EVOLUTION OF BOOLEAN NK–MODELS IN TIERRA ENVIRONMENT

DEDICATED TO PÁL RÉVÉSZ ON THE OCCASION OF HIS 65-TH BIRTHDAY

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Summary

Random dynamics called "Boolean NK–model" are introduced using the concepts of the book of S.A. Kauffman entitled The origins of order (Ch. 5. pp 188–209, see also papers of U. Bastolla–G. Parisi). We discuss theoretical aspects of the $N = K$ chaotic regime in more detailed form. Introducing a fitness function for NK–models we modify T. Ray's Tierra model (see Kauffman's book pp 276–277, papers of T. Ray, and G. Rowe's book), that is the Boolean NK–model is embedded into the Tierra environment. In our process individual dynamics are competing each-other to optimize the fitness function. We describe computer experiences with an implementation of the model and discuss open questions in the critical regime.

1. Introduction

Life is struggle of self-reproducing protein colonies. One of the basic questions of evolution is the origin of proteins. If we connect random pairs of elements of a finite set eventually we get a path connecting all points of the finite set. Even a child can see this simple fact. Erdős and Rényi were the first who recognized that a critical issue is emerging here. Kauffman believes that this critical issue gives an explanation to the origin of life. According to his central intuition, from interacting organic compounds a self-reproducing closed system develops, what he calls autocatalytic system. And autocatalytic systems are self reproducing, thus struggle for survival is launched. Finally the system, based on the dual pillars of amino acids and nucleotides won: the amino acid–nucleotide duo became the successful one from the competition of several other autocatalytic systems. May be it is the truth, to say the less nobody proved so far that this concept is incorrect (Kauffman refers to computer experiments of W. Fontana).

2. Random Boolean NK–Model

Optimization For a mathematician "struggle for life" is essentially optimization. If the universe is finite, as Buddhist philosophers teach then the state of a living organism can be represented by binary codes. Let N be the number of bites representing an organism. Let us denote the state of the organism by $\varepsilon = (\varepsilon_1, \ldots, \varepsilon_N)$, and denote the set of all N-dimensional binary vectors by U, thus U has $n = 2^N$ elements. To measure the fitness of an organism let us introduce a real valued function $f(\varepsilon)$ on U, the task of evolution was to optimize the function $f(\varepsilon)$ on the finite set U. (A delicate aspect of the problem is the increase of dimension N with growing complexity. We shall not touch this question here.)

Optimization walks According to a fairy tale Aladdin optimized with the help of the greedy algorithm when he was walking in the cave. But how to construct a strategic walk on the vertices of the unit cube in the positive orthant of the N-dimensional space? We can "jump" from a vertex to a randomly chosen other one, or we can construct a systematic walk by substituting 2-base form of the integers from 0 to $n-1$ into the function f. Surely, we can not do better if the values of f are independent and identically distributed random variables, independent of ε. We can ask, in this case as well, what happens if we walk systematically as Aladdin did it in the cave. When Aladdin was staying in one cavity, he was investigating the neighbouring ones only, and decided to continue the walk in that neighbour where f took its largest value.

NK–model of fitness Let us suppose that the fitness function f has the following structure:

$$f(\varepsilon) = \sum_{i=1}^{N} g_i(\varepsilon_{\nu(i,1)}, \ldots, \varepsilon_{\nu(i,K)}), \quad \text{where} \quad 1 \le K \le N, \quad K \text{ fixed.} \tag{1}$$

It is called the NK–model of fitness. In this model for each index i $(\nu(i,j),\ j = 1, \ldots, K)$ denotes a K-tuplet of different elements chosen from the N coordinates, and g_i-s are K-variable real valued functions defined on K-dimensional binary vectors.

Boolean NK–model It is better to have more than one Aladdin, but we do not let them walk freely, since the basis of the strength of a good army is its organization. Only a hierarchically built centralized organism is able to use effectively its resources. It is not known whether living organisms operate this way. Individual components of organisms may be linked by an apparently homogeneous network. For the sake of simplicity we suppose that each component has two possible states, and the system operates in discrete time. In each step the next value of each coordinate of the state vector ε is given by a specific rule. The simplest way to formulate a rule for this purpose is to omit the summation in formula (1), and to use K-variable binary functions as g_i-s (that is each g_i has two possible values):

$$f_i(\varepsilon) = g_i(\varepsilon_{\nu(i,1)}, \ldots, \varepsilon_{\nu(i,K)}), \quad i = 1, \ldots, N, \tag{2}$$

where f_i denotes the i-th coordinate of the N-dimensional vector valued function f. This is the so-called Boolean NK–model. In other words f is a function defined on U and with values in U. Such a function defines a dynamical system: starting from an arbitrary element of U, we can walk on U according to f. In each step if we are located in position ε then the value of the function $f(\varepsilon)$ defines the next position of the walk.

The basic difference between the two forms of f is that (1) is an example, how to construct a real valued function with several variables with the help of functions of relatively small number of variables, while in (2) an apparently similar structure defines a function from U into U. In the latter case coordinates of ε change individually by transforming ε into $f(\varepsilon)$, they are like several Aladdins in the cave. But now poor little Aladdins are no longer permitted to stroll in the whole U, each of them controls one coordinate with two possible values 0 or 1 only. ε, the collection of Aladdins denotes the state of the organism, the structure of dynamics are defined by the functions g_i-s and by the indices $\nu(i,j)$ of the controlling inputs. Let us observe that in the course of transition from (1) to (2) the optimization problem got lost. This approach was obvious for Kauffman, but we think there is a gap that we would like to fill in this paper.

The main goal of Kauffman's model is to describe enzymatic processes in living organisms. The metabolism of a cell is driven by changes in activation of enzymes. Enzymes are proteins produced by living organisms and functioning as biochemical catalysts in living organisms. They are either active or inactive. Therefore the enzymatic state of a cell can be described by a binary vector ε where the coordinates reflect the activity of enzymes. An organism with state ε may be a unicellular one, where ε_i-s indicate the activity of the different enzymes inside the cell. However the model can describe a multicellular organism, where the structure (controlling inputs and codes of operations) of each cell is the same, but the states of the cells are different. Each individual cell has its own life, their states are changing according to dynamics defined by the same structure and in functionally identical cells the order of changing states is the same.

