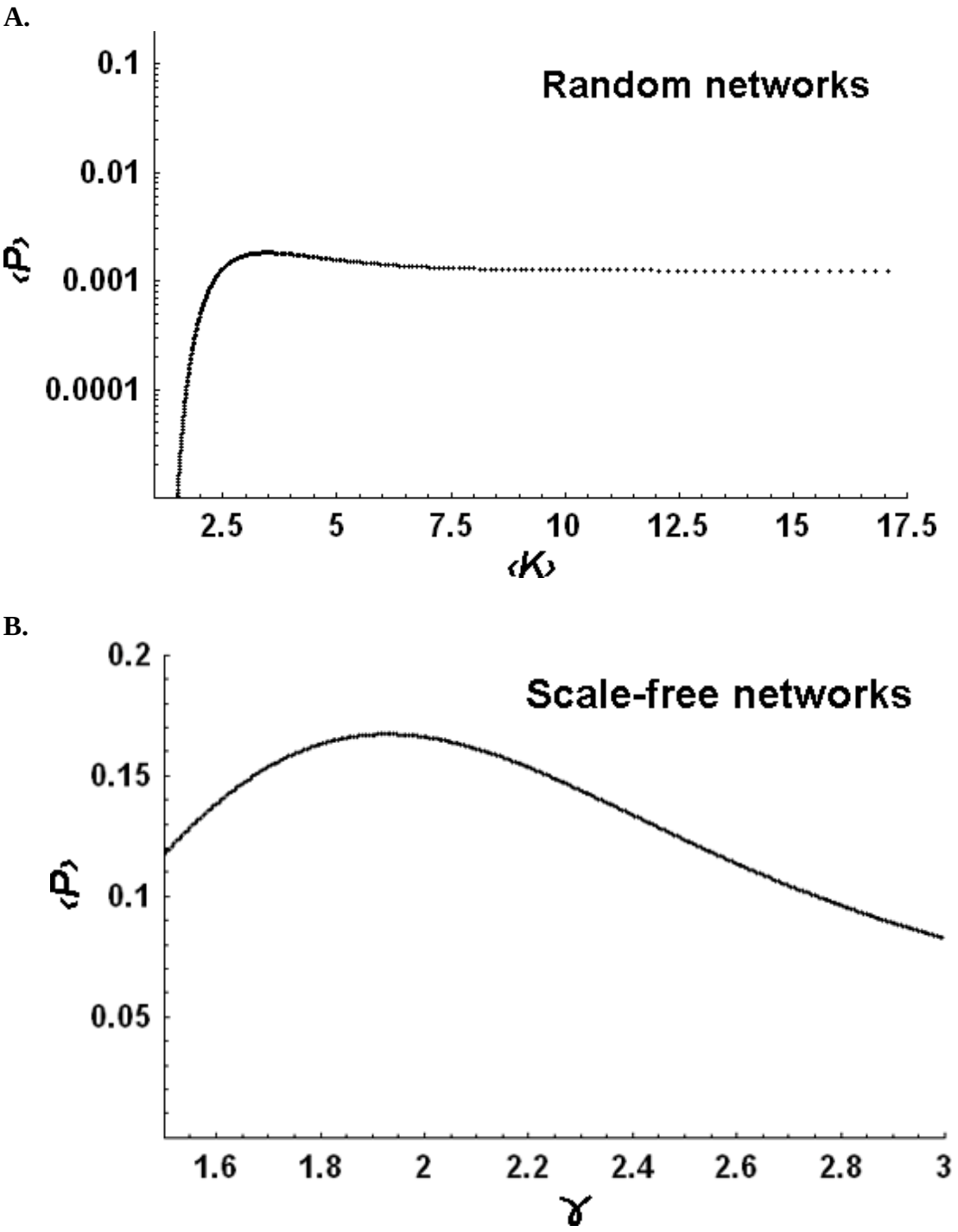


Figure S10: Probability that a random mutation affects the output signal as a function of $\langle K \rangle$ or γ for random and scale-free networks respectively.

