

Extended notion of attractors in noisy random Boolean networks

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Abstract. Since real networks are noisy systems, in this work we investigate the dynamics of the random Boolean networks affected by different size of small random fluctuations. In this case jumps among different attractors are possible, thereby leading to an asymptotic dynamics different from that of the underlying deterministic model. The significance of the jumps among attractors is investigated. The notion of “ergodic set” is discussed and generalized in terms of “threshold ergodic set”, a concept that take into account the system lifetime. In order to evaluate possible differences due to the topology of the nets the experiments are effectuated on Erdos-Renyi and scale-free topologies, showing similar behaviours.

Keywords: random Boolean networks, noise, attractors, emergent computation, ergodic set

1 Introduction

In this work we are interested in investigating the influence of noisy processes in dynamical systems able to process information. The interest in such a kind of dynamical systems had a big explosion in the 80's, because of the first successful applications of neural networks to various challenging problems; the resemblance of such systems to biological neural circuits was to be found providing an approach to information processing radically different from the symbolic one (then prevailing). The differences between human and artificial cognition received a particular emphasis: between the major keywords of that time there were “parallel processing” and “distributed systems”.

However, there was also a perhaps complementary reason of interest, that is, the idea that dynamical systems may provide a powerful principle of self organization, which might be applied to the artificial simulation of cognitive processes [1] [2].

In this case the core of the approach should no longer be the strict adherence to “neuron-like” elements but should be found in the use of dynamical systems.

Another major role for which the neural network movement must be credited is that the notion of network was put at the center of the study with great emphasis. And networks provide indeed a very effective (although not all-encompassing) representation

of complex systems. Networks had already been previously used in AI (semantic nets, Petri nets) but they then became a major focus of attention in many areas of complex systems, including biology, economics and artificial life.

In the same period a very similar framework was applied to biological organization able to process information, that is, the Random Boolean Network model (briefly, RBN). Based on the same key concepts (dynamical, distributed, network-based, complex), RBN is one of the most accurately studied models of complex systems [2] [8]. The nodes of RBN models have only two possible values, and therefore they could be compared with Boolean neural network, such for example the symmetric Hopfield model. In this direction, although the learning algorithms proposed so far for RBNs have been less effective [9], they displays a much richer dynamics with respect to the dynamics of the Hopfield framework. Used also in social systems modeling, in recent years the relations among neural networks and RBN are receiving a growing interest by the researchers [15].

They are particularly interesting due to their rich dynamic behaviour, which ranges from ordered to chaotic relatively to the variation of some parameters. The critical surface in parameter space, which separates the two regions, sometimes called the “edge of chaos”, has also attracted considerable interest. The attractors of finite RBNs are cycles; however, by considering the robustness with respect to small changes in the initial conditions, and by taking into account the scaling of the cycle period with the system size, it is possible to introduce a notion of ordered vs. disordered attractors, which represents in a sense the analogue (in a finite discrete system) of the distinction between regular and chaotic attractors in continuous systems. Section 2 will review the main dynamical properties of RBNs.

RBNs were inspired by network of interacting genes, which affect each other’s activation. In this context the network attractors are associated to cellular types. It has also been observed [10] that in order to associate real systems and artificial ones it is necessary to take into account the role of noise: given that biological systems (genes, proteins, neurons, etc.) are easily affected by noise, the relevance of the attractors has to be checked in the presence of noise. In this paper we present a thorough investigation of the dynamics of the random Boolean networks affected by different size of small random fluctuations

On the basis of the previous remarks, it has been previously suggested by one of us [11] that the really interesting properties of these networks should not be related to single attractors, but rather to sets of attractors which are easily reachable from one another under the influence of a small amount of random noise. The observable behaviour of the system under the action of random noise should then be described by these “relevant”sets of attractors. In this paper we present a detailed study of the behaviour of the system affected by only a small type of perturbation, i.e. a transient flip: at a given time step the value of one or few randomly chosen nodes is changed, and the network is then left free to evolve according to its deterministic dynamics.

