

SELF-ORGANIZATION AND EMERGENCE IN LIFE SCIENCES

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SELF-ORGANIZATION AND EMERGENCE IN LIFE SCIENCES

Edited by

BERNARD FELTZ

*Université Catholique de Louvain,
Louvain-la-Neuve, Belgium*

MARC CROMMELINCK

*Université Catholique de Louvain,
Bruxelles, Belgium*

and

PHILIPPE GOUJON

*Facultés Universitaires Notre-Dame de la Paix,
Namur, Belgium*

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LIST OF CONTRIBUTORS

ATLAN Henri, Human Biology Research Center, Hadassah University Hospital, Jerusalem, Israël and Centre hospitalier universitaire Broussais, Hôtel Dieu, Paris, France.

BERSINI Hugues, IRIDIA, Université libre de Bruxelles, Bruxelles, Belgium.

BAUCHAU Vincent, Netherlands Institute of Ecology, Heteren, Netherland.

BOUQUIAUX Laurence, Université de Liège, Belgium.

BRANDON Robert, Philosophy Department and Zoology Department, Duke University, Durham, USA.

COHEN Irun, Cellular Biology Department, Weizmann Institute of Sciences, Rehovot, Israël.

CROMMELINCK Marc, Laboratoire de Neurophysiologie, Université catholique de Louvain, Bruxelles, Belgium.

DUCHESNEAU François, Département de Philosophie, Université de Montréal, Montréal, Canada.

FELTZ Bernard, Institut Supérieur de Philosophie, Université catholique de Louvain, Louvain-la-Neuve, Belgium.

GOUJON Philippe, Facultés Universitaires Notre-Dame de la Paix, Namur, Belgium.

HEUDIN Jean-Claude, Institut d'Électronique fondamentale, Université de Paris XI, Orsay, France.

KOKOSZKA Valérie, Institut Supérieur de Philosophie, Université catholique de Louvain, Louvain-la-Neuve, Belgium.

LEFÈVRE Philippe, Unité d'Automatique, de Dynamique et d'Analyse des Systèmes, Université catholique de Louvain, Louvain-la-Neuve, Belgium et N.I.H., Washington, USA.

LIVET Pierre, Centre des Lettres et Sciences humaines, Université de Provence (Aix-Marseille I), Aix-en-Provence, France.

MAESSCHALCK Marc, Institut Supérieur de Philosophie, Université catholique de Louvain, Louvain-la-Neuve, Belgium.

MEIRE Philippe, Département de Psychologie clinique, Université catholique de Louvain, Louvain-la-Neuve, Belgium.

MENGAL Paul, Université de Paris XII, Faculté de Lettres et de Sciences humaines, Créteil, France.

MISSAL Marcus, Laboratoire de Neurophysiologie, Université catholique de Louvain, Bruxelles, Belgium.

RICHARDSON Robert, Philosophy Department, University of Cincinnati, USA.

THOMAS René, Chimie Physique, Université Libre de Bruxelles, Bruxelles, Belgium.

THOMPSON Paul, Scarborough College, University of Toronto, Toronto, Canada.

TU C, Unité d'Automatique, de Dynamique et d'Analyse des Systèmes, Université catholique de Louvain, Louvain-la-Neuve, Belgium.

VAN DE VIJVER Gertrudis, NFWO, Gent University, Belgium.

VARELA Francisco (†), Laboratoire de Neurosciences cognitives, CNRS, URA 654 et Centre de Recherche en Épistémologie Appliquée (CREA), École Polytechnique, Paris, France.

WEISBUCH Gérard, Laboratoire de Physique Statistique, École Normale Supérieure, Paris, France.

BERNARD FELTZ, MARC CROMMELINCK, PHILIPPE GOUJON

INTRODUCTION

The concept of self-organization takes a growing place in the evolution of contemporary sciences. Coming from the second cybernetics, which developed in USA at the end of the 1950th, this concept had first implications in biological sciences in the context of the Biological Computer Laboratory founded by Von Foerster and in the works of three symposia on the Self-Organizing systems from 1960 to 1962. During the 1970th, this approach was developed especially by the chilian school of biology. Since the 1980th, the Santa Fe Institute gives a new impulse to these perspectives. These works go on linked with the progress in the algorithm's theories, in artificial intelligence and in the analysis of non linear systems, in particular by the Brussels school. They lead, on the beginning of the 1990th, to books whose explicit purpose is a fundamental new approach of the living.

