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# Brain-like large scale cognitive networks and dynamics

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**Abstract.** A new approach to the study of the brain and its functions known as Human Connectomics has been recently established. Starting from magnetic resonance images (MRI) of brain scans, it is possible to identify the fibers that link brain areas and to build an adjacency matrix that connects these areas, thus creating the brain connectome. The topology of these networks provides a lot of information about the organizational structure of the brain (both structural and functional). Nevertheless this knowledge is rarely used to investigate the possible emerging brain dynamics linked to cognitive functions. In this work, we implement finite state models on neural networks to display the outcoming brain dynamics, using different types of networks, which correspond to diverse segmentation methods and brain atlases. From the simulations, we observe that the behavior of these systems is completely different from random and/or artificially generated networks. The emergence of stable structures, which might correspond to brain cognitive circuits, has also been detected.

## 1 Introduction

In the study of the central nervous system, the idea of large scale interconnected neuronal populations, organized in networks to perform cognitive functions, is progressively gaining momentum [1]. In fact, it has been demonstrated that the structure of the brain, intended as networks of cognitive processes, is decisive for allowing a deeper insight into the neural basis of brain functioning [2]. In this view, cognitive functions are mainly due to distributed processing, involving dissimilar brain areas binded by synchronization [3], which create large-scale networks that carry out processes related to the specific behavioral goals [4–7]. According to [8], cognitive functions are carried out by transient synchronization of neuronal discharges, which dynamically and synchronically bind distant neuronal areas in coherent groups. Such synchronized groups, in turn, create the neural correlates of the given processes,

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implying simultaneous dynamics in different specialized areas of the brain and the integration of responses across the cortical regions involved. Furthermore, while sensory processing is going on, attentional mechanisms and motor areas are affected as well, widening further the cognitive networks with a flexible sensory-motor coordination [9]. Many cognitive processes, organized as large networks [10–17] have been acknowledged by networks neuroscience [18,19]. These findings, together with the recent progresses in the study of structural and functional brain connectivity [20], are allowing the emergence of a new paradigm in cognitive neuroscience, which is progressively substituting conventional models: brain activity would be the result of the joint functioning of brain areas working as large-scale networks, within and between distributed brain systems.

In addition, other biophysically plausible computational models of cognitive networks have been realized to account for synchronization and transition phenomena (registering the emergency of synchronized and desynchronized brain areas according to specific tasks), and for certain types of functional impairments. In particular, some exemplary works concern the role of neuronal gap junctions in maintaining stability in network dynamics [21], the description of the transition dynamics between epileptic seizures [22] and the appearance of the chimera states, namely coexisting synchronized and desynchronized domains, in dynamical networks of nonlocally coupled oscillators [23].

The main problems raised by this approach are related to the lack of knowledge on the emergence of cognition from large-scale brain networks. In fact, the mechanisms that underlie the connections or disconnection of brain areas that constitute the networks are still unknown, as well as the key processes underlying the cooperation, competition, or coordination activities among different networks during complex cognitive behavior. Furthermore a noteworthy variability on short and long time scales is reported in the study of oscillatory synchronization in large-scale cortical networks [24]. To overcome these issues, computational approaches are becoming increasingly important, since they allow for the integration of the structural and functional divide [25], considering cognitive processes as due to both aspects. In this work, by using the brain connectome as structural network formed by nodes and edges [2], Boolean networks (BN) are used to investigate: (a) the dynamical behavior of the emerging large-scale cognitive networks along the BN parameters space; (b) the emergence of brain large-scale cognitive networks; (c) what kind of computation is going on locally and globally in the brain; (d) whether rhythms of interaction among brain areas exist, or if the interactions are purely random or chaotic. Consequently, in this paper we propose to model neural dynamics, maintained across a variety of different brain configuration states, at different levels of temporal and spatial scales, considering several sets of structural connectomes. From the simulation runs, plentiful rich dynamics emerged, giving a lot of information on the above-mentioned issues and prospecting interesting results for the realization of artificial brain-based intelligent systems.