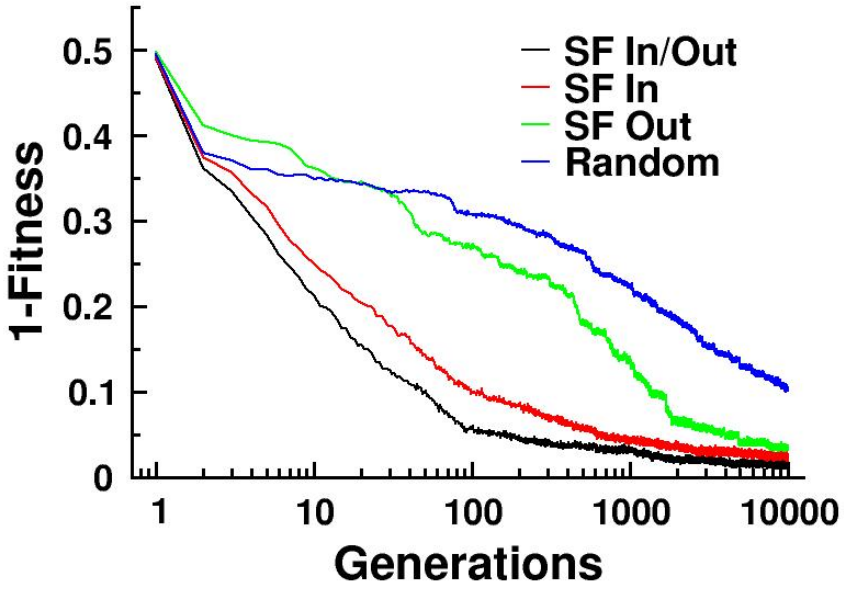


Figure S11: Mean evolutionary path for populations of networks ($\gamma = 2.5$ - $\langle K \rangle = 1.9$) with both in and out degrees power law distributed (black), in degree distribution scale-free and out-degree random (ref), out degree distribution scale-free and in-degree random (green) and both in and out random (blue). The plot shows the average fitness of *50* independent evolutionary paths ($N_{pop} = 50$, $N = 500$, $L_c = 10$ and $\mu = 0.02$). The in-degree distribution appears to determine the evolutionary path of the networks.