Section 3 show the results of extensive computer experiments obtained introducing small types of random noise on the dynamic of RBN and we discuss the outcomes showing the interaction between attractor. In section 4 we discuss the concept of “ergodic set” and verify some of its limitations, which will lead us to introduce a new

concept of “Threshold Ergodic Set” (TES). In Section 5 we discuss the outcomes of the same experiments related to scale-free random Boolean networks. Eventually, in Section 7 we present the conclusions that can be drawn from our simulations.

2 Random Boolean Networks

There are excellent reviews of RBNs in the literature (for example [3] [12]), so here we will very briefly summarize only some of their main properties.

The models were originally developed by Stuart Kauffman as a model of genetic regulatory network to describe the interactions among genes in cells [13]. Besides their biological interest, they have been used to model different complex phenomena [12].

A RBN is a directed graph with N nodes, which can assume a binary value; the value $x_i(t) \in [0, 1]$ indicates the value of the node i ($i = 1 \dots N$) at time t . Each node has k_{in} input connections $I_i = \{\gamma_{i1}, \gamma_{i2}, \dots, \gamma_{ik_{in}}\}$. In the classical model here used k_{in} is the same for all nodes and the input nodes are chosen randomly with a uniform probability between the remaining $N - 1$ nodes; consequently, outgoing connections follow a Poisson distribution $P_{out}(k) = e^{-A} \frac{A^k}{k!}$. To each node is also associated a Boolean function f_i , that is an updating rule that determines the node value at time t considering the value of its own input at the previous time $t - 1$ as follow: $x_i(t) = f_i [x_{\gamma_{i1}}(t - 1), x_{\gamma_{i2}}(t - 1), \dots, x_{\gamma_{ik_{in}}}(t - 1)]$. The Boolean functions are chosen randomly according to some probability distribution between all the $2^{2^{k_{in}}}$ possible Boolean functions of k_{in} arguments (uniform probability in the classical model). Note also that the dynamics depends upon the choice of the allowed set of Boolean functions: besides linearly separable ones, other interesting sets of functions (canalizing and, more recently, biologically plausible ones) have been analyzed [5]. For example, a careful analysis of some known real biological control circuits has shown that there is a strong bias in favour of the so-called canalizing function [14]. A Boolean function is said to be canalizing if there is at least one value of one of its input nodes that uniquely determines its output, independently of the other input values.

The updating of the network is synchronous, the time is discrete and neither the topology nor the logic rules associated to each node change in time (this is the so-called *quenched model*).

In such a way each global state $X(t) = [x_1(t), x_2(t), \dots, x_N(t)]$ determines univocally the successive state $X(t + 1)$. In this deterministic system the dynamic admits as possible asymptotic states only fixed points or cycles. In general terms, we indifferently refer to “cycle” or “attractor”, we call “period” the length of the attractor and we call “phase” each state of the cycle.

Briefly, in the RBN the organism’s genome is represented by a set of nodes, the genes, which have an activation that describe the possible states of gene expression in a Boolean approximation: express (1) or non express (0). The expression of a gene is controlled by the expression of some other genes and the main interpretation proposed by Kaufmann is the relationship between attractors and cell types. In fact as the model admits the presence of many stable configurations starting from a single information

structure, in the same way all cell types of a multiple cell organism have the same genome and in different cell types are active different groups of genes.

Considering the robustness with respect to small changes in initial conditions and other factors (as a scaling of the cycle period with the system size and others), it is possible to distinguish three different dynamical regimes: an ordered and a chaotic one, divided by a critical zone. In the ordered regime the system is characterized by a scarce sensitivity to initial conditions, a high robustness to perturbations and a large number of static (or fixed) nodes. On the other hand, in the chaotic regime one finds a very large number of attractors, sensitivity to initial conditions and a high fraction of oscillating nodes. Here, similar states tend to very different attractors and the network is highly sensitive to perturbations. The most interesting behaviour has been shown by nets in a critical regime, that is the zone of transition between order and chaos. In this regime small changes can propagate without necessarily involving the whole system. Critical RBNs show an equilibrium between robustness and adaptiveness [16]; for this reason one of the most important hypotheses is that living organisms live and evolve in a dynamical regime close to the boundary between ordered and chaotic phases. Recent results from gene knock-out experiments support the view that biological genetic regulatory networks operate close to the critical region [15].