The roll of dynamics On the whole, life of a cell is a mapping for a mathematician. Starting with some $\varepsilon(0)$ this mapping drives the states of the system:

$$\varepsilon(t+1) = f\left(\varepsilon(t)\right), \quad t = 0, 1, \ldots \, . \tag{3}$$

In reality only few enzymes are interacting in one instance and the result is a collection of new enzymes. One may readily wonder how it is possible that the new enzymes are already among the coordinates, that is the system of enzymes is catalytically closed in a living organism. As a result of the evolution, dynamics of enzymes are autocatalytic in living organisms. For the sake of simplicity it is supposed in the model that the number of enzymes controlling the activity of one enzyme is fixed, it is the K component of the NK–pair. K is small (typically $1 \leq K \leq 4$), N is large ($N = 100,000$, say).

Neural networks Several papers deal with networks of automatons, among those the most well-known ones are the neural networks, where the network is developing by a learning process. May be there is a profound connection between Boolean NK–models and neural networks, but a conspicuous difference is that in neural networks the two states of neurons are asymmetric and the effects of interactions are summing up monotonously. If the sum of activity impulses exceeds a certain threshold value then the neuron becomes active. There is no such orientation of g_i-s in Kauffman's model. Another difference is that attractors of neural networks consist of one point and cycles are not typical, as a consequence of orientation.

Random Boolean NK–model Let us return to model (2). Dynamics of an organism depend on two features:

(i) the wiring diagrams of interacting enzymes $(\nu(i,j),\ i=1,\dots,N,\ j=1,\dots,K)$,

(ii) and the collection of Boolean functions $(g_i(\eta_1,\dots,\eta_K),\ i=1,\dots,N)$, indicating the interactions of the enzymes, where g_i and η_j have two possible values, 0 and 1.

The system consisting of the elements described in (i) and (ii) will be referred as the structure of dynamics. In random Boolean NK–models the structure is generated in the following way:

(A i) for each index i $(i=1,\dots,N)$ the collection $\nu(i,1),\dots,\nu(i,K)$ of indices of coordinates (enzymes) effecting the i-th coordinate (enzyme) are chosen with uniform probability from $\binom{N}{K}$ possible K-tuplets of indices and they are chosen independently for different indices,

(A ii) for each index i $(i=1,\dots,N)$ the 0 or 1 outputs of the Boolean function g_i are given independently with probability $(1-p,p)$ for the 2^K possible inputs and they are chosen independently for different indices,

(A iii) the wiring diagram $(\nu(i,j),\ i=1,\dots,N,\ j=1,\dots,K)$ and the set of Boolean functions $(g_i,\ i=1,\dots,N)$ are generated independently of each others.

Random Boolean NK–model has random structure but its dynamics are nonstochastically driven by (3) once the initial state $\varepsilon(0)$ is chosen. Exploring dynamics random initial values are used but it is only a technique of Monte Carlo character.

Two examples Table 1 presents two examples, in both cases $N = 72$, $K = 3$. The "codes of operations" mean that Boolean functions of three variables are represented by integers μ_i $(0 \leq \mu_i < 2^{2^3}$, see explanation in Table 2), r_i denotes the frequency of 1 in the 2-base form of μ_i. Both examples were observed during 3,000 cycles, i.e. dynamics were repeated 3,000 times from a randomly generated $\varepsilon(0)$ upto a cyclic point, and the numbers p_i were the relative frequency of 1 in the cycles. Later on we return to these quantities and to the explanation of the capital letters accompanying with some numbers in Table 1.

3. Dynamical Systems

Mapping (3) results in a dynamical system. The most important feature of a dynamical system is the structure of its attractors. Starting the system one-by-one from all possible initial value $\varepsilon(0)$ the system eventually reaches cyclic points as the number of states is finite (where a cyclic point means an already visited one). Starting from a cyclic point the system is periodic and the visited sites form an attractor. Different initial values may result the same attractor, the collection of such initial values forms the basin of attraction. The size of the different attractors, their basins of attraction and the number of attractors together is called attractor structure.

According to Kauffman the attractor structure is manifested in living organisms, namely one attractor means a given cell-type, the size of that attractor is proportional to the time which is necessary to the division of that cell-type. Consequently the number of attractors corresponds to the number of different cell-types (this number for humans is 250). There are some evidences that in different living organisms the number of different cell-types is proportional to the square root of the size of DNA (cf. Figures 12.7 and 5.6 in Kauffman's books, respectively).

Table 1. Two examples for Boolean NK–model

	Connections $\nu(i,j)$			Codes of operations				Connections $\nu(i,j)$			Codes of operations		
i	1	2	3	μ_i	r_i	p_i	i	1	2	3	μ_i	r_i	p_i
1	54	10	41	128	1	0.00	1	17	56	51	64	1	0.00
2	59	6	7	A247	7	0.63	2	39	58	72	191	7	1.00
3	50	24	40	127	7	1.00	3	48	56	69	127	7	1.00
4	52	12	19	223	7	1.00	4	10	61	18	239	7	1.00
5	59	39	29	251	7	1.00	5	3	61	18	1	1	0.45
6	18	54	17	223	7	0.94	6	71	32	60	64	1	0.00
7	67	29	54	8	1	0.00	7	55	50	67	191	7	1.00
8	70	1	11	4	1	0.00	8	57	20	33	250	6	1.00
9	18	2	24	17	2	0.63	9	63	13	7	239	7	0.43
10	29	34	41	191	7	0.08	10	43	59	71	255	8	1.00
11	54	22	72	10	2	0.06	11	14	A20	68	64	1	0.06
12	18	65	66	254	7	1.00	12	28	38	31	128	1	0.00
13	B52	5	43	253	7	1.00	13	64	30	22	18	2	0.43
14	18	68	48	251	7	1.00	14	58	59	3	32	1	0.00
15	58	1	C12	33	2	0.00	15	4	26	24	191	7	1.00
16	36	19	58	222	6	0.00	16	70	B19	46	254	7	1.00
17	55	26	14	8	1	0.00	17	26	62	6	4	1	0.00
18	59	51	63	32	1	0.00	18	40	5	11	127	7	0.44
19	43	59	18	191	7	1.00	19	64	49	23	253	7	0.57
20	4	51	43	4	1	0.56	20	63	69	24	221	6	0.46
21	56	10	50	239	7	1.00	21	34	8	29	251	7	1.00
22	8	D15	68	254	7	1.00	22	60	23	27	16	1	0.00
23	25	41	48	16	1	0.00	23	46	5	C22	20	2	0.00
24	63	21	32	32	1	0.92	24	65	43	20	1	1	0.31