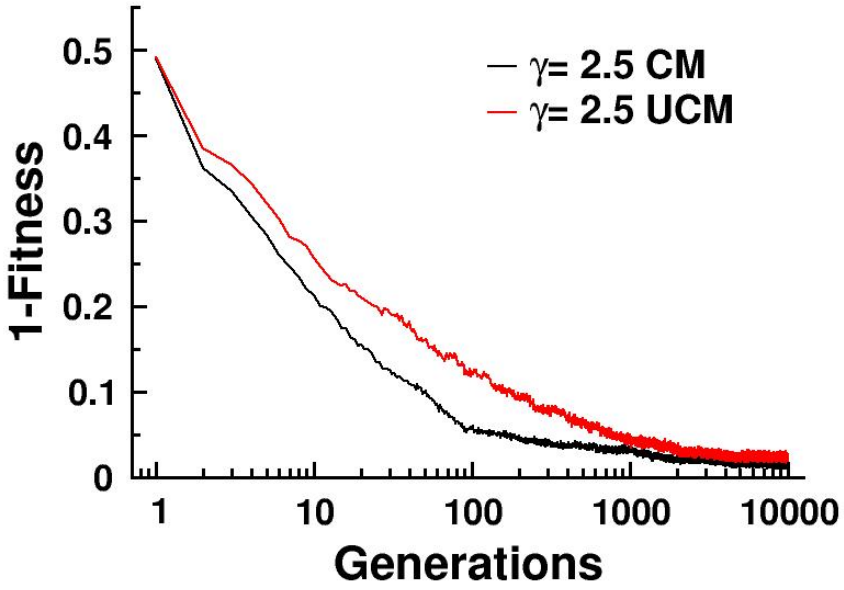
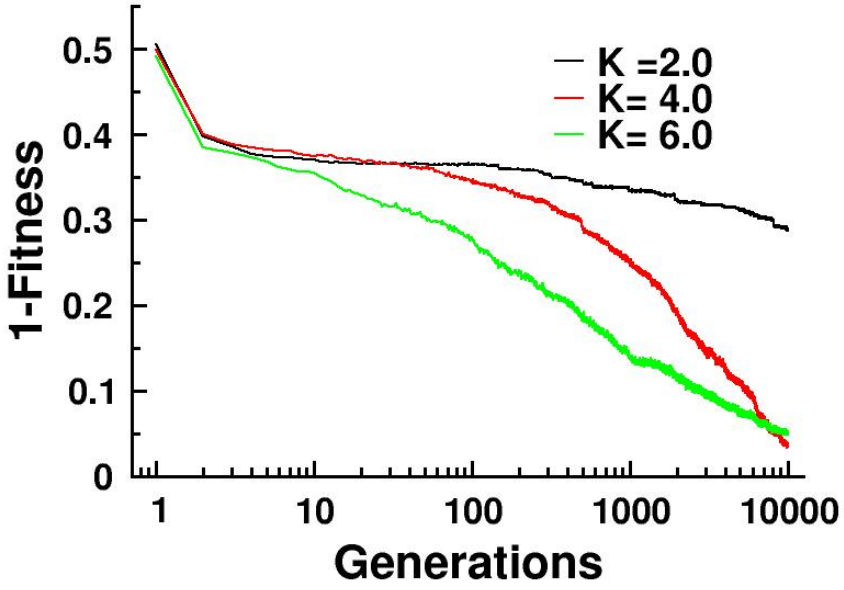
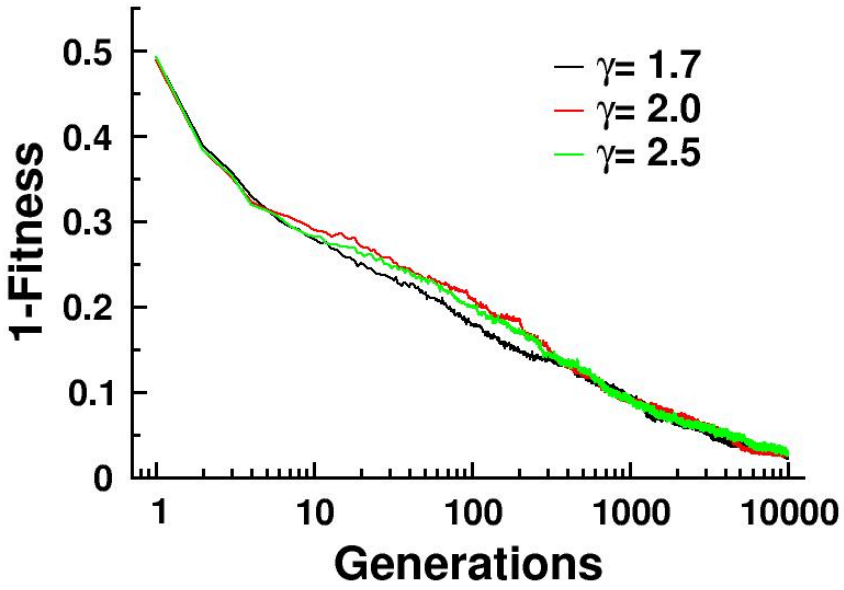


Figure S12: Mean evolutionary path for scale-free networks ($\gamma = 2.5$) generated using the configuration model (CM, black) or uncorrelated configuration model (UCM, red). The plot shows the average fitness of *50* independent evolutionary paths *(N_{pop}= 50, N= 500, L_c = 10* and μ *= 0.02)*. The introduction of a cut-off on the degree distribution for the UCM does not affect the evolutionary path of the networks.