The dynamical regime of a RBN depends primarily on two parameters: the average connectivity of the network and the magnetization bias p , which is the probability that the Boolean functions f_i , have the outcome 1. Many works have shown that if all Boolean rules are accepted the critical regime holds when $k_{in} = 2$ and $p = 0.5$, or that in a more general way the formula $k_{in} = [2p(1 - p)]^{-1}$ holds [12].

3 The influence of noise on the dynamic of random Boolean networks

3.1 Single flip

For the purpose of the present study we will consider initially only a very small amount of noise, i.e. the flip of a single node. In fact, in order to implement noise in the model of random Boolean networks we add small random fluctuations that modify the value of a node for a single time step. So one noisy event corresponds to a single bit flip of the value of one (and only one) node: at time t the state of a node randomly chosen is changed and its state at time $t + 1$ will be determined by the network's own dynamics. We apply the flip perturbations during the stable state of the system because of the system spends a lot of time in its stationary configuration. Moreover, we assume that noisy events are rare; so, after a bit flip, the system can relax on an attractor earlier than another noisy event can affect its dynamics. In such a way, a system which would be in a stable state under the usual deterministic dynamics acquires the possibility of leaving the current attractor to move to a different one.

In order to analyze this new not-completely-deterministic dynamic, we generate critical noisy random Boolean networks ($k_{in} = 2, p = 0, 5$) with different size and we investigate the behaviour of each network affected by random noise. For each network we characterise the dynamics by finding the whole set of attractors, or a subset for

large networks. For each attractor found we perturb every node in every phase (one flip at time) and control the identity of the attractor the perturbation is leading to; this information is memorised in an adjacency matrix, whose rows and columns correspond to the whole set of attractors of the net⁴.

From the adjacency matrix we can obtain a graphical representation of the transitions between attractors. Figure 1 shows an example of such structure: each vertex represents an attractor of a network; there is an edge from vertex a to vertex b if there exists at least one node belonging to one state cycle of the attractor a that, if perturbed, leads the system to the attractor b . The edge labels correspond to the percentages of the number of attractor's perturbations that lead the system from one attractor to itself or to another one, calculated upon total number of possible attractor perturbations (equal to N times the period of the attractor).

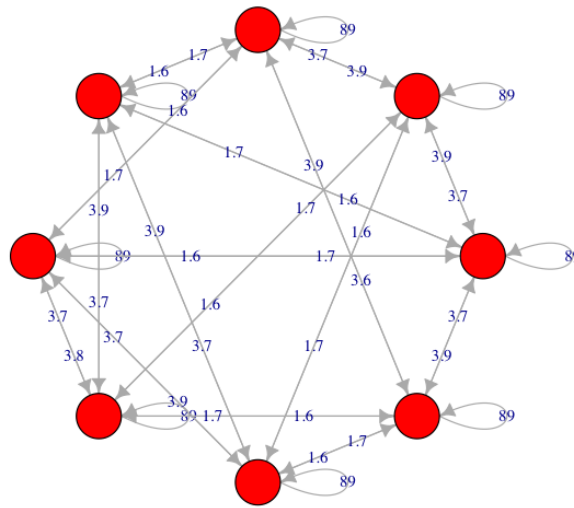


Fig. 1. Graphical representation of the attractor landscape: each vertex represents an attractor. There exist an edge from vertex a to vertex b if perturbing at least one node in one phase of the attractor a the system goes to attractor b . The edge labels correspond to the percentages of the frequency of transitions between two attractors .

Analyzing the diagonal of the adjacency matrices, we found that the higher the network size, the higher is (on average) the percentage of perturbations that don't cause the system to leave the attractor.

