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INSTABILITY, COMPLEXITY, AND EVOLUTION

Abstract. In this paper, we consider a new class of random dynamical systems which contains in particular neural networks and complicated circuits. For these systems we consider the viability problem: we suppose that the system survives only if the system state is in a prescribed domain Π of a phase space. The approach developed here is based on some fundamental ideas proposed by A. Kolmogorov, R. Thom, M. Gromov, L. Valiant, L. Van Valen, and others. Under some conditions it is shown that almost all systems from this class with *fixed* parameters are unstable in the following sense: the probability P_t to leave Π within time interval $[0, t]$ tends to 1 as $t \to \infty$. However, if it is allowed to change these parameters sometimes ("evolutionary" case), then possibly that $P_t < 1 - \delta < 1$ for all t ("stable evolution"). Furthermore we study the properties of such stable evolution assuming that the system parameters are coded by a dicsrete code. This allows us to apply the complexity theory, coding, algorithms etc. Evolution is a Markov process of this code modification. Under some conditions we show that the *stable* evolution of unstable systems possesses such general fundamental property: the relative Kolmogorov complexity of the code cannot be bounded by a constant as time $t \to \infty$. For circuit models we define complexity characteristics of these circuits. We find that these complexities also have a tendency to increase during stable evolution. We give concrete examples of stable evolution.

To the memory of A. N. Livshitz

1. Introduction. Structural stability, instability, and complexity

1.1. Some main ideas

The aim of this paper is to connect concepts of structural stability and genericity with the Kolmogorov complexity theory in order to explain main properties of biological evolution. To describe mathematically biological systems, we consider classical main models of mathematical biology (circuits, reaction-diffusion equations). This paper develops our previous results [67, 64, 65] and uses basic concepts proposed by M. Gromov–A. Carbone, and L. Van Valen [70, 27]. Also we apply some ideas from ergodic theory.

Recall that R. Thom [16] proposed the concept of structural stability to describe complex structures observed in biology and other applications. This approach has been successfully applied by many authors (*catastrophe theory*). However, this fundamental concept also meets some serious difficulties (see an interesting discussion in [54]).

Quite opposite ideas were proposed in [70] and [27]. Basing on some experimental data L. Van Valen concluded that biological species are unstable but evolution can stabilize them. This assertion (the so-called Red Queen hypothesis) drew upon the apparent constant probability of extinction in families of related organisms.

Another variant of this idea is recently proposed by M. Gromov and A. Carbone: "Homeostasis of an individual cell cannot be stable for a long time as it would be destroyed by random fluctuations within and off cell. There is no adequate mathematical formalism to express the intuitively clear idea of replicative stability of dynamical systems" (see [27, p. 40]).

These ideas [70, 27] lead to two hypothesis. First, that functioning of biological systems are unstable (in particular, under random perturbations). Second, these systems can be stabilized by replication (evolution). Here we concentrate our attention to M. Gromov–A. Carbone variant since it is more mathematically tractable.

Recall that homeostasis (a basic concept introduced by celebrated french physiologist Claude Bernard) means supporting of life functions of a system. It is well known that biological molecules and chemical mechanisms in the cell are fragile under environment variations. Thus, in order to support their functioning, some main characteristics of the cell (temperature, pressure, pH, reagent concentrations) must be within some sets (*viability* domains) [2–5].

We denote these domains by Π. In general, they can depend on time. Moreover, one can consider a more complicated model, when there is a probability $0 < q(u) < 1$ to be viable even outside of Π and then the state must leave Π many times before to be destroyed.

1.2 Outline of approach and main results

Using ideas of the Pfaffian function theory, we introduce a new class of random dynamical systems. This class contains both polynomial differential systems and circuits of neural or genetic type.

It is shown that our systems enjoy many remarkable properties. For example, for them one can define natural complexity characteristic [67, 64, 65]. They can simulate all Turing machines [39], generate any structurally stable dynamics [69] and spatio-temporal patterns [68, 63, 67].

For our systems a natural measure of the stochastical stability can be defined. This measure is a probability $P_T(\Pi, u_0)$ that for $t \in [0, T]$ the system state (that can evolve in time) stays in the domain Π if $u(0) = u_0$. This measure is well known and studied [73]. For brevity, if the system state stays within Π for $t \in [0, T]$, we say that our system survives on $[0, T]$ (or the system is viable on $[0, T]$, see [2, 3]).

Genericity concept also plays here an important role. The systems under consideration can depend on some parameters $\mathcal{P}$. We use some measures μ on the set of all possible values of $\mathcal{P}$. Then a property is generic if this property holds for almost all systems with respect to μ (see [36], where one can find an interesting discussion of this topic).

Results can be outlined as follows.

I. Systems with fixed parameters are unstable

We show that the survival probability $P_T(\Pi, u_0) \to 0$ as $T \to \infty$ for a generic system from our class *if system parameters $\mathcal{P}$ are fixed.* For some classes of circuits this property holds for all circuits and the probability $P_T(\Pi, u_0)$ can be estimated.

II. Complexity increasing in evolution of unstable systems

However, *evolving* systems with changing (from time to time) parameters can be stable even as $T \to \infty$. This means that

$$P_T(\Pi, u_0) > \delta > 0 \tag{1.1}$$

for all times $T > 0$. We find a connection between such a stable evolution and the Kolmogorov complexity (in the next subsection we discuss it in more detail). One can establish, under some assumptions, certain general properties of stable evolution (satisfying (1.1)). Surprisingly, one can show that such a stable evolution should have main features of biological evolution (systems must almost always make copies, the mutation probability is small).

III. Evolution of circuits

Above we have outlined some general results, but it would be interesting to find concrete examples of the stable evolution. We find such an example for circuits. When the domain Π is a simple structure, we give an example of stable evolution of circuits which are important in neural and genetic networks. There occur connections with the preferential attachment growth [6, 18], greedy algorithms and the Hebb rule for neural networks. This evolution strategy can be named centralization.

IV. Evolution of spatially extended systems

Dissipative infinite dimensional dynamical systems can be used as models of spatially extended biological systems. The most popular and well known models in population dynamics are given by reaction-diffusion equations and systems. We consider such systems with random parameters of two kinds. The first ones describe a random influence of an environment and the second ones are discrete variables that determine a random Markov evolution. Under some biologically natural assumptions we describe a stable evolution process leading to more and more complex patterns.

Biological and physical interpretations of these results are given in Conclusion, where we also make a comparison with experiments.

1.3. Evolution and complexity: outline of model

Let us precise the result **II**. We assume that evolution is a modification, from time to time, of a discrete parameter which codes parameters of our systems. Our evolution model consists of a random dynamical system, where the form of this system depends on a discrete parameter, together with an associated Markov process of this parameter time evolution (see Sec. 2.4).

We can suppose, without loss of generality, that this parameter is a binary string s, the string length is $l(s)$. Such assumptions allow us to apply ideas of the Kolmogorov complexity theory.

Let us remind briefly some basic notions. Nonformally speaking, given a programming language F, the complexity $K_F(s)$ of a binary string s is the minimal length of a program to compute s [42, 80] (called *Kolmogorov complexity with respect to* F). (In a more formal statement, we should say about Turing machine recursive functions etc. instead of programs and computers.) The fundamental invariance theorem asserts, roughly speaking, that K_F, is independent of programming language choice (up to constant): $|K_F(s) - K_G(s)| < C$, uniformly in $l(s)$, where F and G are two universal languages, C is a constant. So, we may talk about some universal complexity $K(x)$. Such a complexity invented by R. Solomonoff, A. Kolmogorov, and G. Chaitin in 1960s, is a surprisingly deep notion having connections both with key mathematical notions as randomness, Godel's incompleteness theorem, Turing's halting problem, and fundamental physics (entropy, Shannon information). We use here the incompressibility theorem which asserts that the most of words are incompressible, in other words $K(s)$ is close to $l(s)$ for almost all words of a given length $l(s)$.