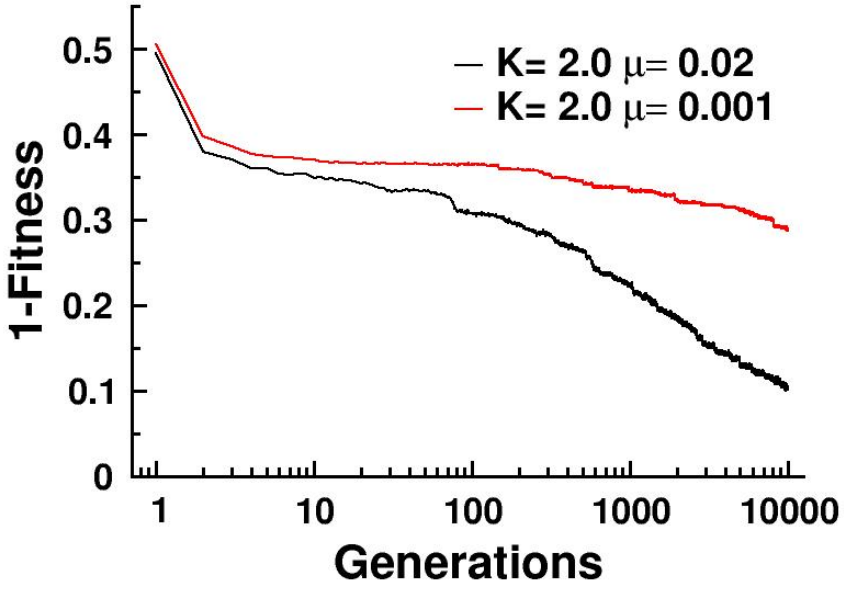
A.


K =2.0
K= 4.0
K= 6.0
1-Fitness
0.5
0.4
0.3
0.2
0.1
0
1
10
100
1000
10000
Generations

B.


γ= 1.7
γ= 2.0
γ= 2.5
1-Fitness
0.5
0.4
0.3
0.2
0.1
0
1
10
100
1000
10000
Generations

C.



D.

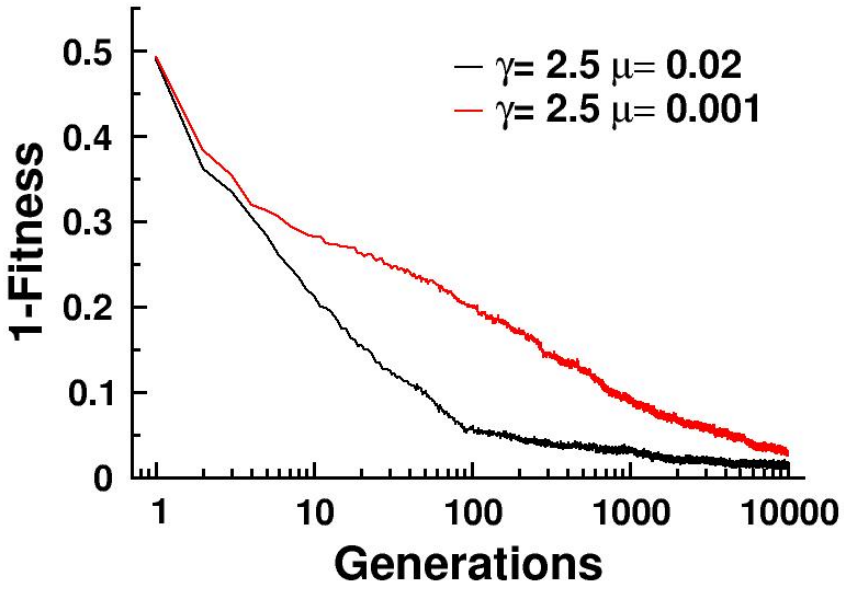
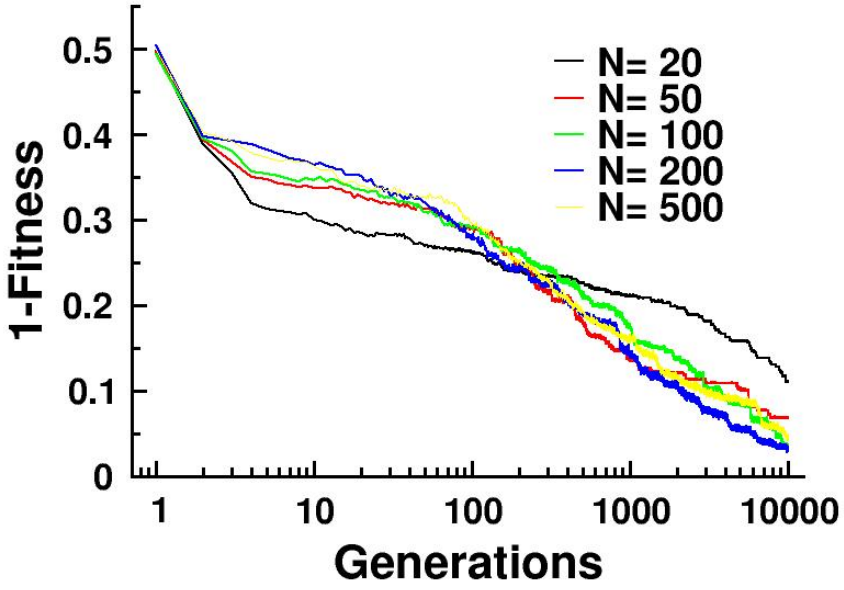