The paper is organized as follows: after the Introduction, BN from a formal point of view and the connectomics methods are presented, together with the adopted modeling process. Experiments and main results follow, with the emergence of complex phenomena.

## 2 Formal aspects of Boolean networks and connectomics

The concerns previously expressed about the necessity to make use of models that are explicitly defined in a computational framework are strictly tied to the requirements of accurately choosing the variables to be the more congruent possible with brain data. For satisfying this requirement, we choose Boolean network (BN). In fact, the human brain is a complex system whose functioning is based on the acquisition and processing of sensory information that are transformed into behavioral responses. From a computational point of view, to mimic brain dynamics it is necessary to simulate the interaction between a large number of interacting elements that collectively gather, record, process and act on the flow of incoming information. In a simplified view, it can be assumed that neurons behave in a binary way: active or inactive. For this reason, the BN satisfy the requirements of intercepting the complexity of the brain and the emergence of brain dynamics.

In the form of random Boolean networks (RBN), the system has been introduced long ago [26], with the aim to study the regulation of gene networks. In this pioneering method applied to DNA, each gene had two states 0 and 1, where the value 1 stood for the gene activation state and the value 0 stood for an inhibition state. Since then, many studies have used the model proposed in [27] in the area of systems and synthetic biology [28–31], especially for its ability to intercept the gene networks dynamics. The status of the nodes in a Boolean network changes at each time step, in relation to the status of the nodes connected to it. The number of possible states of a Boolean network having $n$ nodes is equal to $2^n$.

Formally, a Boolean network is a triplet $(G, S, f)$, composed by a graph $G$, a set $S = \{0, 1\}$ and an evolution rule $f : C \to C$, where $C$ is the space of the all-possible configurations. As it is well known, $G = (V, E)$ is made by the set $V = \{v_1, v_2, \ldots, v_n\}$ of $n$ elements called vertices and by the set $E = \{e_1, e_2, \ldots, e_m\}$ of any edges between two vertices: $e_i = v_j \to v_k$. Each vertex $v_i$ can take a Boolean value of state $s_i = 0$ or $s_i = 1$. The critical arrangement of the initial state will produce different emerging configurations of the system. This setting is particularly suitable for simulating brain dynamics.

Human connectomics [32–34], the current framework adopted to define structural nodes and edges in the brain, is the skeleton of large-scale connected brain areas that enables information flows along preferred pathways for carrying out specific cognitive functions. Nodes and edges constitute the skeleton of the connectome. Nodes, typically considered brain areas, are defined by the cyto-architectonics of the neural areas, the local circuit connectivity, and both the common input and the output target of neuronal projections. The choice of the network nodes is made according to different atlases that allow carrying out a segmentation of the brain by different areas, the so-called regions of interest (ROI). These atlases encode different areas of the brain related to specific morphological features or functionalities. Once the networks have been obtained, different analyses can be carried out to determine key aspects of the brain topology, by using the small-world, scale-free models and the network parameters. For an extensive review see [35]. In this work, however, we do not deal with the basic connectomes parameters as our attention is focused on how the topology of the connectomes and the BN dynamics organize themselves to achieve ordered, complex and chaotic behaviors.

Even simplified with respect to the extreme complexity of the problem, the approach we have used is as follows: (1) regions of the brain are the basic units of information, with two states, active (1) or inactive (0); (2) each brain region connects to other regions through a series of links, contained in the connectome's connection matrix; (3) although the regions can work at different time scales in realizing cognitive processes, we hypothesize that they work in a massively parallel mode, and their states evolve in a synchronized way, as discrete time evolves per unit steps; (4) the spreading of the activation among different regions constitutes a large scale cognitive system; (5) the system is deterministic in the sense that, at a given configuration at time $t$, follows a single structure at time $t + 1$. Extending the cellular automata rules of life [36], we consider a brain region as active, or remaining active, if it shares a link (its neighborhood, including itself) with different active regions. If the number $s$ of links with active regions is lower than the threshold of $a$ or above the threshold of $b$, the region is switched off, both if it is active or not. For a region to be active, the