Our result asserts that if a Markov evolution (performed by a discrete code g in a class of generically unstable systems) is stable, then the Kolmogorov complexity and the length of the corresponding code $g(T)$ cannot be a priori bounded: for each C there is a moment $T(C)$ such that $K(g(T)) > C$.

1.4. Organization of the paper and main mathematical tools

In the next section, we consider main models that will be under consideration. In Sec. 3, we formulate main results: theorems on instability of systems with fixed parameters and complexity increasing in the stable evolution of such systems. We prove the results on instability in Sec. 4. Here the main problem is to describe a large class of unstable systems, simultaneuosly important for applications and mathematically tractable. To resolve this dilemma between generality and tractability, we use here the fruitful tool due to Ascold Khovanski [38]: Pffafian and Noetherian function theory. This theory has many applications in pure mathematics: computations and algorithms in algebraic geometry, O-minimality etc. The contemporary overview of this approach can be found, for example, in [20, 22], some results in [23–26] and applications for biology in [64, 65, 67]. By this approach we introduce a new class of random dynamical systems which contain many previously studied important systems (neural and genetic circuits) and, on the other hand, for such systems we can prove some general results on instability.

In Sec. 5, we prove general results on complexity increasing in stable evolution of such unstable systems. It can be done by elementary probabilistic estimates and basic facts of the Kolmogorov complexity theory [42]. We also discuss here connections of this approach with some simple stochastical models of biological evolution and random dynamical system theory [73], with the second law of thermodynamics.

Sections 6 and 7 give two examples of the stable evolution. The first one describes a stable growth of a graph associated with a neural (gene) network. The second one concerns with spatially extended biological models. They can be defined by infinite dimensional dynamical systems. First we give an estimate of stochastic stability using standard ideas of the attractor approach [28, 40, 59, 31]. This estimate allows us, in the second part of this section, to describe a mechanism of a stable evolution. Here we use some biological arguments fundamental probabilistic tools (concentration inequalities, see [11, 57, 58, 10] and also ideas of the recently developed theory of the phase transitions in hard combinatorial problems [77, 13, 14]).

The last section is a conclusion, where we discuss mathematical results in connection with biological experimental data.

2. Systems under consideration

2.1. Some random dynamical systems

Let us remind the notion of a Pfaffian chain [38, 22–26].

Definition. *A Pfaffian chain of the length r and degree $d \geqslant 1$ is a sequence of real analytic functions $f_1(x), f_2(x), ..., f_T(x)$ in $\mathbf{R}^n$ with the following property: every f_j, $1 \leqslant j \leqslant T$ satisfies a Pfaffian equation*

$$\frac{\partial f_j}{\partial x_k} = g_{kj}(x, f_1(x), ..., f_j(x)), \tag{2.1}$$

where g_{kj} are polynomials of degrees $\leqslant d$. Then T is called the length and d the degree of the Pfaffian chain.

Pfaffian functions are well studied. They enjoy the following properties: the sum and the product of two Pfaffian functions f_1 and f_2 of lengths r_i and degrees d_i are again Pfaffian functions of length $r_1 + r_2$ and degree $d_1 + d_2$ for both the sum and the product. Superpositions of Pfaffian functions also are Pfaffian (see [22] for details).

Consider some elementary examples. The exponent $\exp(ax)$, $x \in \mathbf{R}$ is a Pfaffian function of length 1 and degree 2. More generally, any real analytic function $f(z)$, $z \in \mathbf{R}$ satisfying an equation

$$\frac{df}{dz} = g(z, f) \tag{2.2}$$

is a Pfaffian of degree $deg(g)$. We observe thus that many classical sigmoidal functions are Pfaffian. For example, $f = (1 + \exp(z))^{-1}$ satisfies (2.2) with $g = f^2 - f$. Superposition $\sigma(\exp(ax))$ also is a Pfaffian, etc. Notice, however, that there exist many important analytical functions that are not Pfaffian (for example, $f = \sin z$). They can be included in a more general class of Noetherian functions [20, 22].

Note that there is a connection with the Kolmogorov complexity concept. In fact, let us consider an analytic function $f(z)$ (for example, $f = \exp(z)$). We can compute this function, up to a small correction, by the Taylor series (presenting f by a polynomial, and writing down all polynomial coefficients). On the other hand, we have a very short description of this function by a differential equation $f' = f$.

We consider random dynamical systems with discrete time

$$u_i(t+1) = f_i(u(t), \xi(t)), \quad t = 0, 1, ... \tag{2.3}$$

where $u = (u_1, u_2, ..., u_n) \in \mathbf{R}^n = H$, $\xi(t) = (\xi_1(t), \xi_2(t), ..., \xi_m(t))$, $\xi_k(t)$ are random processes with discrete time. Initial conditions are

$$u_i(0, x) \equiv \phi_i. \tag{2.4}$$

We shall formulate assumptions on ξ below. One can investigate a more general case, where u are elements of a Banach space B, for example, u_i can be functions of t and x, $x \in \Omega \subset \mathbf{R}$, $\phi_i = \phi_i(x)$.

Let us consider the following class of systems (2.3):

Class Kh (in the honour of A. Khovanski).

The class **Kh** *consists of random dynamical systems (2.3), where f_i are Pfaffian functions in u, ξ.*

This class is sufficiently general: it contains subclasses important in applications. On the other hand, investigating these systems we can use the powerful tools from the theory of Pfaffian and Noetherian functions [38, 22, 20, 23–36]. The first subclass **KP** is given by f polynomial in ξ, u:

$$f_i = \sum_{l, l', |l| \leqslant d, |l'| \leqslant d'} b_{ill'} u^{l'} \xi^l \tag{2.5}$$

where $l = (l_1, ..., l_m), l' = (l'_1, ..., l'_n)$, are integer multindices, $\xi^l = \xi_1^{l_1} ... \xi_m^{l_m}$, $l_i, l'_j \geqslant 0$ and $|l| = l_1 + l_2 + ... + l_m$.

The simplest, well studied in control theory [14, 56] subclass of **K** (we refer it as class **KL**) is defined by f of the form

$$f_i = g_{0i}(u) + \sum_{k=1}^{m} \xi_k g_{ki}(u), \tag{2.6}$$

where g_{ki} are polynomials.

Moreover, the class **Kh** contains a number of other physically and biologically interesting systems, in particular, some neural and genetic circuit models. Genetic circuits were proposed ([21, 60, 16, 47–53] among many others, see [55] for a review) to take into account theoretical ideas and experimental information on gene interaction. Model [16] uses Boolean algebra (so-called Boolean switch network). Models [47–53] can be considered as a generalization of the Hopfield model of attractor neural network [33]. We consider here the following model

$$u_i(t+1) = \sigma\Big(\sum_{j=1}^{N} K_{ij} u_j(t) + h_i - \xi_i(t)\Big), \qquad (2.7)$$

where $t = 0, 1, 2, ..., T$, $i = 1, 2, ..., N$, for positive integers T, N and $u_i(0) = \phi_i$. To use methods of the Pfaffian function theory, we must suppose here that the function σ is a strictly monotone increasing function such that $\lim_{z\to-\infty} \sigma(z) = 0$, $\lim_{z\to\infty} \sigma(z) = 1$ and satisfying the differential equation

$$\sigma' = P(\sigma), \qquad (2.8)$$

where P is a polynomial. The well known example can be given by $\sigma(z) = \frac{1+\tanh(z)}{2}$ (here $P = \sigma(1-\sigma)/2$). The polynomial P satisfies the following properties: $P(0) = 0, P(1) = 0$, and $P(z)$ is positive for any $z \in (0, 1)$.

Under condition (2.8), Khovanskii's [38] results can be applied to system (2.7). In fact, it is obvious that Eqs. (2.7) define a Pfaffian function of u, ξ.

Let us introduce complexity of chain (2.7) as the tuple of integers

$$\mathrm{Comp} = \{\, N, T, \deg P\}, \qquad (2.9)$$

where $\deg P$ is the degree of the polynomial from (2.9) that defines σ.