Figure S13: Reduced Mutation Rate- Mean evolutionary path of populations of random (A) and scale-free (B) networks for various average connectivities ‹*K*› and degree exponents *γ*. Average fitness of *50* independent evolutionary paths *(N_{pop}= 50, N= 500, L_c = 10* and *μ = 0.001)*. Mutation rate is reduced by an order of magnitude compared to the evolutionary runs in the main text, so that the expected mutation rate per generation for each network is 0.5. Comparison of different mutation rates for random (C) and scale-free networks (D).

A.



B.

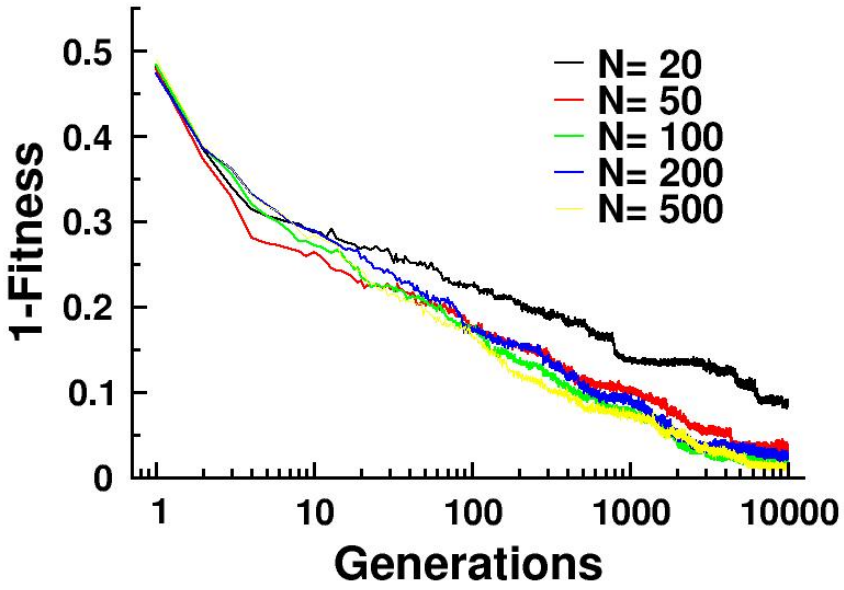
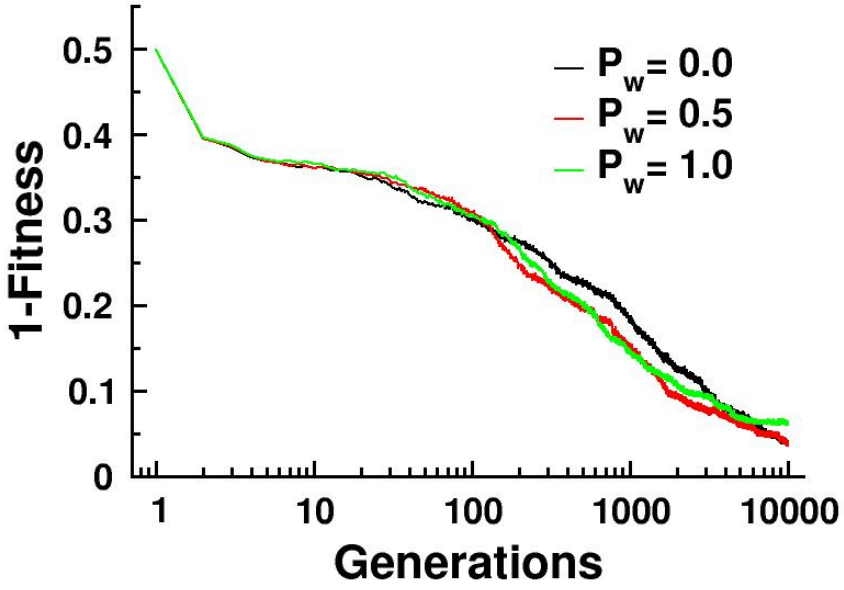