⁴ For small networks ($N = 10, 20$) we test all possible initial conditions, so all the attractors are found. For large networks we explore a predefined numbers of different initial conditions (5000 for networks with $N = 100$ and 10000 for networks with $N = 200$ and $N = 1000$). Note that these latter networks have a small probability of not finding attractors after the perturbation (within the search parameters). These occurrences are very few and are not considered in the adjacency matrix.

To verify this kind of behavior with respect to the dynamical regime of the network, we examined the same characteristic considering a set of nets in an ordered regime⁵. Note that, as it should be expected, for each size the ordered networks are less sensible to the noisy events (Table 1).

This observation might lead one to dismiss the effect of noise as relevant only for small networks, but this would be misleading. Let us suppose for simplicity that in a cell each node has a certain probability of changing its state independently from the other nodes. Let b be the probability that a node chosen at random changes its state during the cell lifetime. Then we expect on average a total Nb flips during the cell lifetime. From Table 1 we see that, by enlarging N from 10 to 1000, b decreases about tenfold in the case of critical nets. But since there are 100 more nodes, the total number of expected flips Nb increases tenfold when N is increased from 10 to 1000. This line of reasoning is robust with respect to the details of the calculations (it only requires that the decrease of b with N be sublinear). Therefore we come to the conclusion that large networks are more susceptible to the transitions induced by flips than smaller ones.

Table 1. Mean percentage of perturbations that lead the system to another state cycle in critical and ordered nets for different size networks.

N	Ordered nets	Critical nets
10	12,5	19,2
20	10,5	18,5
100	5,1	10,3
200	2,65	6,5
1000	0,29	1,8

Another result regards the behaviour that we can call “phase dependence”: perturbing a single node the behaviour of the system depend upon the attractor phase in which the node is perturbed (this behaviour being shown both by fixed nodes and oscillating ones). It is intriguing to remark that also real cells may have different reactions to perturbation if perturbed in different instants of their cellular cycle.

3.2 Double flip

In order to test the robustness of the just shown behaviour, we simulated a larger noise intensity. We used *double bit flips*, in which two different nodes are flipped at the same time; the nodes are chosen randomly with uniform probability and they belong to the same attractor phase. The biological situation corresponding to this process could be a noisy event simultaneously influencing two different sites, or two independent noisy events that occur at the same time.

⁵ We test a set of 100 ordered network ($k_{in} = 2$ and $b = 0,7$) for each size nets, except for the networks with 1000 nodes, for which we tested 20 nets.

The analyses permit a comparison between the perturbations sensibilities associated with these two kinds of flip. The results are shown in Table 2⁶.

Table 2. Mean percentage of perturbations that lead the system to a different attractor in different size networks with different noisy intensity (single bit flip and double bit flip).

N	Single flip	Double flip
10	36,6	36,3
100	15,1	16,4

As we can observe, there are no substantial differences between one flip and double flip results. The behaviour of the nets perturbed by such a kind of noise parallels that described in the previous paragraph, indicating a certain robustness with respect to this kind of change.

4 Ergodic sets and threshold ergodic sets

In presence of noise the system can jump from an attractor to another one; therefore, the interesting properties of noisy RBNs should not be related to a single attractor, but rather to sets of attractors which are easily reachable from one to another under the influence of small fluctuations. It is therefore appropriate to define such a set of attractors. Let $A_i (i = 1 \dots M)$ be the M attractors of a given network (under the action of the deterministic transition functions), and let A be the set of such attractors. Let us now consider a network that, after a finite transient, is in attractor A_i . We say that A_j is *directly reachable* from A_i if there is (at least) a node such that the flip of that node at time t (when the system is in attractor A_i) has the effect of bringing (after a transient) the network to the attractor A_j . We also say that A_j is *indirectly reachable* from A_i if there exists a path which leads from A_i to A_j via transitions between pairs of attractors which are directly reachable (for example a first flip may lead the system from attractor A_i to attractor A_b and a second flip (not necessary of the same node) can lead the system from attractor A_b to A_j). In symbols, we represent the fact that A_j is reachable from A_i (directly or indirectly) with an arrow: either $A_i \rightarrow A_j$ or $A_j \leftarrow A_i$.