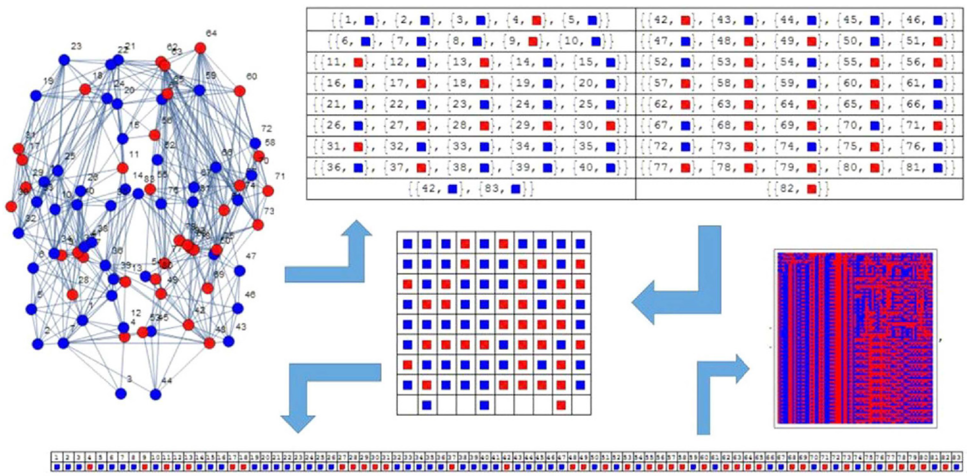

**Fig. 1.** Modeling of the brain dynamics at the global level of brain areas interaction. In this approach, regardless of the Boolean model used, it is possible to follow the global dynamics of the brain connectome. In the image it is possible to see a representation which follows the game of life evolution rule. Left: 83 different areas of the brain are identified on the connectome, each of which is represented, at a given time, by a blue (red) bullet if active (inactive). Right and bottom: the matrix provides the information about the activation state of each area. The different areas, from 1 to 83, are ordered in a row vector (bottom) which gives the initial condition of the network. On the right, the $(n \times 83)$-matrix represents the status of the brain network at $n$ distinct time steps.

number $s$, like in life, must therefore fall within the range $a \leq s \leq b$. The motivation for this choice is again as in life: to activate or to remain active, a region must have a number of active neighbors which lies within a given interval. On the contrary, if too many regions around the considered region are active, then a phenomenon of super activity occurs and the region switches off, even though it is active.

In our model, if all regions of the brain obey the same rule (homogeneous network), then, given an initial configuration of active and inactive regions of the brain, we can detect the behavior of the networks by considering all the evolution rules identified by the different values of $a$ and $b$. As we have seen before, the cardinality of the rules space is small. BN modeling allowed us to grasp the temporal dynamics of brain networks both from the global (following the space-time evolution of all the connections for all nodes) and from the local point of view, isolating a specific brain network and following it in time. From the computational side, we can describe many of their characteristics, usually unfeasible in the real domain, such as managing the effect of direct or indirect interactions among brain areas, and/or examining how different connection topologies can induce different brain dynamics, or obtaining processes of temporal synchronization when different networks are involved. Two kind of dynamical simulations can be undertaken. The first, at the global level, allows the interaction of all the nodes of the connectome, according to specific evolution rules. The results are the spatial-temporal configurations we have reported in Figure 1.

The rules that we consider in Figure 1 are as follows: Activation: a brain node that is inhibited at time $t$ will be activated at time $t+1$ if at least 1 and up to maximum of 4 of its neighbors were active at time $t$. Inhibition: a brain node can be inhibited by: overpopulation: if a node $l$ is active at time $t$ and 4 or more of its neighbors are also active at time $t$, the node will be inhibited at time $t+1$. Persistence: a brain node survives from time $t$ to time $t+1$ if and only if 2 or 3 of its neighbors are active at time $t$.