Table 1. Two examples for Boolean NK–model (continuation)

	Connections $\nu(i,j)$			Codes of operations				Connections $\nu(i,j)$			Codes of operations		
i	1	2	3	μ_i	r_i	p_i	i	1	2	3	μ_i	r_i	p_i
25	54	65	29	191	7	1.00	25	38	72	18	254	7	1.00
26	72	11	53	127	7	1.00	26	21	24	64	192	2	0.00
27	72	18	46	223	7	1.00	27	3	8	10	64	1	0.00
28	53	72	36	128	1	0.00	28	36	7	16	251	7	1.00
29	7	56	6	65	2	0.00	29	71	52	35	D2	1	0.00
30	5	32	7	191	7	1.00	30	9	66	37	191	7	1.00
31	61	14	17	0	0	0.00	31	46	12	E9	191	7	0.69
32	25	35	60	16	1	0.00	32	F30	65	50	239	7	1.00
33	53	57	40	223	7	1.00	33	57	28	14	24	2	0.00
34	61	70	38	191	7	0.01	34	23	6	62	16	1	0.00
35	57	17	24	18	2	0.00	35	64	45	58	247	7	1.00
36	24	28	59	255	8	1.00	36	26	17	33	32	1	0.00
37	71	5	8	1	1	0.00	37	8	52	16	127	7	1.00
38	E62	34	19	255	8	1.00	38	12	69	31	8	1	0.00
39	23	68	16	247	7	1.00	39	G66	60	29	1	1	0.00
40	33	3	27	239	7	1.00	40	33	43	35	8	1	0.00
41	65	71	20	223	7	1.00	41	42	40	13	2	1	0.00
42	5	26	72	4	1	0.00	42	52	11	55	4	1	0.96
43	3	42	19	127	7	1.00	43	5	10	30	127	7	1.00
44	1	9	7	119	6	0.56	44	2	51	60	247	7	0.69
45	23	29	52	223	7	1.00	45	9	63	50	255	8	1.00
46	59	51	58	191	7	0.83	46	22	35	31	64	1	0.00
47	26	13	53	247	7	1.00	47	11	17	61	16	1	0.00
48	21	60	61	3	2	0.60	48	20	39	72	223	7	1.00

Table 1. Two examples for Boolean NK–model (continuation)

	Connections $\nu(i,j)$			Codes of operations				Connections $\nu(i,j)$			Codes of operations		
i	1	2	3	μ_i	r_i	p_i	i	1	2	3	μ_i	r_i	p_i
49	71	38	64	127	7	1.00	49	69	56	3	191	7	1.00
50	42	70	23	185	5	1.00	50	47	43	3	4	1	0.00
51	72	2	25	111	6	0.37	51	56	29	64	2	1	0.00
52	13	60	42	128	1	0.00	52	57	45	43	253	7	1.00
53	15	12	54	239	7	0.94	53	59	37	42	16	1	0.00
54	50	16	51	247	7	0.44	54	56	13	58	H139	4	0.23
55	26	9	68	4	1	0.00	55	48	72	50	175	6	1.00
56	54	25	51	127	7	1.00	56	49	55	28	0	0	0.00
57	53	18	20	4	1	0.60	57	8	66	22	251	7	1.00
58	44	1	55	251	7	1.00	58	7	17	18	4	1	0.45
59	46	35	42	8	1	0.72	59	7	48	37	111	6	1.00
60	3	41	48	253	7	0.60	60	45	52	19	126	6	0.56
61	69	28	12	243	6	0.08	61	56	42	6	189	6	1.00
62	36	14	18	1	1	0.00	62	33	66	17	127	7	1.00
63	14	40	10	1	1	0.01	63	10	22	67	32	1	0.00
64	2	52	59	251	7	0.49	64	52	25	31	253	7	0.47
65	35	19	58	191	7	1.00	65	62	36	69	254	7	1.00
66	58	50	19	16	1	0.00	66	30	I38	37	127	7	1.00
67	F21	46	50	8	1	0.00	67	13	12	19	239	7	1.00
68	54	14	20	0	0	0.00	68	40	11	32	16	1	0.04
69	61	66	71	247	7	0.99	69	68	34	72	J239	7	1.00
70	36	31	50	72	2	0.00	70	42	65	K45	4	1	0.00
71	32	33	51	33	2	0.56	71	12	27	10	223	7	1.00
72	69	5	61	132	2	0.00	72	5	30	59	8	1	0.00

Table 2. Explanation of operation code $\mu_i = 191$ in Table 1
(2-base form of 191 is 10111111)

Input signs			Output
η_1	η_2	η_3	sign (g_i)
0	0	0	1
0	0	1	0
0	1	0	1
0	1	1	1
1	0	0	1
1	0	1	1
1	1	0	1
1	1	1	1

Critical equation It is crucial for the corroboration of a mathematical model to choose the parameters of the model to reproduce the physiological findings. Kauffman proposes certain random Boolean NK–models, what he calls critical. According to the conjecture of U. Bastolla and G. Parisi (1997), the equation

$$2p(1-p) = \frac{1}{K} \tag{4}$$

characterizes the critical p-s for random Boolean NK–models. The conjecture means the following.

Let $0 < p_K \leq P_K < 1 \quad (p_K + P_K = 1)$ be the roots of (4) for $K \geq 2$ (for $K = 1$ the system is convergent). Then the system is

(i) convergent for $0 < p < p_K$ and $P_K < p < 1$,

(ii) chaotic for $p_K < p < P_K$, and

(iii) critical for $p = p_K$ or $p = P_K$.

Chaotic regime resembles to spin glass models. It is characterised by empirical observations that for fixed K the average cycle length increases exponentially with N. The phenomena is most transparent for $K = N$, when the dynamics have simple equivalent forms. This is the so called prototype model.