We now define an *ergodic set* (ES) as a subset of A composed by attractors which are reachable from any other member of the ES, not necessarily in a single step [10] [11]. Also, the ergodic set is such that (one or more successive) single flips can't make the system leave the set itself. Formally:

$$ES \equiv \{A_i \in A \mid \exists A_j \in ES, A_j \rightarrow A_i; A_i \rightarrow A_k \Rightarrow A_k \in ES\}$$

⁶ For the double flip experiments, in the networks with 10 N, we perturb 25 random couples of nodes. In the nets with 100N we perturb 250 * LA (LA = attractor's period) random couples of nodes. So, the exploration of the perturbations is not exhaustive, but sufficient robust given that in the simulations with 200 * LA random couples of nodes perturbed the result doesn't change

In the language of the graph theory, the ergodic set of a network represents a strongly connected component (SCC) of the graph of the transitions between attractors, with the additional constraint that there are no possible outgoing connections from a node of the SCC to a node not belonging to the same SCC. On the contrary there may be incoming connections from an outside node to a node belonging to the SCC. In other words, the ergodic sets can be seen as knots of the attractor landscape graph: a knot of a directed graph being a subgraph with the propriety that every vertex in the knot has outgoing edges, and all outgoing edges from vertices in the knot terminate in other vertices of the knot; thus it is impossible to leave the knot while following the directions of the edges. Formally, we extend this notion to subgraphs with only one vertex, that is, we admit the possibility of having an ergodic set made by a single attractor.

If all single bit flips are permitted, for every size of network, the overwhelming majority of networks analysed present only one ES (with very few exceptions having two ESs); in this case the model loses the possibility to have many different asymptotic states. Nevertheless, since our search of perturbations has been exhaustive, we can see that the percentage of transitions between attractors provides an estimate of the probability that such transition will occur, that is, the probability that a flip of an arbitrary state belonging to a cycle leads the system in another state cycle.

Note that the transitions among attractors which are associated to the flip of just a single specific node could be too rare to occur with appreciable probability during a cell lifetime, and that the same remark applies to those transitions which are associated to the flip of a few nodes. In order to take into account only those transitions which have a reasonable chance to happen and extend in such a way the notion of ergodic set, we introduce the definition of Threshold reachability (T- reachability). We say that A_j is directly T_θ -reachable from A_i with threshold θ if there are at least a fraction θ of different flips each one of which leads the system, when it is in attractor A_i , to attractor A_j . In symbols, we represent the fact that A_j is T_θ -reachable from A_i with threshold θ (directly or indirectly) by means of an arrow: either $A_i T_\theta \rightarrow A_j$ or $A_j \leftarrow T_\theta A_i$.

We can now introduce a new concept related to the asymptotic state of the noisy random Boolean network which takes into account only the transitions which take place with appreciable frequency during the cell lifetime: the *Threshold ergodic set*. A Threshold ergodic set of attractors (T_θ -ergodic set, or briefly TES_θ) of the network is a subset of A composed by attractors which are T_θ -reachable from any other member of the TES_θ , not necessarily in a single step. Also, the ergodic set is such that the flip of less than θ nodes can't make the system leave the T_θ -ergodic set⁷. Formally:

$$TES_\theta \equiv \{A_i \in A | \exists A_j \in TES_\theta, A_j T_\theta \rightarrow A_i; A_i T_\theta \rightarrow A_k \Rightarrow A_k \in TES_\theta\}$$

Within this definition, we can describe an ergodic set as a TES with $\theta = 0$.