Therefore we present a classification of networks based on dynamical parameters. This classification can be performed through the study of different characteristic dynamic behaviors that the system presents during the process of evolution. In an orderly dynamics, network configurations will tend to stabilize at fixed points or limit cycles after few time steps, while in a chaotic regime, the configuration of the network will continue to change for a longer interval of temporal steps. For particular network parameters, we found the presence of complex dynamics, typical of life systems. Our hypothesis is that when the system is complex, emergent phenomena as self-organizing structures can occur, thus creating brain functional networks. These configurations of brain areas in turn create a super flow of information that allows for the management of cognitive tasks. As these systems are critically organized, their behavior differs according to the architecture of each brain, different for each subject (the structural part of the connectome), according to the mathematical model chosen for the simulation (in our case the BN), according to the selected initial data, and also according to the BN basic parameters $a$ and $b$. Therefore, the determination of routes to chaos and the corresponding dynamic behavior of the related networks helps to understand the trends of several organizational processes, to be reproduced in intelligent systems.

## 3 Some experiments

A Boolean network with N nodes has up to $2^N$ configurations (or different states). If the system is deterministic it is obvious that, at most in a time $t \sim 2^N$, the system will return to the same configuration, achieving a limit cycle that can be extremely large. For example, in the case of 83-node BN the result will be $t \sim 10^{25}$.

By realizing different simulation runs, we had the possibility to discover if the patterns of evolution of the BN yielded to large-scale cognitive networks. To start the simulations, let us consider a particular network of 83 vertices.

Random initial conditions (IC) of the Boolean network have been considered. The evolution rule is as follows: a node turns on if only one node in its neighborhood is on, which corresponds to the choice $a = 1, b = 1$. This specific rule has the aim to regulate the activation of neural areas, decreasing hyper activation of the brain circuit. This achieves a kind of economy in brain dynamics, allowing extreme flexibility and improving the overall efficiency of the system. In this case, we observe that after a short time, the nodes are all turned off. To follow this evolution, a cellular automaton-like representation has been used (on the right of Fig. 2). By placing the nodes on the horizontal line and considering time from the top to down, evolution is presented by drawing in black nodes turned on (value 1), and in white nodes turned off (value 0).

More interesting are the other cases presented in Figure 3, in which $1 \leq b \leq 24$ and $a = 1$. If we analyze these set of evolutions, it can be noted that, while the first pattern has a behavior that tends towards a fixed point (as said before), as the value of $b$ increases, the patterns tend to become ordered, with spatial-time periods gradually smaller.

This behavior, beyond the specific details for each network, is common to all the twelve networks, considering the above mentioned values of $a$ and $b$. After a certain time, at the maximum equal to $t = 2^N$ (where N is equal to 83 for this example), the system will tend towards a limit cycle. Instead, the transient pattern created to reach this limit cycle is a clear indicator of chaos or complexity of the system.

From these spatio-temporal patterns, it is possible to detect a route from chaos to order, the opposite of what usually happens in the evolution of dynamical systems, normally going from order to chaos as a parameter is varied [37]. In continuous dynamical systems, in fact, by changing the control parameters chaos appears through