Moreover, the class **Kh** also includes complicated circuits with nonpair interactions, for example

$$u_i(t+1) = \sigma_i(S_i), \quad S_i = \sum_{j} K_{ij} u_{j_1}(t)...u_{j_n}(t) + \sum_{l=1}^{m} M_{il}\xi_l + h_i, \qquad (2.10)$$

where j is a multiindex. If $\sigma_i = H$, where H is the step function, $H(z) = 0$ for z, 0, and $H(z) = 1$ for $z \geqslant 0$, Eqs. (2.10) give a model of boolean networks.

2.2. Some results on (2.7)

In a part of this paper we focus our attention on model (2.7) (although many results can be generalized to (2.10)). Let us remind some known facts.

It is well known that (2.7) with $\xi_i = 0$ can simulate any complicated dynamics on bounded time intervals and generate complicated patterns [19, 30, 34]. They can generate any structurally stable dynamics [69] including some chaotic attractors. The most fundamental fact about (2.7) is that these systems can simulate, in a sense, all Turing machines [39], i.e., perform any computations.

2.3. Assumptions to random processes ξ.

We suppose the following. Let δ be a small positive number. Let $V(\theta, \delta)$ denote the δ – neighborhood of $\theta \in \mathbf{R}^m$.

Assumption 2.1. *Suppose that $\xi_i(t)$ are Markov processes with discrete time, $t = 0, 1, 2, ...$ Assume, moreover, that for each $\delta > 0$ and for each $t > 0$, $\delta > 0$ the probability that the process $\xi(t)$ attains the neighborhood $V(\theta, \delta)$ is positive:*

$$\mathrm{Prob}\{\xi(t) \in V(\theta, \delta)\} > c(\delta) > 0, \tag{2.11}$$

where a constant $c(\delta)$ is uniform in t.

Results for (2.7) hold under a weaker condition formulated in the corresponding section. Physically these assumptions can be interpreted as existence of strong fluctuations. They hold for many stochastic processes.

2.4. Evolution

Let us suppose that the parameters of systems (2.3) can depend on some variables s ("internal parameters"). Let us consider first the case, where s takes some discrete values $s_i \in S$, S is a finite or countable set. Denote by $N(S)$ the number of such states. We can suppose that s are binary strings. Let us denote by S_∞ the set of all possible finite binary strings such as 01...0 (of all possible lengths l) and suppose $S \subset S_\infty$. We extend our phase space H, where $u \in H$, to $H \times S$. Notice that possibly $S = S_\infty$. Suppose that, for fixed s, the time evolution of u is defined by Eqs. (2.3), where coefficients of polynomials g depend on s.

Then in (2.3) the right hand sides f_i also depend on $s \in S_\infty$ through g that define f by (2.5). An evolution of s is defined by a Markov chain $\mathbf{M}$ with discrete time and with countable state set S_∞, with transition probabilities $p_{s's}(u)$ to go in s' from s and, in addition, a Markov process (2.3) that defines an evolution u. Transition probabilities at moment t can depend on the current state $u(t)$.

To describe the effect connected with the viability domain Π we follow the standard construction [73]. We introduce formally an absorbing state

a such that $p(a \to s, u) = 0$ for each s. If u leaves the viability domain $\Pi(t)$, this means that the system state attains this absorbing state.

So, our model is defined by:

1) a family of random dynamical systems (2.3) in $\mathbf{R}^n$ with $f_i = f_i(u, \xi, s)$, $n = n(s)$, where f_i are defined by (2.5), $i = 1, 2, ..., n(s)$;

2) by the set $\Pi \subset \mathbf{R}^n$;

3) the Markov chain $\mathbf{M}$ with the state space $S \cup a$ and the transition matrix $\mathbf{W}(u)$ with entries $p_{s's}(u)$ (the transition probability from s' to s depending on u) such that $p_{as}(u) = 0$. Moreover, we suppose that if $u(t) \in \Pi$ then the process stops, $s(t) = s(t+1) = ... = a$.

About dependence of f on s we suppose the following. All possible values of the coefficients $b_{ill'}$ defined by (2.5) form an Euclidian space E_L of dimension $L(d) > 0$, which can be equipped by the standard Lebesgue measure ν_L. It is reasonable to assume that these coefficients are some random functions of s. Let L_l be the set of all the binary strings with lengths $\leqslant l$. Let us introduce measures μ_l on the sets of all possible maps $b : L_l \to E_L$. Suppose that there holds.

Assumption 2.2. *Suppose A is a set of ν_L − measure 0 in the space E of the coefficients $b_{ill'}$. Then for each length l the probability that the value of the map β lies in A is zero:*

$$\mu_l(B) = 0, \quad B = \{b : \text{ there exists } \ s \in L_l \text{ such } \ \text{that } b(s) \in A\}.$$

This assumption admits a very simple interpretion. Suppose we choose a random point b inside a finite dimensional space and we aim into a set A. Then it is impossible to expect that we will have a success ($b \in A$), if the set A of zero measure and if we make only a bounded number of such random attempts.

For (2.7), we assume that evolution is performed by changes in a directed graph (V_N, E) associated with the matrix K_{ij}. The vertices of this graph is the set $V_N = \{1, 2, ..., N\}$, an edge $(i \to j) \in E$ if and only if $K_{ij} \neq 0$.

Each step of evolution may consist of: 1) either (V_N, E) stays the same, 2) either one adds a node to V_N that gives V_{N+1}, the edges E conserve, 3) or one adds an edge $i \to j$ to E with a new weight K_{ij}.

Definition 2.3. *Denote by $P_T(\Pi, u_0)$ the probability that $u(t) \in \Pi$ for all $t = 1, 2, ..., T$ if initial data $u(0) = u_0 \in \Pi$. We say that the evolution is stable, if there is a positive δ such that $P_T(\Pi, u_0) > \delta > 0$ for all integers $T > 0$ and all u_0.*

If such an δ does not exist we say that the evolution is unstable.

Notice that it is natural sometimes to introduce a probabilistic measure η on the set of initial data u. We suppose that the measure η has a support in Π. In this case, the averaged probability to survive during the time interval $[0, \Pi]$ is defined by $P_T(\Pi) = \int_\Pi P_T(\Pi, u)\eta(u)du$.

3. Main results

3.1. Instability of systems with fixed parameters

Here we consider the case when the evolution is absent, i.e., $S = \emptyset$. Let us denote by $d_{\max}$ the maximum of the degrees of g_{il}. Let us consider a nondegenerated gaussian measure ν in the space E of coefficients of polynomials g_{il} of the degree $d_{\max} = d + d' + d''$. Let us denote by $P_\Pi(u, t)$ the probability to stay in Π at the moment $t + 1$, under condition that, at the previous moment t, the system was in a state u.

Theorem 3.1. *Let us consider systems* (2.3) *of the class* **KL**, *where* f *is defined by* (2.6). *Suppose* $m \geqslant 2$, *i.e., there are at least two noises and the set* Π *is bounded:* $\Pi \subset B_R$, *where* B_R *is a ball of radius* R. *Then for almost all (with respect to a measure* ν *in the space of coefficients) polynomials* g_{ki} *from* (2.6) *one has:*

$$P_\Pi(u, t) \leqslant 1 - \delta(g) < 1 \tag{3.1}$$

where $\delta(g) > 0$ *is uniform in* $u \in \Pi$, $t = 0, 1, 2, \ldots$.

Thus, a generic system (2.3) with fixed parameters is unstable, i.e., $P_T(\Pi, u_0) \to 0$ as $T \to \infty$.

Theorem 3.2. *If* $m \geqslant 2$ *and* $d > 0$, *the same assertion holds for systems of the class* **KP**.