4. Prototype

Consider $n = 2^N$ iid random variables: $X_1, X_2, \ldots, X_n$ with distribution

$$p_j = P(X_i = j), \quad i, j \in V = \{1, 2, \ldots, n\},$$

(observe that the number of possible values of X_i-s is the same as the number of variables). Let Y_0 be independent of X_i-s with the same distribution $p_j = P(Y_0 = j)$. We define the random function $f(i)$ by $f(i) = X_i, \quad i \in V$, and we define the sequence of random variables Y_t by the recursion

$$Y_t = f(Y_{t-1}), \qquad t = 1, 2, \ldots.$$

As V is a finite set, there is a random index $\tau \geq 0$ such that

$$Y_{\tau+1} \in \{Y_0, \ldots, Y_\tau\} \qquad \text{and if} \quad \tau > 0 \quad \text{then} \qquad Y_0, \ldots, Y_\tau \qquad \text{are different.}$$

Let $0 \leq \sigma \leq \tau$ such that $Y_{\tau+1} = Y_\sigma$. For $t \geq \tau$ cycles with length $\beta = \tau + 1 - \sigma$ will be repeated in the sequence. Let us denote by $\mathcal{B}$ the random set $\{Y_0, \ldots, Y_\tau\}$, then

$$P(\mathcal{B} = B) = p_B \prod_{i \in B} p_i, \quad \text{where} \quad p_B = \sum_{i \in B} p_i \quad \text{and} \quad B \subset V.$$

This distribution is called birthday distribution. Furthermore:

$$P(\beta = b \mid \mathcal{B} = B) = \frac{1}{|B|}, \qquad b = 1, \ldots, |B| \qquad \text{for all} \quad B \subset V.$$

Let us say that $i \in V$ is cyclic element for the set $(X_1, \ldots, X_n)$ of random variables if there is an integer k, $k \geq 1$ and there are elements $i_j \in V, j = 1, \ldots, k+1$ such that $X_{i_j} = i_{j+1}, j = 1, \ldots, k$ and $i_1 = i_{k+1} = i$. Let us denote by $\mathcal{C}$ the random set of all cyclic elements. It is a curious fact that $\mathcal{C}$ has the same distribution as $\mathcal{B}$. In proving this theorem, the calculation of the probability of the event $\mathcal{C} = C$ is based on following components:

– the set $\{X_i, i \in C\}$ equals C, thus the probability of this event is $\prod_{i \in C} p_i$,

– there is no circle in $G = V \setminus C$, and the probability of this event is p_C, as it is stated in the following lemma, furthermore

– the above two events are independent.

Lemma 1 For any subset G of V the probability that there is no cycle in G is p_C where $C = V \setminus G$.

Proof Let us denote the number of elements of G by m. We prove the statement by induction on m. Let $s \in G$ be arbitrary, and let us denote by T the event that there is no cycle in G (i.e. G is transient). Then $P(T \mid X_s = s) = 0$. If $X_s \neq s$, we unite the point s with X_s. This does not change the occurrence of T but reduces the number of elements of G. By induction

$$P(T \mid X_s \in G \setminus \{s\}) = p_C, \quad P(T \mid X_s \in C) = p_C + p_s.$$

Thus the statement follows because $(p_G - p_s)p_C + p_C(p_C + p_s) = p_C$. $\square$

Explanation Such a simple fact like this needs some other explanation beyond a proof by induction. Here is one. Two players are playing. Player 1 wins with probability p, Player 2 wins with probability $q = 1 - p$, the pay-off is one unit (payed by the bank). They could readily flip an accordingly prepared coin but Player 1 is a bit shaky, she is afraid of loosing her chances in one single step. She chooses a small number r, $0 < r \leq p$, and she would like to win with probability r immediately. Player 2 agrees on the modification under the following conditions: they flip a "three faced coin" and

(i) with probability r Player 1 wins,

(ii) with probability $p - r$ nothing is changed, and the game is continued,

(iii) with probability q the chances will be updated to $(p - r, q + r)$ and if $r < p$ then the game is continued with the new chances.

Let us count the expected value of the modified chance of Player 1: with probability r it is 1, with probability $p - r$ it is p, and with probability q it is $p - r$. It means that Player 1's winning chance increases by q with probability r and with probability q it decreases by r. Seemingly this process is fair enough (this is a martingale).

In case Player 1 does not win immediately they proceed in the same way. Player 1 may choose any sequence of r-s as long as they remain smaller then her actual chances. Eventually either Player 1 wins or she looses everything in the sequel of many small steps. Let us return to the lemma. Player 1 bets that there is a cycle in G, Player 2 is against it. Let $s \in G$ be arbitrary. If $X_s = s$, Player 1 wins immediately risking $r = p_s$ amount. If $X_s \neq s$ but $X_s \in G$, then nothing really changes. If $X_s \in C$ then any path reaching s leads to C, thus we can swap s from G to C. We continue with t in case $X_s = t \in G \setminus \{s\}$ and with an arbitrary element t of $G' = G \setminus \{s\}$ in case of $X_s \in C$. As long as we remain in G a chain F will be formed and its probability p_F will be the actual bet r of Player 1. The three faced coin is served by X_t where t is the last element of F. In case $X_t \in F$ Player 1 wins immediately, in case $X_t \in G' \setminus F$ the chain F is extended with X_t, and in case $X_t \in C'$ the entire chain F is appended to C' while it is subtracted from G', where G', C' stand for updated versions of G, C. Eventually either Player 1 wins because a cycle is formed in G or G' becomes empty and Player 2 wins. The process is fair thus total winning probability of Player 1 is p_G. (This explanation resembles the proof of ballot theorems, see papers of L. Takács.)

For uniform distribution this lemma is due to B. Harris (1960), the general case is due to Y.B. Burtin (1980) and S.M. Ross (1981). We extended Lemma 1 for exchangeable random variables.

Lemma 2 Let n be an integer, $n > 1$ and let $X_1, \ldots, X_n$ be exchangeable random variables with values in $V = \{1, \ldots, n\}$, and let G be a non empty subset of V. We say that there is a cycle in G if there is an integer k, $k \geq 1$, and there are elements i_j in G such that $X_{i_j} = i_{j+1}$, $j = 1, \ldots, k$, with $i_{k+1} = i_1$. The probability of the event that there is a cycle in G is $P(X_1 \in G)$.