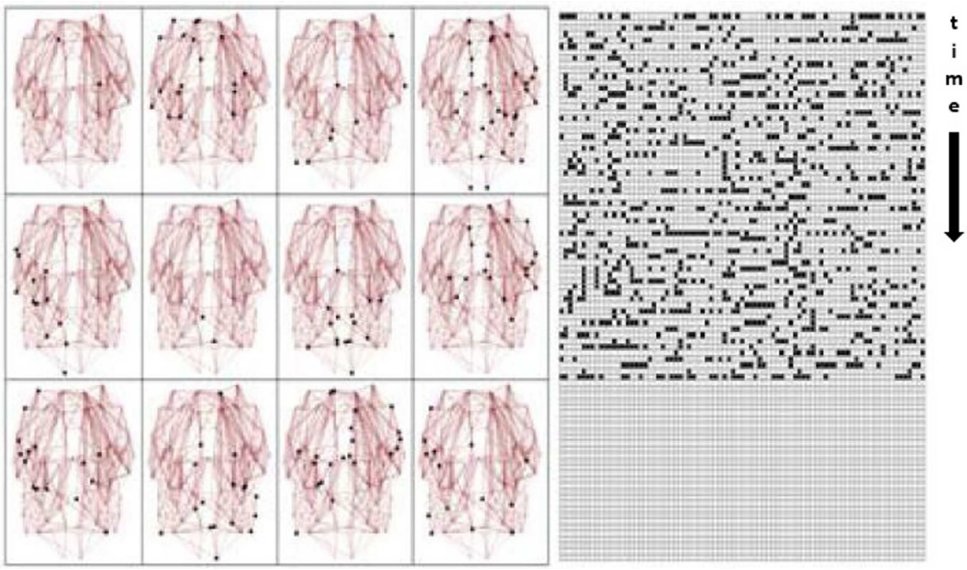


**Fig. 2.** Left: evolution of the network with $a = 1, b = 1$ for the first 12 time-steps, as it can be visualized in the brain connectome. Right: spatio-temporal diagram that emerges when a cellular automaton representation is adopted. Here in black (white) are depicted those node that are turned on (off). Time runs from top to bottom. The dynamics ultimately converges towards a steady state where all the nodes are switched off.

different well-defined behaviors, known as routes to chaos [38]. The best-known route to chaos is the Hopf bifurcation, which allows the system to go from a fixed point to a limit cycle and, finally, through a period doubling cascade, to chaos. Figure 3 identifies a possible way to chaos for the BN, where the control parameters are now $a$ and $b$. It is important to note that $a$ acts as a control parameter for the system dynamics, identifying the number of active regions in a given connectome leaving each region in the active state if it is active, or turning it active, if it is inactive.

As already pointed out, brain dynamics is characterized by the presence of many temporal scales. Since our goal was to identify global dynamics for all possible rules and to investigate the insurgence of routes to chaos and complexity, in our model we considered that the system is massively parallel and upgrades synchronously at each time step. For $a = 1$, excluding the case in which $b = 1$, the simulations gave us a chaotic pattern in which we observed the emergence and slow disappearing of increasingly complex structures. The maximum complexity has been detected for $b = 4$. In this configuration, we have identified the emergence of periodic structures which maintained for a long time and disappeared after some slightly modifications. This phenomenon was more evident for $b = 6$, where the structures, becoming simpler, persisted for a longer time. In fact, while up to 300 simulation steps, we did not observe any repetition in the pattern, for $b = 6$, after a long transient, the structures exhibited a repeating periodical pattern of 16 time steps. This aspect was confirmed for $b > 6$, when the patterns were simplified and the period became 4.

We tested the proposed model considering also different networks in the parameter range $4 \leq b \leq 7$. The observed trend was not dissimilar from what above specified: again, we witnessed the transition from chaos to order. In general, we noticed that, for $b \geq 6$, the system became periodic and, in general, as $b$ increased, it showed a lower periodicity. In some other cases, the increase of $b$ resulted in oscillating increasing and decreasing of periodicity. It is as, out of the chaotic regime, the system went toward