To prove instability of circuits (2.7) we should seek new arguments since these theorems are not applicable to this case. For circuits (2.7) one can give more explicit estimates that hold for all circuit systems, not only for generic ones. Let $N_k = \{i_1, i_2, \ldots, i_k\}$ be a set of different indices, i_l, $1 \leqslant i_l \leqslant n$. We refer these corresponding nodes as key ones. Let us consider the sets Π such that

$$\Pi \subset \{u_{i_l} > \delta_l > 0\}, \quad i_l \in N_k. \tag{3.2}$$

In this case, we define the complexity of circuit (2.7) as the minimal valency V of the key nodes:

$$V = \min V_i, \quad i \in N_K, \tag{3.3}$$

where the valency of the node is the number of links connecting this node with other ones; in our case the valency of ith node with the state u_i is the number of nonzero entries K_{ij}.

In this paper, we extend our previous estimates [65], which show that the survival probability of each circuit (2.7) of a fixed structure tends to zero as $T \to \infty$. Therefore, "homeostasis" performed by a fixed circuit (2.7) will be inevitably broken for sufficiently large times. The more is the complexity V the stabler is the circuit with respect to perturbations.

3.2. Complexity increasing in the process of evolution

Under assumptions of Theorem 3.1 or 3.2 let us consider systems (2.3) from class **KP** or **KL** with f_i, g_{ik} depending on s, where the binary string s evolves according to a Markov process as described above (see Sec. 2.4). We consider more general Pfaffian systems in the end of Sec. 5.

There holds

Proposition 3.3. *If the Markov chain* $\mathbf{M}$ *and* (2.3) *generate only strings with a priori bounded lengths* $l(s) < C$ *then for almost all maps* $s \to b(s)$ *of strings* s *to the coefficients* b *the corresponding evolution is unstable (the corresponding system is not viable):* $P_T(u, \Pi) \to 0$ *as* $T \to \infty$.

Theorem 3.4. *If the Markov chain* $\mathbf{M}$ *and system* (2.3) *generate only strings with a priori bounded relative Kolmogorov complexities* $K_F(s) < C$ *then for almost all maps* $s \to b(s)$ *of strings* s *to the coefficients* b *the evolution is unstable (the corresponding system is not viable):* $P_T \to 0$ *as* $T \to \infty$.

Remark 1. Coefficients b are defined by (2.12) and "almost all" with respect to some measure μ_l (see Assumption 2.2).

Remark 2. Actually, in Theorem 3.4 instead of K_F one could take any function K' enjoying the following property: for any n there exists at most a finite number of s such that $K'(s) = n$. Clearly, this property together with inequality $K'(s) < l(s) + \text{const}$ (which usually holds for relative Kolmogorov complexities) would imply the incompressibility (cf. above).

Below under complexity we mean K_F for a certain fixed F.

Theorem 3.4 gives only a general property of stable evolution that says nothing about existence of such an evolution.

Notice that for biologically realistic models the question on existence of stable evolution is not obvious. We give natural examples of such stable evolutions in Secs. 6 and 7.

4. Instability

4.1. Instability in general case

Let us prove Theorem 3.1. We start with the following preliminary lemma, which immediately implies the theorem.

Lemma 4.1. *Suppose* Π *is a compact set. Let us consider a system of polynomial equations*

$$g_i(u) = 0, \quad i = 1, ..., N, \tag{4.1}$$

where g_i *are polynomials of* $u = (u_1, u_2, ..., u_n)$. *Assume that the number of equations* N *in* (4.1) *is more than the number of variables* n. *Then the probability that this system has a solution* $u_* \in \Pi$ *equals* 0.

The formal proof of this obvious assertion is as follows (notice that there is another easy proof using the resultant theory, see Van der Waerden [75]). Let us introduce an auxiliary function of the variables u and the coefficients b_α of the polynomials g_i:

$$\phi_\epsilon(b, u) = \exp(-\epsilon^{-2} S(u)) \tag{4.2}$$

depending on a parameter ϵ, where $S(u) = \sum_{i=1}^{N} g_i(u)^2$. Let us consider now the integral

$$I_\epsilon = \int_\Pi \int \phi_\epsilon(u, b) d\nu(b) d^n u. \tag{4.3}$$

Since ν is an exponentially descreasing function, we can change the order of integration in (4.3).

Suppose that there is a set A of coefficients b_{ik} of polynomials such that $\nu(A) > 0$ and that there is a solution $u_*(b)$ of system (4.1) for all polynomials with coefficients $b \in A$. Then $\phi_\epsilon > \delta > 0$ in a ball of radius ϵ centered at $u_*(b)$. Thus, by integrating first over u and then over all b_{ik}, one obtains that

$$I_\epsilon > c\epsilon^n \nu(A). \tag{4.4}$$

Let us find now an upper estimate of this integral. Integrating first over all coefficients $b_{i,000..0}$ corresponding to terms of zero degree in u, we see that

$$\int \phi_\epsilon d\nu < C\epsilon^N. \qquad (4.5)$$

Therefore, due to compactness of Π, one has

$$I_\epsilon < C_1\epsilon^N. \qquad (4.6)$$

For $N > n$ estimates (4.4) and (4.6) lead to a contradiction as $\epsilon \to 0$. The lemma is proved. □

To demonstrate Theorem 3.1, let us observe that if $g_1(u) \neq 0$ or $g_2(u) \neq 0$ for each $u \in \Pi$, $\inf_{u\in\Pi}(|g_1(u)| + |g_2(u)|) \geqslant \kappa > 0$ since Π is contained in a compact set. But then Assumption 2.1 entails that $P_\Pi(u) < 1 - \delta(g)$. □

Proof of Theorem 3.2. Due to boundness of Π, there is a $R > 0$ such that if $|u| > R$ then $u \notin \Pi$. Let us prove that, generically, for each $u \in \Pi$ there is a value ξ such that $|f(u,\xi)| > R$. Let us set $m = 2$. One has

$$f_i = \sum_{l,|l|\leqslant d} h_{il}(u)\xi^l, \qquad (4.7)$$

where $h_{il}(u)$ are some polynomials. Let us consider a finite set $A = \{a_1, a_2, ..., a_{d+2}\}$, where a_j are mutually distinct positive numbers. Let us set $\xi_1 = z$, $\xi_2 = a_j z$, and let $z \to +\infty$. Then one has from (4.7) that

$$h_{il}(u) = 0, \ i = 1, ..., n, |l| = d. \qquad (4.8)$$

So, we have $n(d+1)$ polynomial equations with n unknowns u_i. Now we apply Lemma 4.1 and we obtain that generically (4.8) has no solutions and, therefore, generically $|f(u,\xi(z))|$ are not bounded as $z \to \infty$. Thus if $u(t) \in \Pi$ then, due to Assuption 2.1, there is a nonzero probability $P(u)$ that $|u(t+1)| > R$ and, consequently, $u(t+1) \notin \Pi$. □

4.2. Instability for circuits

In this section, we simplify and improve some results of [65] on instability of circuits (2.7). We suppose that circuits are under "strong" noises. Mathematically, this can be formulated as follows. Denote by $W_i(a)$ the set $W_i(a) = \{\xi : \xi_i < a\}$. We also assume that the domain Π is defined by (3.2).

We estimate the stability via the following parameters: the circuit complexity V (see 3.3), the maximum $|K_*|$ of absolute values of the entries K_{ij}, the maximum h^* of $|h_i|$. We can suppose, without loss of generality, that the set I of the key indices is $I = \{1, 2, ..., N_{\text{key}}\}$.

Assumption 4.1. *Assume that ξ is a time discrete Markov process with values in $\mathbf{R}^N$ such that for each i and a*

$$\text{Prob}\,\{\xi(t) \in W_i(a),\ t = 0, 1, 2..., T-1\} = \Phi_i(a, T) \to 0, \tag{4.9}$$

where $i \in I$, as $T \to \infty$.

Assumption 4.1 holds, for instance, when $\xi(t+1)$ are independent on $\xi(t)$ and ξ can take unboundly large values, for many Markov processes and walks. A large class of such ξ can be described as a section, at $t = 1, 2, ...$, time continuous diffusion processes. In this case, a rough asymptotics of Φ can be found by standard methods [8, 73,9].