The concept of emergence refers to the coming out of new properties linked to the complexity of an organization. In scientific context, self-organization models have an important place in the formalization of emergence. The order from chaos, presented by Self-Organizing models, is often interpreted in terms of emergence, *id est* the advent of a higher level of organization.

These two concepts can be analysed according to different perspectives. This explains the structure of this book in three parts: scientific, historic and epistemologic. It will be first analysed in what extent the concepts of self-organization and emergence have some impact in experimentations in the different fields of contemporary life sciences. Second, historical origins, distant or more recent, will be envisaged. This concerns remote intuitions of antiquity, the first approach in philosophy of life in the modern period, as the more recent developments of the first and second cybernetics. Finally, in a third part, emergence and self-organization will be epistemologically analysed in relation with the questions of teleology and explanation.

* * *

The scientific approach presents two parts. The first one is an introduction to different formalisms of self-organization and emergence. Physicist G. Weisbuch introduces to the dynamic complex systems. V. Bauchau analyses boolean automata networks in biology and H. Bersini presents the problematic of artificial life. The second part analyses experimental biology and medical practice. R. Thomas shows the importance of positive feed back in the cellular differentiation process. Ph. Lefevre and his colleagues develop an example of emergent properties of neuronal networks and F. Varela studies neuronal synchronization in cognitive functions. Ph. Meire analyses the relevance of self-organization concept in psychiatric practice. Finally, H. Atlan shows the fecundity of self-organization perspective in immunology. The dominant image is one of great potentialities with already actual results but specially a great hope of promise.

For historicist, such a fecundity is not surprising. Self-organization and emergence problematic indeed concerns fundamental debate on specificity of living since antiquity to contemporary period. G. Van De Vijver shows that precisely in a detailed analysis of kantian position. More linked to the history of science, the contribution of F. Duchesneau studies the concepts of “formative force” and “essential force” in the epigenesis theories in the 18th century, while P. Mengal shows how, in the 19th century, the concept of emergence oscillates between biology and theology. This historical survey shows that self-organization and emergence, in their philosophical intuitions, lead to a concept of scientific approach of living which takes distance with mechanistic project. On the contrary, analysis of more recent origin of these concepts places us in a radically mechanistic perspective. The first cybernetics is the starting point of a more complex elaboration which tends to integrate the problematic of self-programmation. J.C. Heudin develops such perspectives in relation with artificial life, while P. Livet studies the relations between self-organization and the logic of deconstruction. Historical approach exhibits clearly ambiguities of self-organization and emergence. Distant origin refers to concepts which lead to vitalism, while proximate context places these concepts in a deliberate mechanistic research programme.

This ambiguity is precisely in the core of epistemological analysis of the third part. All the scientists and philosophers of this book keep away from vitalism without renouncing to the question of the specificity of living which presents new formulations. R. Brandon analyses the relation between self-organization and teleology, which is at the core of living, while

M. Maesschalck and V. Kokoszka envisage the relation between self-organization and the phenomenological intentionality. Moreover, epistemological analysis of emergence is linked to the question of explanation which focalises the last contributions. P. Thompson studies the concept of model in Self-Organizing systems. R. Richardson analyses the relation between explanation and causality in these systems. Finally, B. Feltz proposes an articulation between self-organisation and selection in evolutionary theory and analyses the implication of these concepts in the question of emergence.