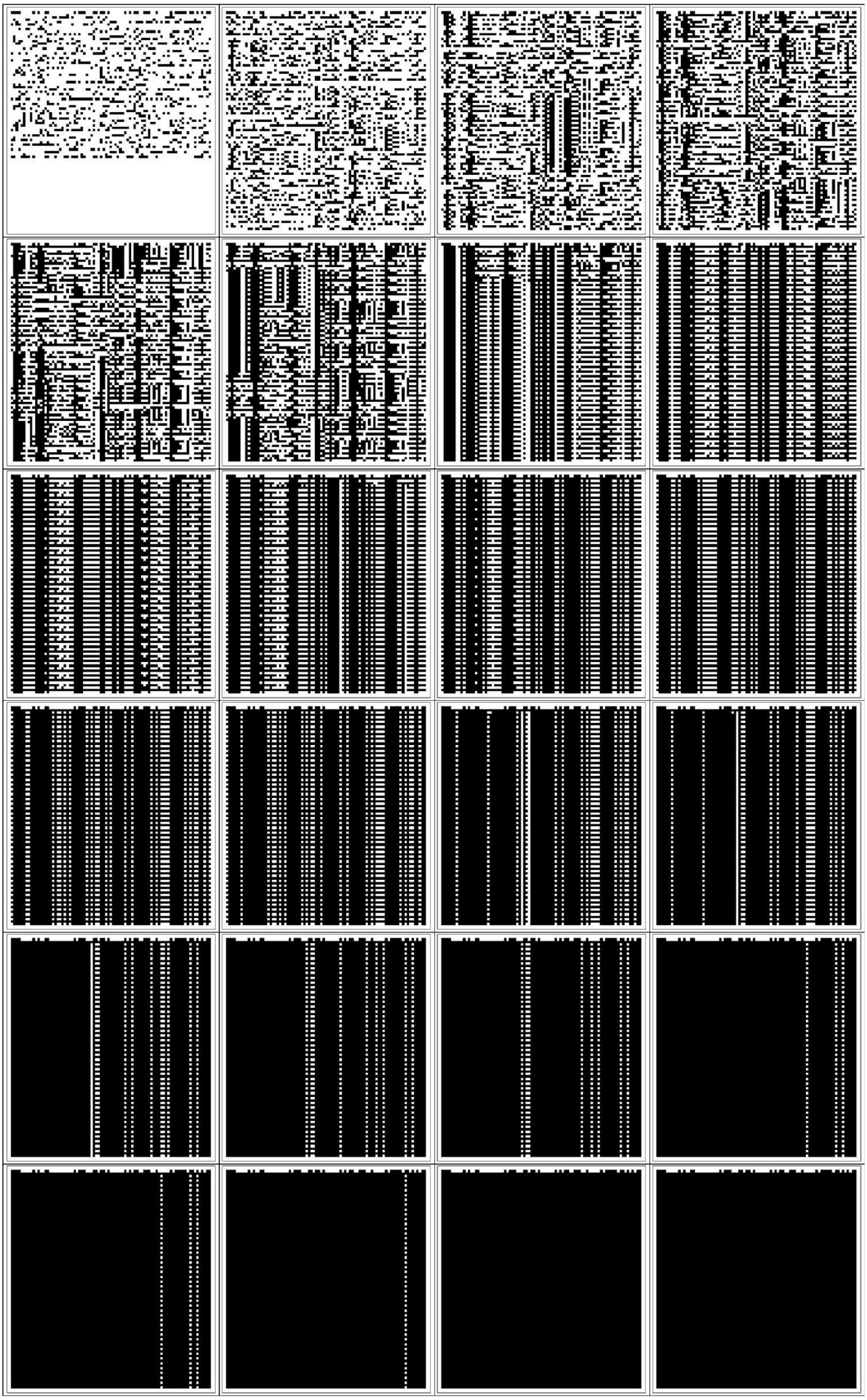

**Fig. 3.** Evolution of 24 different BN for $a = 1$ and $b = 1, 2, 3.....24$. As in Figure 2, in black (white) are reported active (inactive) nodes and time runs from top to bottom. It can be noted that, varying $b$, the process results in qualitatively different evolutions, going from chaos to complexity to order.

**Table 1.** Values of the period detected for network parameters $a = 1$ and $4 \leq b \leq 7$. As it can be noted, different periodical structures emerge as the parameter space is spanned.

| Network | $b = 4$ | $b = 5$ | $b = 6$ | $b = 7$ |
|---|---|---|---|---|
| 1 | No period | No period | 16 | 4 |
| 2 | 12 | 2 | 8 | 4 |
| 3 | 4 | 12 | 4 | 4 |
| 4 | 4 | 4 | 12 | 20 |
| 5 | No period | 40 | 4 | 4 |
| 6 | 4 | 8 | 8 | 4 |
| 7 | 12 | 6 | 4 | 4 |
| 8 | 4 | 64 | 4 | 12 |
| 9 | 10 | 4 | 4 | 12 |
| 10 | No period | 4 | 12 | 8 |
| 11 | 36 | 4 | 4 | 4 |
| 12 | No period | 20 | 28 | 4 |

increasing and then decreasing oscillating complexity/ordered behavior. We do not have results for $b < a$. For larger values of $a$, the emergence of complexity required higher values of $b$, although the overall trend was confirmed.