The stability (survival in Π) depends on the structure of Π and asymptotical properties $\Phi_i(a, T)$ for large a, T.

Proposition 4.2. *Each circuit* (2.7) *with fixed parameters is unstable as $T \to \infty$, i.e., $P(T, \Pi) \to 0$ as $T \to \infty$.*

To prove this assertion, assume, without loss of generality, that $V_1 = \min_{i \in I} V_i = V$. Notice that $0 \leqslant u_i(t) \leqslant 1$ for all $t > 0$ (since $0 \leqslant \sigma \leqslant 1$). Thus, $|\sum_{j=1}^N K_{1j} u_j(t) - h_i| < VK^* + h^* = r$. Therefore, if $\xi_1(t) > a = r - \sigma^{-1}(\kappa)$, then one has $u_1(t+1) < \kappa$ and thus $u(t+1) \notin \Pi$. So, $u(t) \in \Pi$ for all $t = 0, 1, ..., T$ entails $\xi(t) \in W_1(a)$ for each $t = 0, 1..., T-1$. This gives

$$\text{Prob}\,\{u(1), ..., u(T) \in \Pi\} < \Phi_1(a, T) \to 0$$

as $T \to 0$. □

5. Properties of stable evolution

5.1. Proof of Theorem 3.4

First let us show that, for unstable systems, stable time evolution is possible only when the code complexity is unbounded in time. Consider systemes of the class **KP**. They are defined by (2.3) and (2.5), dependence of g_{ik} on s is defined by a random map $s \to b(s)$, where $b(s)$ are coefficients (see (2.12)), and this map satisfies Assumption 2.2.

First let us prove Proposition 3.3. Suppose that the lengths of all codes s a priori bounded by an integer l. Let us denote by $p(s(t), u(t), t)$ the probability to survive (to stay in Π) at the moment $t+1$ under the condition that, at the moment t, the system is in the state $u(t)$ and the system is coded by $s = s(t)$. Then, since our process is a Markov one, the probability $P_T(\Pi)$ to be in Π at time moments $0, 1, ..., T$ is the product

$$P_T = p(s(1), u(1), 1)p(s(2), u(2), 2)...p(s(T-1), u(T-1), T-1).$$

(in fact, the probability to be in Π at moment $t+1$ depends only on the current state $u(t)$, $s(t)$, and t). One observes then that the evolution is stable if

$$\log P_{T+1} = \sum_{t=1}^{T} \log p(s(t), u(t), t) > -C, \quad C > 0 \tag{5.1}$$

uniformly in T. Using Theorem 3.1 one has

$$\log P_{T+1} = \sum_{t=1}^{T} \log p(s(t), u(t), t) \leqslant \sum_{t=1}^{T} \log(1 - \delta(g(s(t)))$$

$$\leqslant T \log(1 - \min_{s \in L(l)} \delta(g(s))) \leqslant \mathrm{const}\, T\kappa(l), \quad \kappa(l) = \min_{s \in L(l))} \delta(g(s)), \tag{5.2}$$

where $L(l)$ is a finite set of strings of lengths bounded by l, and here g denotes polynomials $g_{ik}(u)$ depending on s. This means that the coefficients b of polynomials g in (2.6) are real valued functions of s. Remind that these functions satisfy Assumption 2.2. Relation (5.2) entails that, if the evolution is stable, $\kappa(l) = 0$. Indeed, for a stable evolution $T\kappa \geqslant logP_{T+1} \geqslant -C$ for all T that gives us $\kappa(l) = 0$.

Let us compute the probability (with respect to the measure μ_l on the space of all maps $s \to b(s)$, see Assumption 2.2) that $\kappa(l)$ equals 0. Then one finds that this probability is zero. In fact,

$$\mathrm{Prob}\,\{ \min_{s \in L(l))} \delta(g(s)) = 0\} = 1 - \Pi_{s \in L(l)} \mathrm{Prob}\,(\{\delta(g(s)) > 0\}).$$

But, according to Assumption 2.2, the probability that, for a random map $s \to b(s)$, one has $\delta(g(s)) > 0$ (defined by the measure μ_L, see Assumption 2.2) equals 1. This completes the proof. □

Let us prove Theorem 3.4. First let us note that the lengths $l(s)$ of strings of the Kolmogorov complexity not exceeding K is a priori bounded: $l(s) < N_K$.

Therefore, all strings of complexity $< K$ are in a finite set $\mathcal{B}_K$ of binary strings. Thus we can repeat the arguments from the previous proof.

Remark. Notice, however, that between Proposition 3.3 and Theorem 3.4 is a key difference. For some relative Kolmogorov complexities K_F there are no effective bounds of $l(s)$ via $K_F(s)$, in particular, for the Kolmogorov complexity $K = K_F$ it follows from the well known Rabin theorem [76] (proved as well by G. Tseitin).

Thus it is impossible to estimate evolution stability, even in average, through the Kolmogorov complexity. However, at least theoretically, it may be possible to make it via $l(s)$.

5.2. Entropy and the second law of thermodynamics

In the next subsections, let us consider connections between the Kolmogorov complexity, entropy and the second law of thermodynamics. We make it first in the framework of simple Markov models. We shall show how one can obtain this simplified models from (2.3) in the end of this section.

Consider first the following simplified evolution model based on a Markov chain with a finite number of states $s \in L$, thus $length(s) \leqslant l$. Here L is a state space, the number of states will be denoted by $N = |L|$. Let $p(s,t)$ be the probability to be in the state with the code s at the moment t. We write down

$$p(s,t+1) = \sum_{s'} w_{s's} p(s',t) \tag{5.3}$$

where $w_{s's}$ are transition probabilities (from s' to s). We suppose (see above) that there is an absorbing state a such that $w_{as} = 0$ for all $s \neq a$. We denote by W the linear operator in the right-hand side of (5.3). Then (5.3) can be rewritten as $p(t+1) = Wp(t)$.

If we are dealing with an unstable system, then $w_{sa} = v(s) > 0$ is a positive (in biology, it is an "extinction probability"). Suppose that, if the absorbing state is excluded, chain (5.3) is ergodic and there is an equilibrium solution $p_{eq} = \pi(s)$ of (5.3) such that all $\pi(s) \neq 0$. This solution, defined by $\pi = W\pi$, is an eigenfunction of the operator W with the eigenvalue 1. Moreover, let us make the standard assumptions that all the rest eigenvalues λ_j of W satisfy $|\lambda_j| < 1$. Then our chain is not only ergodic but also it is exponentially mixing: one has $|p(s,t) - \pi(s)| < C\exp(-ct)$ for some $C, c > 0$.

If $v = 0$, the following classical assertion expresses mathematically the second termodynamic law for model (5.3). Let us consider two distributions $p_1(s)$, $p_2(s)$ of probabilities of codes s. Naturally, $\sum_{s\in L} p_i(s) = 1$ and $p_i(s) \geqslant 0$. If $p_2(s) > 0$ for all s, then we can introduce Kullback's information in p_1 with respect to p_2

$$H(p_1,p_2) = \sum_{s\in L} p_1(s)\log(p_1(s)/p_2(s)). \tag{5.4}$$

It is well known that the map $p_1 \to H(p_1,p_2)$ is convex and nonnegative. This functional can be interpreted as a conditional information (minus entropy) p_1 on p_2. One can show [9] that, under some conditions on

$w(s \to s')$, if $p_1(s,t), p_2(s)$ are two solutions of (5.3), that Kullbac's information $H_K(t) = H(p_1(t),\, p_2(t))$ is a nonincreasing in time t function. In particular, for any solution $p(s,t)$ of (5.3) the information

$$H(p(t)) = \sum_{s \in L} \pi(s) \log(\pi(s)/p(s,t)) \tag{5.5}$$

is also nonincreasing in t. This formula expresses the second law of thermodynamics (in our simplest case). The entropy $\mathcal{E}$ is defined by $\mathcal{E} = -H$. Below we shall find a connection of this function with the Kolmogorov complexity.