* * *

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I. SCIENTIFIC APPROACH

A. SELF-ORGANIZATION AND BIOLOGY: GENERAL STANDPOINTS

GÉRARD WEISBUCH

THE COMPLEX ADAPTATIVE SYSTEMS APPROACH TO BIOLOGY

The purpose of this contribution is to describe the applications of concepts and methods derived from statistical physics of disordered systems and non-linear dynamics to certain issues in Theoretical biology. In those applications, the central issue is to study functional organization of a multi-component system based on a simplified description of the components. The first section gives a few examples of complex systems taken from physics and biology. We then describe three formalisms commonly used in theoretical biology. The central concepts of this approach, the *attractors* is introduced in the section on networks. Rather than emergence, we further discuss generic organizational properties of networks and give some examples which characterize the difference between organized and chaotic dynamical regimes. Before concluding, we discuss two implementations of memory in models of the brain and of the immune system.

1. FROM STATISTICAL PHYSICS TO COMPLEX SYSTEM

1.1 The Physics Approach to Simplicity and Complexity

Statistical physics has accustomed us to mathematical descriptions of systems with a large number of components. The thermodynamic properties of ideal gases were understood as early as the end of the 19th century, while those of solids were understood at the beginning of the 20th century. In both cases, two important properties make modeling easy:

These are systems in which all of the components are identical.

If the interactions between the components are very weak, they can be ignored, as in the case of ideal gases. Otherwise, as in the case of solids, we can use linearization methods to put the problem into a form in which these simplifications can be made.

These early successes compared to the difficulties encountered in the understanding of biological systems would make us consider the above mentioned systems as rather simple.

On the other hand, here are some examples of complex living systems:

The human brain is composed of approximately ten billion cells, called neurons. These cells interact by means of electrico-chemical signals through their synapses. Even though there may not be very many different types of neurons, they differ in the structure of their connections.

The immune system is also composed of approximately ten billion cells, called lymphocytes with a very large number of specificities which interact via molecular recognition, in the same way as recognition of foreign antigens.

Even the metabolism of a single cell is the result of interactions among a large number of genes which results into the cell function.

Although complexity is now a somewhat overused expression, it has a precise meaning within this text: it a complex system is a system composed of a large number of different interacting elements.

In fact, the great majority of natural or artificial systems are of a complex nature, and scientists often choose to work on model systems simplified to a minimum number of components, which allows to observe “pure” effects. This approach is illustrated by a number of Belgian teams (see Nicolis and Thomas). The complex systems approach, on the other hand, is to simplify as much as possible the components of a system, so as to take into account their large number. This idea has emerged from a recent trend in research known by physicists as the physics of disordered systems.

1.2 Disordered Systems

A large class of physical systems, known as multiphase systems, are disordered at the macroscopic level, but some are disordered even at the microscopic level. Glasses, for example, differ from crystals in that interatomic bonds in a glass are not distributed according to symmetries which we observe in crystals. In spite of this disorder, the macroscopic physical properties of a glass of a given composition are generally the same for different samples, as for crystals. In other words, disorder in a system does not lead to unpredictable behavior. The simple models used by

physicists are based on periodic networks, or grids, and simplified components of two different types are placed on the nodes, such as for example conductors or insulators in the problem known as percolation. These components are randomly distributed, and the interactions are limited to pairs of neighboring nodes. For large enough networks, we perceive that certain interesting properties do not depend on the particular sample created by a random selection, but of the parameters of this selection. In the case of the aforementioned insulator/conductor mixture, the conductivity between the two edges of the sample depends only on the ratio of the number of conductive sites to the number of insulating sites.

These primeval examples show the approach taken by a number of theoretical biologists:

We choose to oversimplify the components of the system whose global behavior we would like to model. The formal genes, neurons and lymphocytes discussed below are cartoon-like simplifications of biological polymers and cells.

Nonetheless, these simplifications enable us to apply rigorous methods and to obtain exact results.

Furthermore this approach of biology is dynamical. We start from a local description of the state changes of the components due to their interactions. We expect the global description of the system from the method, that is to say the long term behavior of the system as a whole. The global behavior can be very complex, and it can be interpreted in terms of emergent properties. Within this notion is the idea that the properties are not *a priori* predictable from the structure of the local interactions, and that they are of biological functional significance.