Proof Let us denote by $K(G)$ the event that there is a cycle in G and by m the number of elements of G. For $m = 1$ our statement is a tautology since $K(\{s\}) \equiv \{X_s = s\}$ for $s \in V$. We prove the statement by induction on m with n fixed. Let $m > 1$ and let us suppose that the statement is true for any integer less then m.

Let $G_1,\ G_2$ be disjoint nonempty subsets of G such that $G_1 \cup G_2 = G$. Then we have $P(K(G_i)) = P(X_1 \in G_i)$ for $i = 1,2$ by induction and $K(G_i) \subset K(G)$ for $i = 1,2$ by definition. These imply that

$$P\left(K(G)\right) = P\left(K(G_1)\right) + P\left(K(G_2)\right) - P(A) + P(B),$$

where

$$A = K(G_1) \cap K(G_2), \qquad B = K(G) \setminus \left(K(G_1) \cup K(G_2)\right).$$

We are done proving that $P(A) = P(B)$, apparently it is enough to consider the case when G_1 consists of one element: $G_1 = \{s\}$.

From now on we investigate m-tuplets $w = (w_i :\ i \in G)$ calling them words ($w_i \in V$). The coordinates of words are listed according to increasing order of the indices $i \in G$. For any subset F of G set $w_F = (w_i,\ i \in F)$, this is the subword of w consisting of coordinates of w listed according to increasing order of indices in F. Observe that we are speaking about increasing order of indices i in F while the corresponding coordinates w_i are not necessarily increasing. We say that a subset F of G is proper for a word w if w_F is a permutation of elements of F. If F is proper for w then the mapping $i \mapsto w_i$ is one-to-one on F, in other words w_F is a permutation of elements of F. A one-to-one mapping consists of disjoint cycles: starting from an arbitrary element $i \in F$ we proceed according to the mapping $i \mapsto w_i$ as long as we reach i, then continue with another element of F if any remained. A proper subset F of w is called simple for w if w_F consists of one cycle. Simple proper subsets of a fixed word w are disjoint and their union is the maximal proper subset for w (it may be empty). We say that words w', w'' are congruent if

i) their maximal proper subsets are the same, and

ii) they have the same coordinates outside their maximal proper subsets.

If w', w'' are congruent, then the events $\{X_i = w'_i,\ i \in G\}$, $\{X_i = w''_i,\ i \in G\}$ have the same probability, because the X_i-s are exchangeable and congruence implies that the coordinates of w' are a permutation of coordinates of w''. Observe that event B means that there is a cycle in G but there are no cycles in G_1 and G_2. Thus the maximal proper subset of a random word $X = (X_i, i \in G)$ in B is simple and it contains the index s which is the only element of G_1.

Let us denote by $W(B)$ the set of words with the above properties: a word is an element of $W(B)$ if and only if its maximal proper subset is simple and it contains s. Let us fix a word w in $W(B)$ and let us denote the size of its maximal proper subset F by k, then in $W(B)$ there are $(k-1)!$ words congruent with w. Now let us turn to the event A and let us denote the set of corresponding words by $W(A)$. The maximal proper subset of any word $w' \in W(A)$ is no longer simple for w' because it has $\{s\}$ as one proper subset and it has at least one other proper subset in G_2. There are words in $W(A)$ which are congruent with the fixed $w \in W(B)$ because we can construct them with appropriate rearrangement of coordinates $w_i,\ i \in F$ and leaving the other coordinates unchanged (and vice versa: for any element of $W(A)$ we can construct a congruent element of $W(B)$). The number of words in $W(A)$ which are congruent with the fixed w is again $(k-1)!$ because we may form any permutation of elements of $F \setminus \{s\}$. Thus $P(A) = P(B)$. $\square$

Asymptotics In a recent manuscript J. Pitman(1998) summarises many related problems. Asymptotics for the birthday distribution was investigated by M. Camarri and J. Pitman (1998), they proved that if $\Delta \max_{i\in V} p_i$ goes to 0 as $n \to \infty$ then

$$\lim_{n\to\infty} P(|\mathcal{B}| > \Delta x) = \exp(-\frac{x^2}{2}),$$

where $\Delta = 1/\sqrt{\sum p_i^2}$ (here everything depends on n but we do not denote the dependence). For uniform distribution it means that the size of $\mathcal{C}$ is about $\sqrt{n}$, while in the general case it is approximately Δ. If $\mathcal{C} = C$, then the set of the values of random variables $\{X_i, i \in C\}$ equals C, and the conditional distribution of the random variables $\{X_i, i \in C\}$ given $\mathcal{C} = C$ is uniform on the permutations of elements of C. Asymptotics for random permutations is given by the following theorem of V.L. Goncharov (1944).

Theorem Let us denote by κ_m the number of cycles in a random permutation of m elements. Then

$$\lim_{m\to\infty} P\left(\frac{\kappa_m - \log(m)}{\sqrt{\log(m)}} \leq x\right) = \frac{1}{\sqrt{2\pi}}\int_{-\infty}^{x} e^{-\frac{t^2}{2}}dt.$$

Let $\mathcal{D}$ denote the set of elements of the cycle in a random permutation of m elements containing one specified element s. Then

$$P(|\mathcal{D}| = k) = \frac{1}{m}, \quad k = 1, \ldots, m,$$

and given that $|\mathcal{D}| = k$, the conditional distribution of $\mathcal{D}$ is uniform on the set of subsets of k elements containing s. Roughly $|\mathcal{D}|$ is $m/2$, and subtracting $\mathcal{D}$ from the original set the procedure may be repeated: the random permutation on the remaining elements is again random. If m goes to infinity the length of the smallest cycle remains of finite order. The same statement holds true on attractors: the one reached from one specified initial value has approximately the size $\Delta/2$, the number of attractors is $\log(\Delta)$, and the size of the smallest attractor is of finite order when n goes to infinity. The probability that a random permutation of m element consists of one cycle is $1/m$, thus the probability that there is only one attractor is $1/\Delta$, (this quantity is exactly

$$\sum_{C\subset V} \frac{p_C}{|C|}\prod_{i\in C} p_i,$$

but there is no closed form for it).