Let us turn to the case $v > 0$. If $v(s) > 0$, the probability $p(a,t)$ to be in the absorbing state a is an increasing in time function.

The case, that admits an asymptotical analysis, occurs if $v > 0$ is small enough (of order ϵ, where $\epsilon > 0$ is a small parameter). Then it is not difficult to show (using the standard methods, see[BhM, BK]) that for an arbitrary initial distribution $p(s,0)$, the time evolution of solutions of (5.3) can be described as follows. One has $|p(s,t) - \pi(s)| < C\exp(-ct)$ due to the mixing property. Within a relatively short stage (this time period is independent of ϵ) one has that the entropy $\mathcal{E} = -H$, where H is defined by (5.5), up to ϵ-small corrections.

To describe the dynamics for $t > O\,(|\log \epsilon|)$ we can use an asymptotical solution having the form $p(s,t) = C(t)\pi(s) + \widetilde{p}$, $s \neq a$, where $C(t)$ makes sense of the probability of survival states and $\widetilde{p}$ is a small correction such that $\sum_{s \neq a} \widetilde{p}(s,t) = 0$ for all t. The dynamics of $C(t)$ satisfies the equation

$$C(t+1) = (1-q)C(t), \quad q = \sum_{s \in L} v(s)\pi(s) + O(\epsilon^2). \tag{5.6}$$

Notice that $q = O(\epsilon)$, thus this dynamics of C is slow. Therefore, for the second stage the averaged extinction probability is $q > 0$ and q can be computed by (5.6). Here the survival is not possible: $C(t) \to 0$ as $t \to \infty$.

5.3. Process with countable state space

Let us consider now a more complicated situation, where survival is possible. Suppose that the state number $N(t)$ may increase in time. In the case of increasing state number $N(t)$ an asymptotic approach can be developed if we assume that new states (codes) s appear, in a sense, "seldom." Between these appearences at moments T_j, T_{j+1}, the probabilities $p(s,t)$ can be described by $p(s,t) = p_i(s,t)$, where $p_i(s,t)$ is a solution on $[T_j, T_{j+1}]$ for (5.1) with fixed state number N_j. Let us denote by $p_{eq,j}$ the corresponding stationary solution to (5.1) with the fixed state number and $v = 0$. We suppose that $|v(s)| < c\epsilon$ and $c_1\epsilon^{-1} < |T_j - T_{j+1}| < c_2\epsilon^{-1}$, ϵ is a small paramater, $c_i > 0$.

Then one can use the previous argeuments and one has:

I. For the first evolution stage on $[T_j, T_{j+1}]$, the entropy is defined by

$$\mathcal{E}_j = -\sum_{s \neq a} \pi_j(s) \log(\pi_j(s)/p_j(s,t)),$$

where π_j is an equilbrium state for the Markov chain without absorbing set at j-th stage. The $\mathcal{E}_j$ is a nondecreasing in time. The solution $p_j(s,t)$ tends to $\pi_j(s)$ with an exponential rate.

II. The second stage: $p_j = C_j(t)\pi_j + \widetilde{p}$, where all the evolution reduces to a time evolution of $C_j(t)$ according to (5.6), where $q = q_j$. The entropy $\mathcal{E}_j$ is equal to $\log(1 - C_j) + \text{const}$.

The stable evolution (in our sense) is possible if there is an infinite sequence of s such that $v(s) \to 0$ (a sequence of more and more stable states) and transition probabilities to these states are not too small. A necessary condition for possibility of such evolution is given by the elementary.

Proposition 5.2. *If the evolution is stable there is a sequence s_n such that $v(s_n) \to 0$ as $n \to \infty$.*

This assertion can be interpreted as follows: the stable evolution must generate new stabler states. An example of a stable evolution see Sec. 6.

5.4. Kolmogorov complexity and entropy

Let us discuss in more detail connections between the complexity $K(s)$ and the Kullback information (when π is uniform, this is the Shannon information connected with the classical entropy of statistical physics). Let us remind an important theorem proved by A. N. Kolmogorov [80] that reveals a connection between the Kullback (Shannon) information and complexity of individual codes.

Theorem. *Let r be a positive integer. Let a word x of length $i \cdot r$ consist of i words of length r, where kth word of length r occurs in x with the frequency q_k $(k = 1, 2, ..., 2^r)$. Then*

$$K(x) \leqslant i(-H(q) + \alpha(i)) + C,$$

where $H = -\sum_k q_k \log_2 q_k$, $\alpha(i) = C_0 i^{-1} \log i \to 0$ *as* $i \to \infty$.

Let us consider now a population of codes s evolving according to (5.1). Let us assume that the lengths of all s are a priori bounded by r. Let us compose a large word x connecting all s together and let us consider the complexity of x (complexity of the genetic pool of population).

The Kolmogorov theorem cited above shows that the genetic pool complexity is proportional, for large populations, to minus of the Shannon information (entropy) of this genetic pool.

5.5. Reduction of evolution model (2.3) to Markov chain (5.3), ergodicity and complexity of Pffafian function

Let us discuss now evolution model (see Sec. 2.4) for general systems (2.3). In this more complicated case, there are two variants to reduce evolution (2.4) to the cases considered in previous Secs. 5.1–5.4.

Variant A: Systems with simple attractors

Equation (5.3) can be deduced under some strong assumptions on dynamics (2.3). For example, one can assume that

$$f = f_0(u, s) + \kappa \sum_{k=1}^{m} h_k(u)\xi_k, \quad u = (u_1, ..., u_n) \in \mathbf{R}^n, \tag{5.7}$$

where κ is a small parameter, h_k are Pfaffian functions, all the equilibria of (2.3) for $\kappa = 0$ are hyperbolic rest points U^n for each code s defined by equation $U = f_0(U, s)$. We suppose that all $U^n \in \Pi$.

In this case, the space of discrete states S should be extended. Suppose that for $\kappa = 0$, Eqs. (2.3) and (2.7) generate a dissipative semiflow and thus we consider dynamics (2.3), (2.7) inside a bounded domain $D \subset \mathbf{R}^n$.

With each s we associate the set of possible local point attractors $U^1(s), ..., U^{k(s)}(s)$ of dynamical system (5.7) with $\kappa = 0$. The state of the Markov chain are now $(s, U^j(s))$, $j = 1, 2, ..., k(s)$. For each fixed s the Ventsel–Freidlin theory [73] allows us to estimate the probability p_{jk} of transitions from U^j to U^k for fixed s (they are exponentially small, $\log p_{jk} = O(\epsilon)$). After this extension we obtain (5.3) with a new larger state space.

Variant B: ergodic ideas and Pffafian functions

Again we suppose that for $\kappa = 0$, Eqs. (2.3) and (2.7) generate a dissipative semiflow and thus we can consider dynamics (2.3), (2.7) inside a bounded domain $D \subset \mathbf{R}^n$. We assume $\Pi \subset D$. Also let us suppose that system (2.3) with f defined by (2.7) is ergodic and mixing for $\kappa = 0$. If $\eta(u)$ is a measure describing a distribution of initial data (see Sec. 2.4) and let $\rho(u,t)$ be the measure obtained from η as a result of time evolution according to (2.3) and (2.7). Let us suppose that the following weak mixing proeprty holds: for is an arbitrary continuous function $\phi(u)$ such that $\sup|\phi| \leqslant 1$, one has $|\int\limits_{\Pi} \phi(u)(d\rho(u,t) - d\rho_{eq}(u))| < C\exp(-ct),\ C, c > 0$, where $\rho_{eq}(u)$ is a limit measure, constants C, $c > 0$ are idependent of ϕ. We suppose that the support of ρ_{eq} is a subset $\mathcal{M}$ contained in Π: $\mathcal{M} \subset \Pi$ and that this set contains infinitely many points. For example, it may be a manifold of a positive dimension.