Another interesting fact is that the larger was the values of $a$, the more the network begun to work only on one side of the system, clearly indicating that in the real brain, only some parts of the hemispheres were active, while others were completely neglected. To verify that this was a general behavior not restricted to a specific network, we have extended the search for periodic recurrent structures to other brain networks, considering simulations up to 500 time steps. Data have been summarized in Table 1. As it can be noted, changing the values of $a$ and $b$, the dynamics of each network evolution produced complex structures with different periods, thus giving a picture of the BN parameters space organization.

From Table 1 we can discern different behaviors. In some cases, the simulation does not exhibit any periodic behavior (that is to say that no periodic behavior has been found in the simulation time of 500 time steps). In other simulations, it exhibits large periodical limit cycles ($64, 40, 36, 28$ and $20$). In other cases, the system exhibits small periods. Considering $a = 1$, a general trend is noticed, except for a few exceptions, in which periods decrease by increasing the values of $b$. This behavior is not only maintained in other experiments but is further enhanced as its value grows. These structures have rhythmic patterns with each other, creating a synchrony within the parameter space. So, not only there is a harmony within the evolution time of every network, according to the parameters, but, probably, there is also a similar harmony between the networks, giving us important information about the modular structure and adaptability of the emerging structures in the parameter space. To summarize, the identified behavior can be classified into 6 different categories, which corresponds to different regions (R) of the BN parameters space (Fig. 4):

R1: ordered behavior, going to a fixed point. This behavior occurs for low values of $a$ and $b$ and in some cases, it does not appear at all. Starting from a random initial data and after a certain time, it converges on a fixed point in which all elements of the network are inactive. R2: ordered behavior, going to a limit cycle with moderate period. R3: complex behavior, with the emergence of limit cycles with high value of the period. In this case, we have various self-organized structures (some of which are very large). The total maximum period found is 40 time steps. R4: complex behavior that does not tend to limit cycles. This is the more interesting behavior. We consider this kind of space, the edge of chaos, the place where cognitive networks occur. R5: chaotic behavior. In this case, no self-organizing structure appears. No periods can be found and the system has a high entropy, as population dynamics might show.