2. NETWORKS

2.1 Units

2.1.1 Boolean Automata

A simplified automaton is defined by its sets of inputs and outputs and by the *transition function*, which gives the output at time $t+1$ as a function of the inputs and sometimes also the internal state (*i.e.* the output) at time t . In addition, we will limit ourselves to binary automata, that is to say to two states, for example 0 and 1.

Boolean automata operate on binary variables, that is to say variables which take the values 0 or 1. The usual logic functions AND, OR and XOR

are examples of transition functions of boolean automata with two inputs. A boolean automaton with k inputs, or of *connectivity* k , is defined by a truth table which gives the output state for each one of the 2^k possible inputs. There are 2^{2^k} different truth tables, and then 2^{2^k} automata.

Let $k = 2$. Here are the truth tables of four boolean logic functions with two inputs:

Table 1.

	AND				OR				XOR				NAND			
Input	00	01	10	11	00	01	10	11	00	01	10	11	00	01	10	11
Output	0	0	0	1	0	1	1	1	0	1	1	0	1	1	1	0

On the input line of the table, we have represented the four possible input states by 00, 01, 10, and 11. The four truth tables correspond to the standard definitions of the following logic functions: AND returns a 1 only if its two inputs are 1; OR returns a 1 only if at least one of its inputs is a 1; XOR is 1 only if exactly one of its inputs is a 1; and NAND is the complement of AND. In logical terms, if A and B are two propositions, the proposition (A AND B) is true only if A and B are true.

We will further discuss the application of boolean units to genetics.

2.1.2 Threshold Automata

The state x_i of the i th threshold automaton is computed according to:

$$h_i = \sum_j J_{ij} x_j \quad (1)$$

$$x_i = 1 \text{ if } h_i > \theta_i; x_i = 0 \text{ otherwise}$$

The sum is computed over all of the inputs, subscripted by j . J_{ij} is the weight of the interaction between the i th and j th automata. In other words, the i th automaton has the value 1 if the weighted sum of the states of the input automata $\sum J_{ij} x_j$ is greater than or equal to the threshold θ_i and 0 otherwise.

We will further summarize some applications of threshold units to cognition.

2.1.3 Formal Lymphocytes

Not all networks are made of automata. A number of authors studying neural nets used differential equations as units. In immunology, Perelson and Weisbuch (1997), for instance, started from the following model of lymphocytes proliferation. The time evolution of the population x_i of clone i is described by the following differential equation:

$$\frac{dx_i}{dt} = m + x_i(pf(h_i) - d) \quad (2)$$

where m is a source term corresponding to newly generated cells coming into the system from the bone marrow, the function $pf(h_i)$ defines the rate of cell proliferation as a function of the “field” h_i , and d specifies the per capita rate of cell death.

For each clone i , the total amount of stimulation is considered to be a linear combination of the populations of other interacting clones j . This linear combination is called the field, h_i , acting on clone x_i , *i.e.*,

$$h_i = \sum_j J_{ij} x_j \quad (3)$$

where J_{ij} specifies the interaction strength (or affinity) between clones x_i and x_j . The choice of a J matrix defines the topology of the network. Typically J_{ij} values are chosen as 0 and 1.

The most crucial feature of this model is the shape of the activation function $f(h_i)$, which is taken to be a log bell-shaped dose-response function

$$f(h_i) = \frac{h_i}{\theta_1 + h_i} \left(1 - \frac{h_i}{\theta_2 + h_i} \right) = \frac{h_i}{\theta_1 + h_i} \frac{\theta_2}{\theta_2 + h_i} \quad (4)$$

with parameters θ_1 and θ_2 chosen such that $\theta_2 \gg \theta_1$.

Below the maximum of $f(h_i)$, increasing h_i increases $f(h_i)$, we call this the *stimulatory regime*. Above the maximum, increasing h_i decreases $f(h_i)$; we call this the *suppressive regime*. Plotted as a function of $\log h_i$, the graph of $f(h_i)$ is a bell-shaped curve.