For $\kappa \neq 0$, system (2.3), (2.7) generates a Markov chain. Let $W(u,\Gamma)$ be the transition probability from u to a set Γ. We can compute this transition probability by $W(u,\Gamma) = \mathrm{Prob}\,\{\kappa h(u,\xi,s) \in \Gamma - \{u\}\}$. This probability is small for small κ if $f_0(u) \notin \Gamma$.

Then, for small κ, the probability P_d to leave Π at the moment t admits the following asymptotics for as $t \to \infty$:

$$P_d(t) = \int\limits_{\Pi} W(u, \overline{\Pi}_D)d\rho_{eq}(u) + O(\exp(-ct)), \tag{5.8}$$

where $\overline{\Pi}_D$ is a complement of Π in D: $\overline{\Pi}_D = D - \Pi$. Notice that the first main contribution is constant $\overline{P}_d$. Under above assumption $\overline{P}_d > 0$ (exluding only for a trivial case $h_k \equiv 0$). In fact, if $\overline{P}_d = 0$ thus $W(u, \overline{\Pi}_D) = 0$ for all $u \in \mathcal{M}$. This entails that $h_k(u) = 0$ for all $u \in \mathcal{M}$. Pffafian functions are really analytic, thus, $h_k(u) \equiv 0$ for all $u \in D$.

This implies the instability result for non-polynomial in u Pfaffian case.

Proposition 5.3. *Then under above assumptions the probability to leave Π admits the estimate*

$$\overline{P}_d = \int\limits_{\Pi} W(u, \overline{\Pi}_D)d\rho_{eq}(u) > \delta > 0. \tag{5.9}$$

This result on instability is an analog of Theorem 3.2: a fixed Pfaffian system (2.3), (5.7) generated by Pfaffian functions h_k of a priori bounded complexity cannot be stable. However, if the code $s(t)$ evolves in time then a stable evolution is possible.

Suppose that the maximum of degrees of Pfaffian functions h_k is $\deg_h$ and the maximum of the lenghts is Length_h. There occurs a natural question about existence of estimates δ through $\deg_h$ and Length_h. It is possible only for particular classes of Pffafian functions that can be constructed by chains of a special form (to show it one can use results [26]).

6. Example of stable evolution: centralization strategy

To analyze the evolution process in more detail, let us consider the simplest model, where for each i, j either $K_{ij} = K_*$ or $K_{ij} = 0$. Then changing matrix K with time leads to a time evolution of a directed graph associated with K and vice versa, a growth of a directed graph generates an evolution of a network (2.7). The graph evolution can be then considered as an algorithm adding edges and nodes. As an example, let us consider two well studied evolution algorithms, the Erdös– Rényi one, [18], and the preferential attachment algorithm [6].

In Erdös–Rényi's algorithm, at time moments $0, 1, 2, ...$, one adds to a graph a new edge with a fixed probability p. This leads to a Gaussian distribution for the degree. In the preferential attachment algorithm [6] the probability that a new edge goes to the ith node is proportional to the valency (connectivity) of this node. The graph obtained by this algorithm has so-called scale-free structure [6], which can be illustrated by a map of a country. Looking on the map of a country we can often see a few of great cities and a number of small cities.

The main goal of this section is to demonstrate that a stable evolution is possible under some natural restrictions on the circuit growth. Let us formulate such restrictions. To simplify the statement, let us consider boolean circuits (2.7), where σ is the step function, $\sigma(z) = 1$ for $z > 0$ and $\sigma(z) = 0$ for $z \leqslant 0$. Assume that

R1. The averaged valency of the whole network is a priori bounded for all times:

$$\lim_{t \to \infty} N(t)^{-1} \sum_{i}^{N(t)} V_i(t) < K_c, \tag{6.1}$$

where K_c is a positive constant, $N(t)$ is the number of nodes involved in circuit (2.7). This assumption is consistent with experimental data [6, 35, 37]. Let us notice that the averaged valency of the key nodes is not bounded, according to the results obtained above.

R2. The evolution rate is bounded, i.e., at each evolution step, we add to the graph associated with the circuit at most one edge and at most one node. The weights K_{ij} are a priori bounded: $|K_{ij}| \leqslant K_*$;

R3. The noises $\xi_i(t)$ are random processes discrete time such that each $\xi_i(t+1)$ is independent of all previous $\xi_j(\tau)$ with $\tau < t+1$ and satisfying

$$0 < P(\xi_i(t) > a) < \exp(-\beta a) \tag{6.2}$$

for each $a > 0$ and for each fixed t, where β is a positive constant independent of t and a.

Theorem 6.1. *There is a growing circuit* (2.7) *satisfying* **R1**, **R2**, *and* **R3** *such that its stochastical stability does not vanish for large times:* $P_T > p_0 > 0$ *for all* $T > 0$. *The circuit averaged valency satisfies asymptotical relation* (6.1) *as* $t \to \infty$ *for any* A. *The circuit complexity* V *(defined by* (3.3)*) is unbounded as* $t \to \infty$.

Proof. Let us set $N_{\text{key}} = 1$, $r_i = 1$, $\overline{\theta} = 1, K_* > 0$. Let us suppose that at the initial moment we have $N = V_0$ nodes and the matrix $\mathbf{K}$ is defined by $K_{1j} = K_*$, $K_{j1} = K_*$, $K_{jj} = 0$, where $j = 1, 2, ..., V_0$.

At the time moment t, where $t = 1, 2, ...$, we can add a node and one edge connecting this new node with our key node. Let us denote by $V(t)$ the valency of the key node at the moment t. The total number of the nodes at the time moment t also is $N(t) = V(t)+1$. The nodes $2, 3, ..., N(t)$ are usual ones.

Let us find first an upper estimate of the probability $Q(t)$ that the circuit will be destroyed at a moment $t+1$ under condition that the circuit states were in Π at $\tau = 0, 1, ..., t$. This means that $u_1(\tau) = 1$ for $\tau = 0, 1, ..., t$ and $u_1(t+1) = 0$. Suppose that, at the time moment t, exactly k of the N usual nodes have values 0. The value $u_1(t+1)$ can become zero at the time moment $t+1$ as a result of the noise action on the key node. If $u_1(t+1) = 0$, this noise $\xi_1(t)$ satisfies the inequality:

$$\xi_1(t) > h + K_*(V(t) - k). \tag{6.3}$$

On the other hand, at the time moment t the ith usual node is not active only under the inequality

$$\xi_i(t-1) > h + K_*. \tag{6.4}$$

Therefore, due to our hypothesis **R3** and (6.3), (6.4), the probability $Q(t)$ admits the estimate

$$Q(t) < \sum_{k=0,\ldots,V(t)} \binom{V(t)}{k} \exp(-\beta(h + K_*(V(t) - k))) \exp(-\beta(h + K_*)k).$$

By summing over k one obtains

$$Q(t) < \exp(-\beta(K_* V(t) + h))(1 + \exp(-\beta h))^{V(t)} = \rho^V \exp(-\beta h), \quad (6.5)$$

where $\rho = \exp(-\beta K_*)(1 + \exp(-\beta h))$. Suppose $\rho < 1$. By summing over $t = 1, 2, ..., T$ one finds

$$\log P_T > -\beta h + \sum_{t=1}^{T} \log(1 - \rho^{V(t)}). \quad (6.6)$$

Assume now that the valency of the key node $V(t)$ increases at least linearly: $V(t) > \alpha t + V(0)$ where $\alpha > 0$. Then

$$\sum_{t=1}^{T} \log(1 - \rho^{V(t)}) > -C - 2\sum_{t=1}^{T} \rho^{V(t)} > -C_1,$$

where C and C_1 are positive constants. This uniform in T estimate finishes the proof. □

Remark 1. If the condition **R3** does not hold, this proof is not correct (although the theorem could be true). Indeed, if the noises are correlated, then the probability of destruction of many nodes may be not small.

Remark 2. If $V(0)$ is large, running of this algorithm is similar to the preferential attachment. The preferential attachment can be considered then as a probabilistic variant of the described algorithm.

Remark 3. This algorithm can be interpreted as a greedy algorithm. Let us consider a node without adjacent edges. The algorithm chooses a new edge, adjacent to this node, to increase maximally the node stability, since the stability grows with valency (connectivity).