In case of random Boolean NK–model $n = 2^N$, and in the chaotic regime the number of attractors is $\mathcal{O}(N)$, the size of attractors is $\mathcal{O}(2^{N/2})$. It is believed (and supported by extended computer work) that in the critical regime both the number of attractors and the size of the attractors are $\mathcal{O}(\sqrt{N})$.

One possible explanation of this phenomena is the appearance of frozen bits: if p is small then the majority of bits become fixed as 0, some of them may be fixed as 1. This process is controlled by p, if p is close to $1/2$ (and $K > 2$) then there are no frozen bits at all, and as p decreases the number of frozen bits increases. For small p all bits became frozen, the dynamics are convergent. Of course this is a statistical rule, the actual structure of the dynamics may cause opposite effects. In Table 1 the coordinates of two examples given with $p_i = 0$ are frozen as 0 (observe that corresponding r_i-s are mostly 0, 1 or 2 with exception of case $i = 16$ for the first example), and the coordinates are frozen as 1 for $p_i = 1$. (We use both p_K and P_K but it would not be a restriction of generality to use only one of them.)

5. Tierra

For investigation of critical regime we used evolutionary optimization method proposed by T. Ray (1992). In Ray's proposition the main idea is that in an evolution model fitness have to be defined by the activity of the investigated dynamics. In formula (1) fitness is mechanically evaluated from characteristics of an organism. Ray's idea is to let the investigated organisms to live for a while and to evaluate fitness directly from their success. He is using a simple computer language (LISP) with the property that any sequence of bits may be either a program or an input data. In his process the programs are evolving by interaction of bit strings (this process is a special case of genetic optimization). We are using the same evolutionary process for exploring critical regimes in random Boolean NK–models. We say that we embedded the Boolean NK–model into the Tierra environment because in our process individual dynamics are competing each-other, and the whole population becomes the environment for its members.

Initialization and typical steps We start with a collection of M different Kauffman's dynamics, so called "animals", and step by step

– we choose one of the M animals with uniform distribution,

– we choose a point in U with uniform probability at $t = 0$,

– we let the chosen animal to evolve according to its dynamics upto a cyclic point, then the same dynamics start from another randomly chosen point of U,

– the dynamics operate from time 0 upto a fixed time T (T is called action time).

Selection rule For an animal let us denote by κ the number of different cycles observed from 0 upto T, by $\beta_1, \ldots, \beta_\kappa$ the lengths of cycles and by $\gamma_1, \ldots, \gamma_\kappa$ their frequencies. The fitness of the animal is calculated as

$$\varphi = \sum_{i=1}^{\kappa} \sqrt{\beta_i} \log(\gamma_i), \tag{5}$$

(it is possible that $\kappa = 0$, then $\varphi = 0$).

If the fitness of an organism is larger then the minimal fitness of previous ones then a mutant version of the organism replaces the one with the minimal fitness. We call this step division. Divisions form recurrence points of the process and counting of minimum of fitness restarts after divisions. Animals producing larger fitness than some successive other ones do not change.

Mutation Mutation means that with a fixed (small) probability all elements of the structure of dynamics of the animal are changed in the following way:

– new connection codes $\nu(i, j)$ are chosen with uniform distribution (but taking into account that they should be different),

– the Boolean functions g_i are changed to a new one using the original critical distribution.

First a mutation rate 0.01 was used but after a while we increased it to 0.05. Descendants of one original animal (we call them "stem") form a family. Two animals given in Table 1 are averages of two families accordingly (labeled by 688 and 320), developed in an evolution process with $M = 904$ animals and action time $T = 510$. Capital letters in Table 1 refer to the corresponding values of the original animals, which were the following: A=32, B=6, C=32, D=57, E=71, F=13 for stem animal 688, and A=24, B=39, C=62, D=128, E=16, F=69, G=52, H=239, I=46, J=128, K=3 for stem animal 320. Initial fitness of the first animal was 16.08, it is 72nd in this respect among the 904 animals. Family of this stem animal started to become a winning one when descendants of second stem animal turned the course of the process.

Termination We have no definite termination rule, usually one evolutionary process consists of 200,000 typical steps. Fitness function increases up to 45 and descendents of one stem animal fill the zoo.

6. Results and questions

Stability In the first steps mean fitness of population is linearly increasing, which indicates that the extremal dynamics of the present fitness function (5) may be different from the critical dynamics. Thus we are faced with two possibilities:

– we have to find a fitness function with critical dynamics as its extremal dynamics, or

– we have to find out what population is the extremal one for our fitness function.

Our first fitness function was $\varphi = \kappa$ which resulted in a seemingly unbounded increase of mean fitness of population. We found a case with $\nu(i,1) = i, \quad i = 1, \dots, N$, where the total number of attractors was about 100,000. It indicates that rule (A i) is crucial for the critical regime. In certain cases we tried to find all of the attractors. It turned out that in the majority of cases the number of attractors is close to κ, but for some extreme dynamics it was much larger. For a fixed structure the standard deviation of fitness function is usually 1. Relative randomness of fitness function reflects real life, in each action there are certain elements of chance incorporated. That is why in our Tierra model T is proportional with N, and attractors occurring only once are penalized. For animals presented in Table 1 we have $\kappa = 22$ and $\kappa = 44$ respectively. These animals were developed with fitness function $\varphi = \kappa$, the corresponding values for their stem animals was $\kappa = 10$ and $\kappa = 9$. The example shows that fitness function of the evolutionary optimization "orients" the mutations: here number of attractors was to be optimized without reference to the sizes of attractions basins and resulting animals have large number of attractors with thin attraction basins (for the two animals given in Table 1 the values of new fitness function (5) are 18.78 and 22.46 respectively which barely differs from initial fitnesses 16.08 and 19.60).

Convinced by the inappropriateness of fitness function $\varphi = \kappa$ we tried to find a more appropriate one and used

$$\varphi = \sum_{i=1}^{\kappa} \beta_i \log(\gamma_i),$$

which resulted in rather long cycles. Our last choice was the fitness function (5) and it was used in the majority of our computer simulations. We think that it is the central problem of critical Boolean networks, what is the fitness function that they do optimize. (It is a special case of the more general question, what is the "aim" of the evolution.)