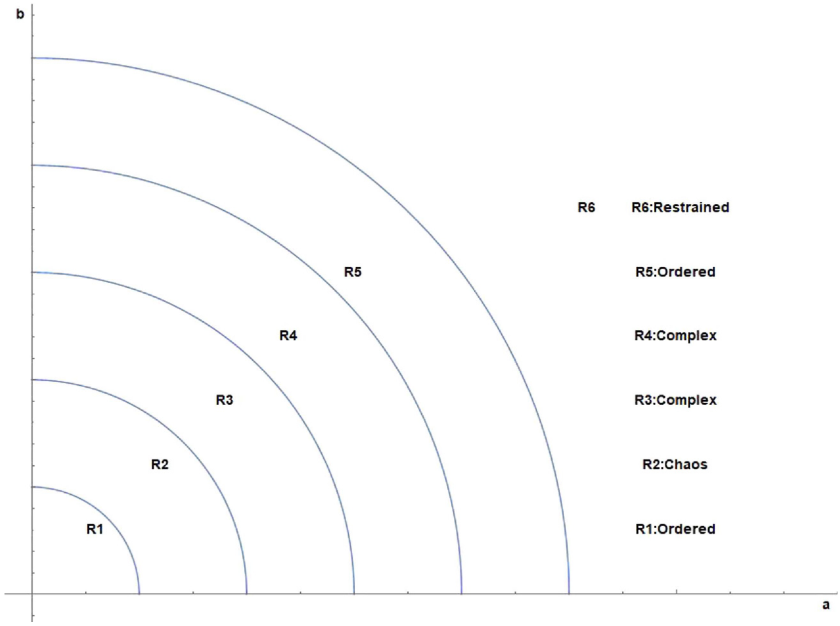


**Fig. 4.** Distinct qualitative dynamical behaviors reported in the parameter space of large-scale cognitive networks: as the parameters $a$ and $b$ are varied, one observes the transition between states characterized by different degrees of order.

A confirmation that the system is chaotic can be indirectly inferred from the correlation matrix, made on the progress of the simulation between 450 and 500 steps: no node has a correlation equal to 0.9. R6: Binding behavior. This is a kind of confined behavior in a specific regions of the connectome, evidencing areas of the brain which are not involved in the process for different reasons such as in a disease or as in specialized behavior. For this networks, for the chosen initial conditions, and for the considered parameters $a$ and $b$, the route to chaos is as follows: fixed point (when there is) $\Rightarrow$ chaos$\Rightarrow$ complexity $\Rightarrow$ complexity $\Rightarrow$ order (low periods) $\Rightarrow$ binding behavior (if it is present). As it happens in the field of dynamical systems, many routes to chaos can be achieved as the Boolean network parameters are varied. The one we have dealt with seems to be the most common to a high number of simulations, with various networks.

## 4 Conclusions

In this paper we have used BN on different structural brain networks to illustrate: (a) the dynamical behavior of the emerging large-scale cognitive networks, in the BN parameters space; (b) the emergence of brain large-scale cognitive networks; (c) what kind of computation was going on locally and globally in the brain; (d) the rhythms of interaction among brain areas. A complex landscape of how cognitive processes arose has been given, considering the emergence of metastable structures [39,40]. These metastable structures, with a hierarchical organization, allowed for the emergence of brain organizations at the next level. At the global level, we have seen that the above described dynamics have achieved this complex organization in the space of the NB parameters, called the edge of chaos, where, according to Langton [41], life processes can be possible. At the local level, we have analyzed the emerging of the cognitive networks, by following their development and hierarchical organization. The main results obtained are as follows. First, we confirmed the existence of large scale cognitive networks by using the BN approach, where by a massive parallelism, provided for the simultaneous interaction of many areas in the brain connectome. Second, many brain areas involved in the realization of cognitive networks need only to be locally connected (as it happens in real life situation, in response to local external or internal stimulation), while the whole process happens at the global level. This shows the efficient power of the brain system, which, while is carrying on a massive parallel process, the number of connections for any local brain area involved can be independent of the whole number of processing elements. Third, as brain areas involved in a cognitive process are distributed in the whole brain, this defines a very highly structured networks of connections, which are determined by the evolution of the networks in time. Connections occur by the dynamical synchronization of brain areas in time, as an orchestra playing behavior. Many sub-synchronizations are possible, following the overall score of the concerto. Furthermore, we have seen that, according to the BN parameters changes, many dynamics can be generated at different levels of the brain connectome, which gave different behavior of the whole system. From the dynamical point of view, at the global level, important qualitative behaviors have been identified, going from chaos, to complexity, to order. Many interesting features, valuable for designing more brain-like artificial devices, can be gathered from the dynamics of these systems.

## 5 Further developments

Given the great flexibility and simplicity of the proposed model, we plan to apply this modeling in real contexts, incorporating the dynamic results in robotic systems that carry out complex activities, such as staying in social interaction environments [42], to develop advanced vision systems based on a chaotic modulation [43], in systems able to realize cognitive functions in short time [44], to mimic the complex dynamics that intercepts the realization of spots in neurodegenerative diseases such as multiple sclerosis [45].

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## Author contribution statement

All authors contributed to the design and implementation of the research, to the analysis of the results and to the writing of the manuscript.

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