Figure S14: Network Size- Mean evolutionary path of populations of random (A) and scale-free (B) networks for various network sizes (*N= 20, 50, 100, 200, 500*). Average fitness of *25* independent evolutionary paths *(N_{pop}= 50, L_c = 10* and *μ = 0.002)*. The convergence of the fitness is insensitive to the variation of network size for *N>50*.

A.



B.

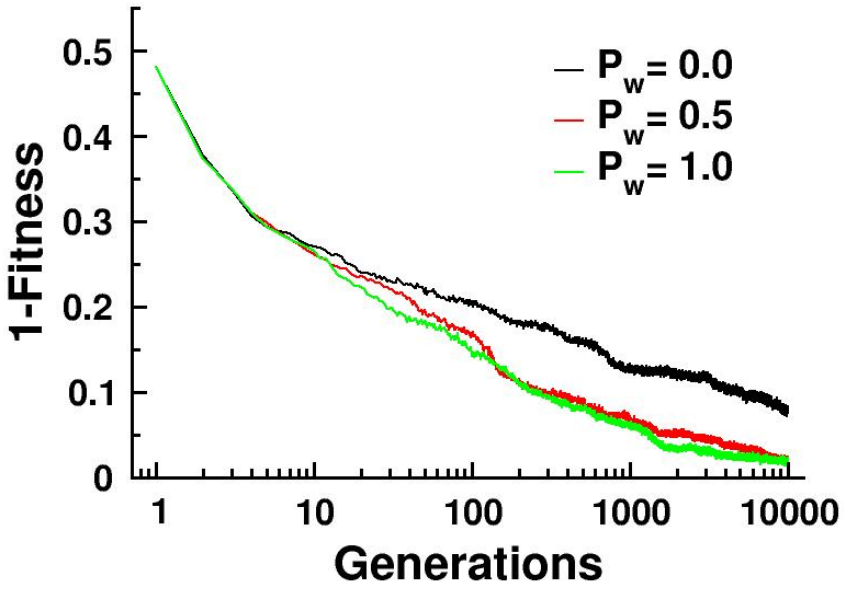


Figure S15: Connection vs. weight mutations- Mean evolutionary path of populations of random (A) and scale-free (B) networks. Average fitness of *50* independent evolutionary paths *(N_{pop}= 50, N= 500, L_c = 10* and *μ = 0.002)*. We vary the relative probability that a given mutation changes either a weight w_{ij} or a connection. P_w is the probability that a mutation changes a weight. Varying P_w only affects the convergence of the fitness function for scale-free networks (when there are no mutations of weight).