Random Boolean NK–models form a tiny subset of mappings from U to U: we are using stem animals coming from this regime but following Ray's strategy we are generating structures evolving outside this tiny subset. Now we are faced with the intriguing question: is it a mistake - or a result? Using fitness function (5) the majority of developing structures had cycle length 4 while the number of cycles was rather large, around 20-30. Dynamics of this character have rather small probability in random Boolean NK–model.

In the random Boolean NK–model structural elements are independent. In the winning structures a random permutation of g_i-s keeping the $\nu(i,j)$-s unchanged usually decreases dramatically the fitness. It shows that in structures optimal for fitness function (5) two components of the structure of dynamics are no longer independent, a given wiring diagram defines the appropriate Boolean functions. Testing the effect in a computer experiment some correlation was forced for the connections, which resulted changes in the critical probability. With new fitness function (5) appropriate mutations for the first animal in Table 1 are the following: $\nu(5,1) = 19$, $\nu(7,1) = 40$, $\nu(14,2) = 50$, $\nu(44,1) = 2$, $\nu(46,1) = 19$, $\nu(47,1) = 11$, $\nu(47,3) = 51$, $\nu(62,3) = 51$, changes in operation codes: $g_{24} = 1, g_{34} = 254, g_{63} = 32$. With these changes $\varphi = 35.24$. Changes for the second animal in connections: $\nu(3,2) = 6$, $\nu(5,1) = 33$, $\nu(8,2) = 15$, $\nu(44,3) = 58$, $\nu(51,2) = 2$, in this case there is no need for changing the operation codes, new fitness is $\varphi = 35.17$.

Winning families In long runs descendants of one stem animal win, but the winning stem animals are different from trial to trial. In Table 3 we give the results of some experiments. In our zoo there were M = 904 animals numbered from 0 to 903, with N=72, K=3 and T=510. We used a fixed collection of M stem animals and ordered them according to their initial fitness, this is "order" and "initial fitness" in Table 3 (we are presenting only a selection of the population in the table). In four different runs (labeled by A, B, C, D) families were formed from descendants of the same collection of stem animals (this is the same population where two examples of Table 1 come from). In Table 3 average fitnesses and total numbers of divisions are given for whole families.

New structures Effects of mutations are clustered in the following way:

– in majority of cases the effect of mutations is neutral,

– in some cases it is lethal, which implies that most investigated structures have convergent structures in their close neighbourhood (fitness of a convergent structure is rather small, that is why convergent mutations are killed with high probability),

– in very rare cases there are extremely high jumps in fitness values which are usually the source of the winning versions of one ancestor: in the long run that family wins which is developing first this new type of structure.

Directed graph of changing bits Let us fix one attractor of the dynamics. We call a coordinate $i \in V$ living if it takes both of its possible values in the attractor, and we call the connection $\nu(i,j)$ living if the ith and $\nu(i,j)$th coordinates are living. Let us define a directed graph with vertices in V and with directed edges $i \mapsto \nu(i,j)$ if $\nu(i,j)$ is a living connection. We call the resulting graph the directed graph of changing bits. It is easily seen that all attractors have at least one cycle in their directed graph of changing bits. If there is only one cycle in the graph of an attractor, then the number of attractors corresponding to one cycle is related to the length of the cycle. (For a cycle of m elements the number of attractors is roughly 2^m.) If the dynamics have different attractors with disjoint cycles and the lengths of the cycles are relative primes then the number of attractors of the dynamics is the product of the number of attractors of the individual cycles.

Fitness function (5) prefers large number of attractors with large basin of attraction. It may be expected that in course of computer evolution animals with disjoint cycles will be generated and once they are generated then they propagate with high speed in zoo. The simplest cycle consists of two coordinates such that they simply forward the bits to each other without changing it. This system has three attractors, two with cycle length 1, and one with cycle length 2. If both coordinates flip the bits, then the situation is similar. In the case one coordinate keeps the bits unchanged while the other flips them, then the system is cycling on its 4 possible states. In a system consisting of three pairs, one from each of the above types, all the attractors have cycle length 4, and the number of attractors is 16 (all states are cyclic). It is no wonder that in most cases winning families have similar structures: in course of lucky mutations pairs of coordinates are formed which effect each other and the majority of other bits become frozen. For such an "ideal" system $\kappa = 16, \beta = 4, \gamma = 5$, and the fitness $\varphi = 16 \times \sqrt{4} \times \ln(5) = 51.5$.

Table 3. Results of four different runs

No	Or-der	Initial fitness	Average fitness A	B	C	D	Number of divisions A	B	C	D
0	324	7.89	8.65	29.49	7.86	7.94	4	1420	2	1
3	65	16.59	15.29	30.98	16.32	13.33	40	2177	17	5
22	184	11.12	8.85	10.02	9.99	9.13	4	3	6	2
70	51	18.78	13.50	20.49	33.91	26.16	15	1	7003	123
105	2	27.84	27.14	26.81	27.94	25.76	146	96	114	100
107	85	15.30	16.57	14.91	12.12	14.95	1	0	19	24
113	90	15.15	13.44	15.00	28.18	15.50	6	4	624	8
119	1	28.36	17.45	12.49	24.80	23.67	26	3	27	33
127	195	10.87	10.78	35.14	10.33	8.81	1	8992	5	6
142	96	14.98	26.47	14.81	14.17	14.54	553	0	1	6
154	109	14.52	20.87	13.22	14.33	26.06	30	2	1	236
155	25	21.06	18.12	22.04	22.51	22.18	3	254	288	52
172	73	15.99	36.29	17.73	16.67	18.61	33320	1	1	53
199	60	17.32	19.46	21.16	32.30	13.54	1	17	6341	5
201	546	4.32	26.64	4.31	4.32	4.33	651	1	1	1
205	139	12.76	31.72	13.28	15.82	12.27	409	1	29	8
279	21	21.78	21.14	19.66	21.60	19.16	62	107	96	36
283	8	25.34	22.16	26.46	26.74	24.40	168	619	608	148
300	171	11.63	16.59	12.00	11.04	11.22	15	1	1	2
320	41	19.60	27.50	34.07	17.42	22.12	1056	11822	5	76
338	4	26.47	26.79	26.43	27.04	25.84	97	200	247	85
365	31	20.38	21.32	18.31	20.47	21.33	51	47	70	43
383	10	25.00	23.12	32.12	28.70	22.13	4	833	682	155
389	52	18.21	16.06	25.98	26.24	23.57	5	172	382	52
409	7	25.57	22.37	21.50	22.17	27.47	9	2	29	159
447	115	14.22	12.08	17.39	13.08	11.57	2	12	3	13
468	3	26.58	26.71	23.48	24.92	22.78	793	144	209	89