2.2 Networks

2.2.1 Structural Properties

A *network* is composed of units interconnected such that the outputs of some are the inputs of others. It is therefore a directed graph, where the nodes are the units and the edges are the connections from the output of one unit to the input of another.

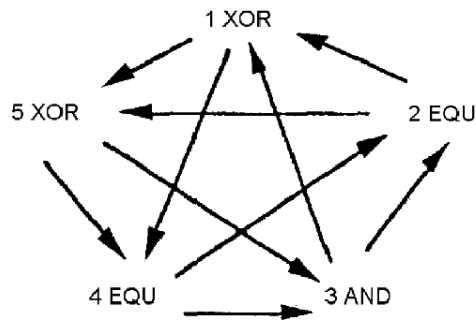


Figure 1. A network of five boolean automata with two inputs. Each automaton has two inputs and transmits its output signal to two other automata. The XOR and AND functions have been previously defined. The EQU(ivalence) function is the complement of the XOR function — it is 0 only if exactly one input is a 1.

Figure 1 represents the graph of the connections of a network of five boolean automata with two inputs.

A network of five boolean automata with two inputs. Each automaton has two inputs and transmits its output signal to two other automata. The XOR and AND functions have been previously defined. The EQU(ivalence) function is the complement of the XOR function — it is 0 only if exactly one input is a 1.

2.2.2 Dynamical Properties

Iteration Mode

Let us discuss here the dynamics of automata networks, since the notion related to attractors are easily defined. Everything discussed here generalizes

to continuous dynamics. In fact historically, most notions were first discussed for continuous dynamics.

The dynamics of an automata network are completely defined by its connection graph, the transition functions of the automata, and by the choice of an *iteration mode*. It must be stated whether the automata change their state simultaneously or sequentially, and in what order. In the parallel mode, for instance, all of the automata change their state simultaneously as a function of the states of the input automata in the previous timestep. Conversely, in the case of *sequential iteration*, or iteration in series, only one automaton at a time changes its state. Sequential iteration is therefore defined by the order in which the automata are to be updated. In the discussion that follows, we will talk only of *parallel iteration*.

Iteration Graph

There are 2^N possible configurations for a network of N boolean automata. The network goes from one configuration to the next by applying the state change rule to each automaton. Its dynamics can be represented by a directed graph, the *iteration graph*, where the nodes are the configurations of the network and the directed edges indicate the direction of the transitions of the network from its configuration at time t to a new configuration at time $t+1$.

Figure 2 represents the iteration graph of the previous network for the case of parallel iteration. This graph contains the $2^5 = 32$ possible states. It illustrates the fundamental dynamical characteristics which we will define below.

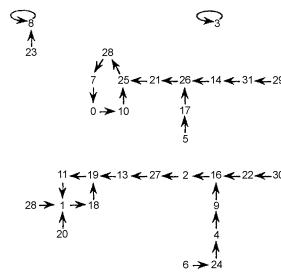


Figure 2. Iteration graph of the network of Figure 1. The numbers from 0 to 31 refer to the decimal representations of the 32 binary configurations of the network. The arrows show the temporal order of the configurations. Note that there are four different basins of attraction. State number 3 is an isolated fixed point. State number 8 is another fixed point. The other, larger, basins are composed of the configurations which converge toward the limit cycles with periods 4 and 5.

Attractors

Since an automata network is a deterministic system, if the network reaches a state for the second time, it will go through the same sequence of states after the second time as it did after the first time. Therefore, the system will go into an infinite loop in state space. These loops are called the *attractors* of the dynamical system, and the time it takes to go around the loop is called the *period* of the attractor. If this period is 1, as is the case for the configuration numbered 8 in the example shown below, the attractor is a *fixed point*. We speak of *limit cycles* if the period is greater than 1. The set of configurations which converge toward an attractor constitutes a *basin of attraction*. The network shown in the example below has four attractors.

Clearly it is only possible to construct a complete iteration graph for small networks. For the large networks we must be content to describe the dynamics of the system by characterizing its attractors.

In this way we can try to determine:

- the number of different attractors,
- their periods,
- the sizes of the basins of attraction (the number of configurations which converge toward each attractor),
- the notion of *distance* is also very important. The *Hamming distance* between any two configurations is the number of automata which are in different states.