The notion of threshold (and the correlated definition of TES) is useful to interpret the presence of noise within the RBN framework. In fact, not all the transitions are possible within the typical lifetime of a cell; therefore, it is more appropriate to associate cell types to TESs rather than to the attractors of the deterministic dynamics. In order to elucidate the differences, Figure 2 shows the variation of η ($\eta = \frac{\#TES_\theta}{NA}$) with respect

⁷ If there is no risk of ambiguity it is possible to skip the θ symbol to brevity purposes, in these cases we use T instead of T_θ and TES instead of TES_θ .

to the variation of the threshold θ for each network size, where η is the ratio between the number of TES_θ and the total number of unperturbed networks' attractors N_A . When η reaches the value of 1 all the attractors are TES_θ , whereas each net starts with a η value that represents only a fraction of the maximum.

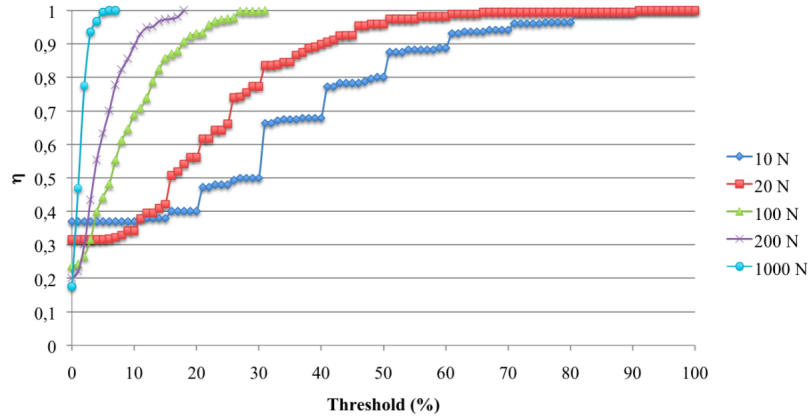


Fig. 2. The fraction η of total possible ESs in the network over the total number of attractors N_A , with respect to the variation of the threshold θ : the higher is N , the lower are the values of θ able to separate all the attractors. All points are averages of 65 different networks, with the exception of the nets having $N = 1000$ for which only 20 networks are analysed.

Now we can vary the threshold θ between 0 and 100 %, and make some interesting observations:

- at $\theta = 0$ the total number of attractors is a growing function of N , whereas the corresponding networks have typically only one TES; therefore η is a decreasing function of N ;
- a high threshold value is not necessary in order to obtain in the same net several different threshold ergodic set;
- at constant threshold values, the fraction of TESs is an increasing function of the network size; it follows that the threshold value which corresponds to the maximum value of η is a decreasing function of N .

The effect of increasing the value of the threshold θ is that of generating new TESs. This is a very interesting effect, because it indicates the possibility of creating “specialised” patterns starting from a more “global” and noisy one. Again, the higher N is the more easily the nets can exhibit this behaviour, a phenomenon that could introduce interesting consequences for the theories of natural and artificial evolving systems.

But there is a further advantage in adopting this viewpoint. Suppose that the threshold is low at an early stage of an organism’s life: then all the attractors belonging to the ES are reachable, a situation that might be associated to a stem cell. Suppose now that

as the organism grows the threshold is increased - we do not make detailed hypotheses on the reasons why this should happen, but it is conceivable that repair and control mechanisms become progressively more efficient. Then we find a few disjoint ergodic sets. By further increasing the threshold, the number of different disjoint ergodic sets increases, a phenomenon which can be associated with cellular differentiation or a sequential specialization of few initial undifferentiated patterns.

5 The effect of noise in Scale-free random Boolean Network

Recent results show that genetic and metabolic networks have a different structure from the Erdos-Renyi topology [17]. In particular these networks are characterized by the presence of some nodes which influence on a high number of other nodes (for example, transcription factors). In terms of network analysis, we have a so-called scale-free topology when a small number of elements (frequently called hubs) are highly connected whereas the major part of the nodes has few links. Formally it means that the probability $P(k)$ that one particular node belonging to the network is connected to k other nodes follows a power law: $P(k) = Ck^{-\gamma}$, where γ is the so called scale free exponent, that characterizes the distribution.