Table 3. Results of four different runs (continuation)

No	Or-der	Initial fitness	Average fitness A	B	C	D	Number of divisions A	B	C	D
517	27	20.80	19.67	18.77	18.45	19.74	35	14	8	82
527	349	7.62	7.88	7.67	26.40	8.35	2	1	177	1
556	23	21.61	25.26	18.84	16.56	21.45	325	34	37	74
572	43	19.59	25.96	18.41	20.10	24.55	338	0	35	32
584	165	11.73	11.29	11.74	26.63	11.68	1	7	58	2
607	32	20.21	23.38	18.08	18.04	17.45	261	60	50	73
609	150	12.36	11.42	12.19	19.15	30.64	4	1	11	1830
632	6	25.64	19.28	19.23	26.76	22.28	79	62	284	18
633	13	24.31	18.42	24.93	21.25	22.69	9	0	66	2
637	9	25.29	24.60	26.54	23.14	23.38	443	979	138	626
642	48	19.19	21.56	27.03	27.50	18.26	190	326	300	28
657	14	24.03	19.63	27.61	24.02	16.82	54	311	273	4
669	5	25.78	25.38	25.36	23.61	23.86	338	91	82	28
670	229	9.57	9.72	9.47	9.69	31.25	1	12	1	3424
688	72	16.08	35.42	16.06	13.56	20.01	10810	11	11	101
694	283	8.23	7.98	8.57	8.13	8.21	1	1	1	1
698	30	20.50	21.51	18.36	18.97	15.40	193	32	12	5
699	28	20.76	23.24	16.12	15.89	21.43	157	15	3	67
714	143	12.63	23.85	22.65	11.46	28.93	221	177	3	602
727	18	22.04	20.64	20.85	22.46	20.23	12	131	102	40
738	57	17.44	26.25	34.47	28.01	15.83	23	8390	871	2
752	54	17.96	36.99	21.70	35.11	27.72	19939	84	10549	270
761	12	24.66	24.42	22.33	25.82	21.83	287	73	23	41
778	39	19.70	33.04	17.73	23.78	29.67	1348	4	102	1995
804	16	23.30	21.49	35.02	22.03	31.20	44	1929	1	2989
840	559	4.31	4.32	4.31	30.15	4.30	1	2	1388	1
880	26	20.95	14.24	23.79	23.05	24.32	15	196	162	348

Actually in Kauffman's theory it is not stated that enzymatic interactions of real living organisms may be described by pure random Boolean networks. According to Kauffman's central intuition evolution was moving inside the critical region where any optimization is more effective. We cannot evaluate the biological merits of disjoint cycles, which are only mathematical consequences of the use of fitness function (5). However it is very likely that dynamics of living organisms have some similar specified structural properties which developed during the evolution as some practical device for metabolism.

New fitness function With all the experiences of discussed runs we think that a fitness function of type

$$\varphi = \sum_{i=1}^{\kappa} \log(\beta_i) \log(\gamma_i), \tag{6}$$

would be more appropriate. It penalizes cycle length 1 in the same way as fitness function (5) did it for frequency 1.

Mutation endurance Evolution in Tierra environment is more than a mere optimization. Usually it is not enough for a family to have one member with high fitness. We are not cloning our animals, they are permitted to reproduce themselves with a rather high mutation rate only. We observed many cases when the structure of one animal was on the top of the fitness landscape, yet practically all descendents of the animal were killed and the entire family died out eventually. For example stem animal 201 in Table 3 had initial fitness 4.32, and it was killed in runs B, C, D but developed an average fitness 26.64 prospering in a short period in run A. Or see stem animal 409 with average fitness equal to initial fitness 25.57 and moderate number of divisions in all of the four runs.

The case $K = 1$ revisited There are two trivial Boolean functions, one is identically 0, the other is identically 1. Coordinates with such g_i-s are frozen immediately. For large K-s if we exclude these functions it does not keep the systems off frozen states but for $K = 1$ their inclusion or exclusion is crucial. Without them only two other Boolean functions remain, the identity and its "opposite" function which orders 1 to 0 and 0 to 1 (we call this function flipping). A system with these functions reduces to the prototype system but now the coordinates are playing the role of states. (In other words we consider a directed graph in N dimension instead of 2^N dimension, see H. Flyvbjerg - N.J. Kjaer(1988).) If the connection graph consists of one cycle then all states are cyclic and usually the cycle length of the dynamics is equal to either the length of cycle of connections or twice of that number depending on the parity of number of flipping functions in the cycle (it may be some divisor of this number). Cycle length of dynamics with many cycles in the directed graph of changing bits is the smallest common multiple of cycle lengths corresponding to individual cycles. Asymptotics of cycle length of the dynamics is connected to the following question.

Let m be a large number. Starting from $Y_0 = m$ let us define a sequence Y_t by the recursion that Y_t is uniformly distributed on the integers $0 \le s < Y_{t-1}$. The process terminates with $Y_\tau = 0$. Question: what is the asymptotic distribution of the smallest common multiple of differences $(Y_{t-1} - Y_t), \quad (t = 1, \dots, \tau)$?

Lipschitzian random fields Let f be an arbitrary mapping from U to U and let us define its potential by

$$Q(f) = \sum_{\varepsilon', \varepsilon'' \in U} 2^{-3\delta(\varepsilon', \varepsilon'')} \frac{\delta(f(\varepsilon'), f(\varepsilon''))}{\delta(\varepsilon', \varepsilon'')},$$

where δ is Euclidean (or what is the same, Hamming) distance. Let the probability of f defined by

$$P(f) = \text{const} \exp(-\frac{Q(f)}{T}),$$

where T is a parameter (temperature). The attractor structure of this random field depends on parameter T, for large T the field is chaotic, for small T it is convergent. With appropriate parameter T the fitness function of this random field is as good as the one for critical random Boolean networks. Our conjecture is that critical behavior corresponds to Lipschitzian constants about 1 in these fields.

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