3. IN SEARCH OF GENERIC PROPERTIES

In view of all the simplifications that were made to define the units of the model networks, one cannot expect all properties of living systems to be modeled. Only some very general properties, independent of the details of the model will show-up. These are the so-called generic properties of the network. In fact, we are interested not in the particularities of a specific network, but in the orders of magnitude which we expect to observe in studying a set of networks with fixed construction principles. We therefore consider a set containing a large but finite number of networks. We choose some of these networks at random, construct them, and measure their dynamical properties. We then take the average of these properties, and we

examine those which are fairly evenly distributed over the set of networks. An example will help to clarify these ideas.

Consider the boolean networks with connectivity $k = 2$, with a random connection structure. The dynamical variable we are interested in is the period, for the set of all initial conditions and networks. Of course, this period varies from one network to the next. We have measured it for 10 randomly chosen initial conditions for 1 000 different networks of 256 randomly connected automata, whose state change functions were generated at random at each node of the network. Figure 3 shows the histogram of the measured periods. This histogram reveals *that the order of magnitude of the period is ten* (this is the generic property), even though the distribution of the periods is quite large.

We can certainly construct special “extreme” networks for which the period cannot be observed before a million iterations. For this, we need only take networks which contain a random mixture of exclusive OR and EQUivalence functions (EQU is the complementary function of XOR; its output is 1 only if its two inputs are equal). But these extreme cases are observed only for a tiny fraction ($1/7^{256}$) of the set under consideration. We consider them to be pathological cases, *i.e.* not representative of the set being studied.

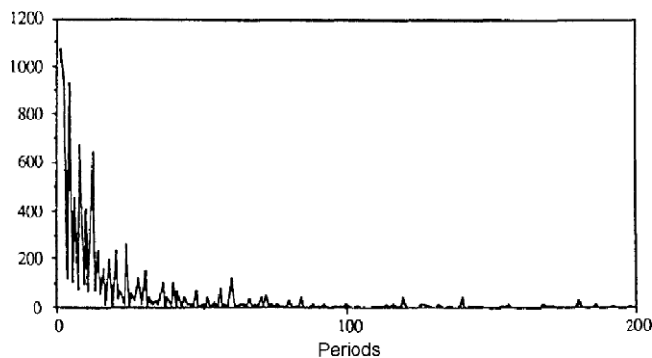


Figure 3. Histogram of the periods for 10 initial conditions of 1 000 random boolean networks of 256 automata.

We then call *generic properties* of a set of networks those properties which are independent of the detailed structure of the network — they are characteristic of almost all of the networks of the set. This notion then applies to randomly constructed networks. The generic properties can be shown not to hold for a few pathological cases which represent a proportion of the set which quickly approaches 0 as the size of the network is increased. In general the generic properties are either:

- qualitative properties with probabilities of being true are close to 1
- semi-qualitative properties, such as the scaling laws which relate the dynamical properties to the number of automata.

The notion of generic properties characteristic of randomly constructed networks is the basis for a number of theoretical biological models. It is similar to the notion of universality classes, developed for phase transitions. Without going into too much detail, we can say that the physical variables involved in phase transitions obey scaling laws which can be independent of the transition under consideration (such as, for example, problems in magnetism, superconductivity, or physical chemistry) and of the details of the mathematical model which was chosen. These laws only depend on the physical dimension of the space in which the transition takes place (for us, this is three-dimensional space) and on the dimension of the order parameter. The set of phase transitions (and their mathematical models) which obey the same scaling laws constitutes a universality class.

In fact, the first attempt to model a biological system by a disordered network of automata by S. Kauffman (1969), a theoretical biologist, predates the interest of physicists in this subject. It is also based on the idea that the properties of disordered systems are representative of the vast majority of systems defined by a common average structure.

3.1 An example: Cell Differentiation and Random Boolean Automata

The apparent paradox of cell differentiation is the following: “Since all cells contain the same genetic information, how can there exist cells of different types within a single multicellular organism?”