In order to introduce within the RBN framework characteristics closer to the real biological system, it is possible to vary the underlying topology. In this work we use a scale-free (power law) distribution of output connectivities and compare the results with those of the Erdos-Renyi topology.

In order to make a correct comparison between classical and scale-free random Boolean networks, in this work we use scale-free random Boolean network with a fixed indegree ($k_{in} = 2$), the same bias ($b = 0,5$) and a power law distribution for the outdegree [18]. Moreover, given that Erdos-Renyi topology involves a Poissonian distributions, which in turn imposes a fraction of nodes without outgoing links, we build scale-free nets with the same number of links and the same fraction of nodes without outgoing links⁸.

Applying the small random fluctuations (single bit flip) to simulate the noise in the model and repeating the same procedure previously described, we get results broadly similar to that of the classical model. In particular, for each analyzed scale-free networks we have only one ergodic set.

Some perhaps minor differences can be observed: analyzing the adjacency matrix, we found that the sum of the off-diagonals terms are (on average) lower than those of classical model's matrices. In other words, TESs are more stable with respect to perturbations. For example, considering nets with $N=100$, in the classical model almost 85% of the perturbations don't influence the asymptotic state of the system. In the scale-free nets with the same parameters the corresponding percentage is 92%.

This difference is observed also for larger networks; for example, with $N=200$ the same percentages are 90% for the classical model and 95% for the scale-free nets, while with $N=1000$ we found almost 97% for classical RBN and 98% for the scale-free nets.

⁸ For a deeply explanation of the network we used, we forward the reader to [18]. The values of γ that we used is $\gamma = 2,2441$ for the nets with 100 nodes, $\gamma = 2,2901$ for nets with 200 nodes and $\gamma = 2,3435$ for nets with 1000 nodes.

We also observe that in classical networks (on average) the percentage of zeros in the off-diagonal terms of the adjacency matrices is larger than that of the scale-free nets. This percentage measures the fraction of the attractors that are not directly linked each other. So the result suggests that even if the scale-free networks have a stronger stability to the perturbations, the noisy events that influence the dynamic can link more attractor.

These features probably reflect the peculiar organization of the scale-free nets, characterized by the presence of hubs and by the presence of a large fraction of poorly connected nodes, unlikely to significantly affect the asymptotic state of the net.

Despite these differences, the behavior of the noisy dynamic of the scale-free nets resulting from the threshold introduction parallels that of Erdos-Renyi nets (Figure 2); the only difference is that, for each size networks, the minimum θ value needed to obtain the maximum relative number of the ergodic sets is smaller. As a follow-up to this work, because of the particular action of hubs, it would be interesting to study the influence of their assortative/disassortative linking on the transition probabilities among attractors.

6 Conclusions

In this work we discuss the influence of noise on the dynamics of critical RBNs, in particular, we investigate the influence of small noisy events on the transition between attractors. The presence of noisy fluctuations in the model allows the system to jump between different attractors. So, we redefine the concept of biological asymptotic state as an ergodic set. In case of a finite lifetime, the less frequent fluctuations could be neglected allowing the formation of many independent patterns. This process could be modelled by means of the introduction of a threshold, allowing the coexistence of more disjoint ergodic sets. This behaviour can be tentatively associated to new models of cell differentiation. In order to better describe the noisy dynamics, we have also introduced the notion of “threshold ergodic set” as an asymptotic state which take into account the system lifetime, and which can be tentatively associated to cell types (rather than associating them to the usual deterministic attractors or to ergodic sets). The concept of “threshold ergodic set” seems to capture all the characteristics necessary to support the biological metaphor, additionally indicating new ways to enlarge the RBN framework. We also observe that larger nets are more susceptible to the transitions induced by flips than smaller ones and that similar (although not identical) properties are present in both classical and scale-free topologies. Last but not least, the fact that the threshold increasing induces a sequential specialization of few initial undifferentiated patterns could have interesting consequences for distributed systems designed for information processing.

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