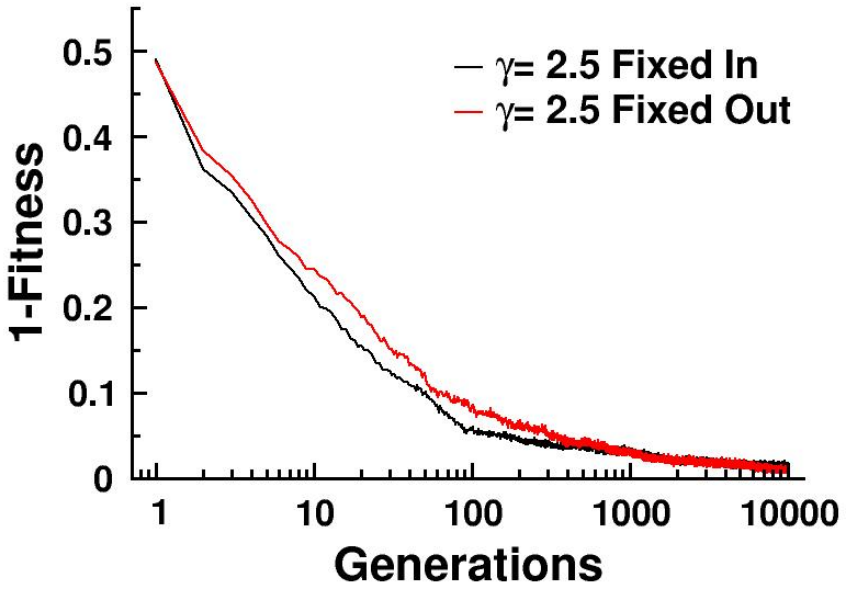
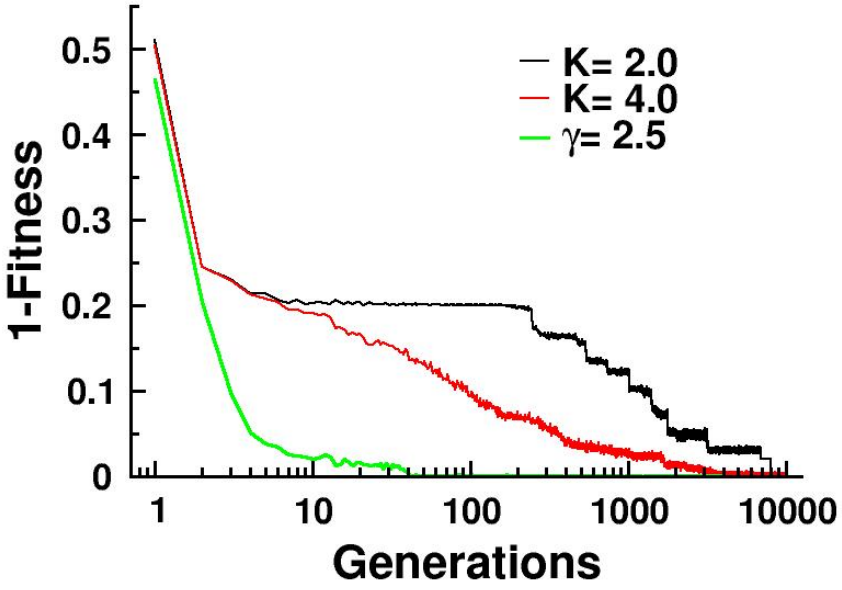


Figure S16: - Mean evolutionary path of populations of scale-free networks. Mutations conserve the in-degree distribution (black) or the out-degree distribution (red). The convergence of the fitness function is insensitive to this change. Average fitness of *25* independent evolutionary paths *(N_{pop}= 50, N= 500, L_c = 10* and μ *= 0.02)*.