Indeed, our body contains cells with very different morphologies and biological functions: neurons, liver cells, red blood cells (...) a total of more than 200 different cell types. Yet the chromosomes, which carry the genetic information, are not different in different cells. Part of the answer is that not all of the proteins coded for by the genome are expressed (synthesized with

a non-zero concentration) in a cell of a given type. Hemoglobin is found only in red blood cells, neurotransmitters and their receptors only appear in neurons, etc.

Several mechanisms can interfere with the different stages of gene expression to facilitate or block it. We speak of activation and repression. The best known mechanisms involve the first steps of transcription. In order to transcribe the DNA, a specific protein, DNA polymerase, must be able to bind to a region of the chain, called the promoter region, which precedes the coded part of the macromolecule. Now, this promoter can be partially covered by a control protein, called the repressor; reading the rest of the chain is then impossible. It follows that, depending on the quantity of repressor present, the gene is either expressed or not expressed. The protein which acts as a repressor is also coded for by another gene, which is itself under the control of one or several proteins. It is tempting to model the network of these interdependent interactions by an automata network.

- A gene is then represented by an automaton whose binary state indicates whether or not it is expressed. If the gene is in state 1, it is expressed and the protein is present in large concentrations in the cell. It is therefore liable to control the expression of other genes.
- The action of control proteins on this gene is represented by a boolean function whose inputs are the genes which code for the proteins controlling its expression.
- The genome itself is represented by a network of boolean automata which represents the interactions between the genes.

In such a network, the only configurations which remain after several iteration cycles are the attractors of the dynamics, which are fixed points or limit cycles, at least when the dynamics is not chaotic. These configurations can be interpreted in terms of cell types: a configuration corresponds to the presence of certain proteins, and consequently to the biological function of a cell and its morphology. Consequently, *if* we know the set of control mechanisms of each of the genes of an organism, we can predict the cell types. In fact, this is never the case, even for the simplest organisms. Without knowing the complete diagram of the interactions, S. Kauffman (1969) set out to uncover the generic properties common to all genomes by representing them by random boolean networks. Since there is a finite number of possible boolean laws for an automaton with a given input connectivity k , it is possible to construct a random network with a given connectivity.

S. Kauffman determined the scaling laws relating the average period of the limit cycles and the number of different limit cycles to N , the number of automata in the network. For a connectivity of 2, these two quantities seem to

depend on the square root of N (in fact the fluctuations are very large). In fact, these same scaling laws have been observed for the time between cell divisions and for the number of cell types as a function of the number of genes per cell.

It is clear that Kauffman's approximations were extremely crude compared to the biological reality — binary variables representing protein concentrations, boolean (and thus discrete) functions, simultaneity of the transitions of automata, random structures\dots The robustness of the results obtained with respect to the possible modifications of the model (these are random networks) justifies this approach. As for the existence of a large number of attractors, it is certainly not related to the particular specifications of the chosen networks; it is a generic property of complex systems, which appears as soon as frustrations exist in the network of the interactions between the elements.

3.2 Generic properties of Random Boolean Nets

In fact, the results obtained by Kauffman show two distinct dynamical regimes, depending on the connectivity.

For networks of connectivity 2, the average period is proportional to the square root of N , the number of automata. The same is true of the number of attractors. In other words, among the 2^N configurations which are a priori possible for the network, the dynamics selects only a small number of the order of N which are really accessible to the system after the transient period. This selection can be interpreted to be an *organization* property of the network.

As the connectivity is increased, the period increases much faster with the number of automata; as soon as the connectivity reaches 4, the period as well as the number of attractors become exponential in the number of automata. These periods, which are very large as soon as the number of automata is greater than one hundred, are no longer observable, and are reminiscent of the chaotic behavior of continuous aperiodic systems. In contrast with the organized regime, the space of accessible states remains large, even in the limit of long times. Further research has shown that other dynamical properties of these discrete systems resemble those of continuous chaotic systems, and so we will refer to the behavior characterized by long periods as *chaotic*.

3.2.1 Functional Structuring

We have shown that when boolean automata are randomly displayed on a grid their temporal organization in period is related to a spatial organization in isolated islands of oscillating automata as soon as the attractor is reached. In the organized regime, percolating structures of stable units isolate the oscillating islands. In the chaotic regime the inverse is true: few stable units are isolated by a percolating set of oscillating units.

3.2.2 The Phase Transition

The connectivity parameter is an integer. It is interesting to introduce a continuous parameter in order to study the transition between the two regimes: the organized regime for short periods, and the chaotic regime corresponding to long periods. B. Derrida and D. Stauffer suggested the study of square networks of boolean automata with four inputs.

The continuous parameter p is the probability that the output of the automaton is 1 for a given input configuration. In other words, the networks are constructed as follows. We determine the truth table of each automaton by a random choice of outputs, with a probability p of the outputs being 1. If $p = 0$, all of the automata are invariant and all of the outputs are 0; if $p = 1$, all of the automata are invariant and all of the outputs are 1. Of course the interesting values of p are the intermediate values. If $p = 0.5$, the random process described above evenly distributes all of the boolean functions with four inputs; we therefore expect the chaotic behavior predicted by Kauffman. On the other hand, for values of p near zero, we expect a few automata to oscillate between attractive configurations composed mainly of 0's, corresponding to an organized behavior. Somewhere between these extreme behaviors, there must be a change of regimes. The critical value of p is 0.28. For smaller values, we observe small periods proportional to a power of the number of automata in the network. For $p > 0.28$, the period grows exponentially with the number of automata.

3.2.3 Distance

The distance method has recently been found to be one of the most fruitful techniques for determining the dynamics of a network. Recall that the Hamming distance between two configurations is the number of automata in different states. This distance is zero if the two configurations are identical, and equal to the number of automata if the configurations are complementary. We obtain the relative distance by dividing the Hamming distance by the number of automata.

The idea of the distance method is the following: we choose two initial conditions separated by a certain distance, and we follow the evolution in time of this distance. The quantity most often studied is the average of the asymptotic distance, measured in the limit as time goes to infinity. We compute this average over a large number of networks and of initial conditions, for a fixed initial distance. Depending on the initial distance, the two configurations can either evolve toward the same fixed point (in which case the distance goes to zero), or toward two different attractors, or they could even stay a fixed distance apart (in the case of a single periodic attractor), regardless of whether the period is long or short. Again, we observe a difference in the behaviors of the two regimes. On Figure 4, the x-axis is the average of the relative distances between the initial configurations, and the y-axis is the average of the relative distances in the limit as time goes to infinity. In the chaotic regime, we observe that if the initial distance is different from 0, the final distance is greater than 10 %. The final distance seems almost independent of the initial distance. On the other hand, in the organized regime, the final distance is proportional to the initial distance.

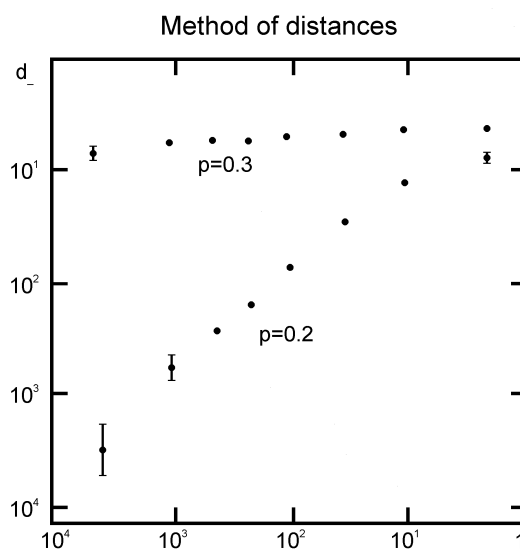


Figure 4. Relative distances at long times as a function of the initial relative distances, in the organized ($p = 0.2$) and chaotic ($p = 0.3$) regimes. (From B. Derrida and D. Stauffer (1986) *Europhys. Lett.*, **2**, 739).