A. $L_c=2$



B. $L_c=3$

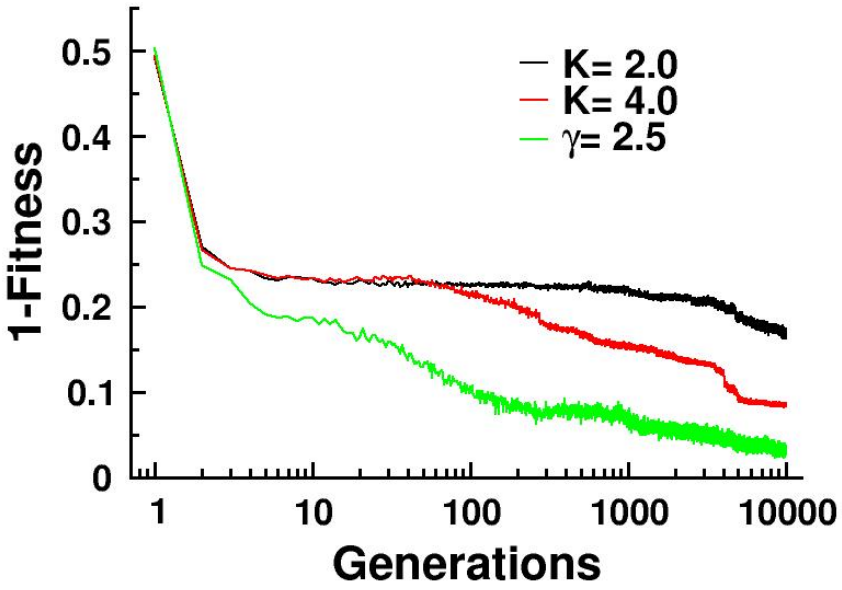


Figure S17: - Mean evolutionary path of populations of random and scale-free networks. Average fitness of 25 independent evolutionary paths *(N_{pop}= 50, N= 500, μ = 0.001)* for target cycles of small length $L_c=2$ (A) $L_c=3$ (B).

1. Kauffman, S. Homeostasis and Differentiation in Random Genetic Control Networks. *Nature* **224**, 177-178 (1969).
2. Kauffman, S. A. Metabolic Stability and Epigenesis in Randomly Constructed Genetic Nets. *Journal of Theoretical Biology* **22**, 437-467 (1969).
3. Aldana, M. Boolean dynamics of networks with scale-free topology. *Physica D-Nonlinear Phenomena* **185**, 45-66 (2003).
4. Fox, J. J. & Hill, C. C. From topology to dynamics in biochemical networks. *Chaos* **11**, 809-815 (2001).
5. Oosawa, C. & Savageau, M. A. Effects of alternative connectivity on behavior of randomly constructed Boolean networks. *Physica D* **170**, 143-161 (2002).
6. Albert, R. & Barabasi, A. L. Statistical mechanics of complex networks. *Reviews of Modern Physics* **74**, 47-97 (2002).
7. Catanzaro, M., Boguna, M. & Pastor-Satorras, R. Generation of uncorrelated random scale-free networks. *Physical Review E* **71**, - (2005).
8. Callaway, D. S., Hopcroft, J. E., Kleinberg, J. M., Newman, M. E. J. & Strogatz, S. H. Are randomly grown graphs really random? *Physical Review E* **6404**, - (2001).
9. Boguna, M., Pastor-Satorras, R. & Vespignani, A. Cut-offs and finite size effects in scale-free networks. *European Physical Journal B* **38**, 205-209 (2004).
10. Derrida, B. & Pomeau, Y. Random Networks of Automata - a Simple Annealed Approximation. *Europhysics Letters* **1**, 45-49 (1986).
11. Rohlf, T. & Bornholdt, S. Criticality in random threshold networks: annealed approximation and beyond. *Physica A* **310**, 245-259 (2002).
12. Bertschinger, N. & Natschlager, T. Real-time computation at the edge of chaos in recurrent neural networks. *Neural Computation* **16**, 1413-1436 (2004).
13. Oikonomou, P. Manuscript in preparation.
14. Aldana, M. & Cluzel, P. A natural class of robust networks. *Proceedings of the National Academy of Sciences of the United States of America* **100**, 8710-8714 (2003).
15. Nakamura, I. Dynamics of threshold network on non-trivial distribution degree. *European Physical Journal B* **40**, 217-221 (2004).
16. Newman, M. E. J., Strogatz, S. H. & Watts, D. J. Random graphs with arbitrary degree distributions and their applications. *Physical Review E* **6402**, - (2001).
17. Aldana, M., Coppersmith, S. & Kadanoff, L. P. in *Perspectives and problems in no n linear science : a celebratory volume in honor of Lawrence Sirovich* xi, 443 (Springer-Verlag, New York, 2003).
18. Beiu, V., Quintana, J. M. & Avedillo, M. J. VLSI implementations of threshold logic - A comprehensive survey. *Ieee Transactions on Neural Networks* **14**, 1217-1243 (2003).