Remark 4. We do not know whether this algorithm is optimal (gives maximal value P_T for large T) or not. Moreover, other stable algorithms are possible. They depend on properties of $\phi(a)$ and on the parameters h, K_*.

Remark 5. Theorem 6.1 holds in a relatively simple situation when the admissible domain Π is fixed. Actually, biological, economical and social systems survive in much more complicated situations when Π depends on time and the Π is an unknown set. The key problem is to find stable evolution algorithms in this case. Some ideas can be found [71, 72].

It is interesting to interprete the growth algorithm from Theorem 6.1 in the framework of our analogy with a development of a strongly centralized country (an Empire) consisting of a number of regions and a bureaucratic center. The evolution goal is to conserve the center. The parameter h can be considered as an internal region resource: for greater h only a great noise ξ_i leads to the region disfunctioning. The parameter K_* determines the connection intensity between the center and the regions. The noises can be considered as instability sources in the regions.

We notice that the Empire should be extending. The described algorithm is as follows: the center obtains resources from all the regions giving, in turn, a minimum of resources for each region. The regions are disconnected. The algorithm works successfully under condition $\rho < 1$. This condition holds if the internal resource parameter h and the connection force K_* are both large enough, if $K_* > 0$ is small and h is very large, or if K_* is very large and $h > 0$ is small. The algorithm, described here, can be called "centralization." Possibly that, in an opposite situation (small resources, strong connections), other algorithms (for exmaple, leading to a cluster formation) can be more effective.

Stability depends on the parameter ρ. Expession for ρ allows us to notice an important fact: to stabilize the circuit, it is more useful to increase of the connectivity parameter K_* than to concentrate resources (to increase h).

Centralization does not work if the noises ξ_i are correlated. Appearence of a correlated noise can be interpreted, for example, as vanishing of resources in a large region or even in the whole country.

7. Decentralization strategy of survival

In this section we show that, in opposite to Sec. 6, for many distributed systems a decentralization strategy can give a stable evolution process. In this case, the stable evolution can lead to more and more complex states. This result follows from the attractor theory for infinite-dimensional dissipative dynamical systems. We shall see that the attractor theory and complexity theory can be connected.

7.1. Systems under consideration

A typical model of a distributed system can be given by a system of partial differential equations together with some boundary and initial conditions. Such a system can be rewritten as an abstract evolution problem in an appropriate Banach or Hilbert space. Taking into account linear random noises, we consider the following class of evolution equations

$$u_t = Au + F(u,s) + \sum_{k=1}^{m} \xi_k F_k(u,s), \tag{7.1}$$

where $u \in H$, H is a Hilbert space with the norm $||u||$, F_0, F_k are nonlinear maps satisfying some restrictions (see below), ξ_k are mutually independent real-valued Markov processes with continuous trajectories. Let us assume that A is a self-adjoint negatively defined unbounded operator with a domain $D(A) \subset H$. We define the fractional subspaces $H_\alpha \subset H$ associated with A [Hen]. The space H_α consists of functions u such that the norm $||u||_\alpha = ||A^\alpha u||$ is bounded (here $\alpha \in (0,1)$). We suppose that F and F_k are bounded C^2-smooth maps from a bounded domain $D(R) = \{u \in H_\alpha : ||u|| < R\}$ to H for some $\alpha \in (0,1)$. We suppose here that all functions F, F_k also depend on a binary parameter $s = (s_1, s_2, ..., s_M)$, $s_i \in \{0,1\}$. They can be considered as "genes" that define the system structure. Below we sometimes omit dependence on s.

Reaction-diffusion equations

$$\frac{\partial u}{\partial t} = d\Delta u + f(u,x,s) + \sum_{k=1}^{m} f_k(u,x,s)\xi_k(t) \tag{7.2}$$

and systems of such equations give a fundamental model for biology and ecology beginning with seminal work [62] (see, for example, [48, 45] among many others). Here, $x \in \Omega$, $t > 0$, Ω is an bounded domain in $\mathbf{R}^d$, $d = 1,2$, with a smooth boundary. In addition to (7.2), we set standard initial and boundary conditions (for example, no flux Neumann's boundary conditions), f, f_k are bounded in the norm $C^1(\mathbf{R})$. It is well known [31], that (7.2) defines a global semiflow if we take, as an appropriate phase space, $H = L_2(\Omega)$. Then for $\alpha > 1/2$ the functions $f(u)$, $f_k(u)$ define bounded maps from H_α to H.

To use ideas of the attractor theory, let us suppose that the operator A has a countable sequence of eigenfunctions (ψ_j), which form a basis in H:

$$A\psi_j = -\lambda_j \psi_j, \quad 0 < \lambda_1 \leqslant \lambda_2 \leqslant ..., \tag{7.3}$$

where $\lambda_j \to \infty$ as $j \to \infty$. For each N one considers projection operators P_N, Q_N, where P_N is an orthogonal projection on Span $\{\psi_1, ...\psi_N\}$, $Q_N = I - P_N$. Then one has a decomposition of H to two subspaces $P_N H$, $Q_N H$

and two corresponding operators $A_1 = P_N A$, $A_2 = Q_N A$. These operators generate evolution semigroups $\exp(A_1 t)$, $\exp(A_2 t)$ satisfying estimates

$$||\exp(A_1 t)u||_\alpha \leqslant \beta_\alpha(\lambda_1, t)||u||, \tag{7.4a}$$

$$||\exp(A_2 t)u||_\alpha \leqslant \beta_\alpha(\lambda_N, t)||u||, \quad \alpha \geqslant 0, \tag{7.4b}$$

where $\beta_\alpha(\lambda, t) = C_\alpha t^{-\alpha}$ for $t \in (0, \alpha\lambda^{-1}]$ and $\beta_\alpha(\lambda, t) = C_\alpha \exp(-\lambda t)$ for $t > \alpha\lambda^{-1}$. We also use estimates

$$||\exp(A_1 t)u||_\alpha \leqslant \lambda_i^\alpha \exp(-\lambda_1 t)||u||_\alpha. \tag{7.5a}$$

$$||\exp(A_1 t)u||_\alpha \leqslant \lambda_i^\alpha \exp(-\lambda_N t)||u||_\alpha. \tag{7.5b}$$

These estimates can be obtained immediately from the spectral decomposition (7.3) [31].

Let us formulate important conditions to dynamics and noises.

Assumption 7.1. *For $\xi_k = 0$, there is a stationary solution u_0 of (7.1) such that*

$$Au_0 + F(u_0) = 0, \tag{7.6}$$

where the linear operator $B = A + DF(u_0)$ satisfies the estimate

$$||\exp(Bt)u||_\alpha < \beta_\alpha(b, t)||u||, \quad t > 0, \quad \alpha \geqslant 0, \quad b > 0. \tag{7.7}$$

Denote by δ_N the following supremum

$$\sup_{n=1,\dots,N,\ k=1,\dots,m} |(\psi_n, F_k(u_0))|, \tag{7.8}$$

where (f, g) denotes the inner scalar product in H.

Assumption 7.2. *Let us denote*

$$\phi(h, \xi(\cdot), q) = \sup_{k,T} \left(\int_T^{T+h} |\xi_k(t)|^q dt \right)^{1/q}.$$

Suppose that for sufficiently small h the trajectories ξ_k satisfy

$$\text{Prob}\,\{\phi(h, \xi(\cdot), q) > \mu h\} < \Phi(\mu), \tag{7.9}$$

where $1/q > 1 - \alpha$ and $\Phi(\mu) \to 0$ as $\mu \to \infty$.

7.2. Estimate of probability to leave a small neighborhood of stationary state

Let us take a positive $h < 1$ and a small $r > 0$ and let us consider estimates of the probability Prob (hT, r) to be in the r-neighborhood B_r of u_0, $B_r = \{u : ||u - u_0||_\alpha < r\}$ within the time interval $[0, Th]$. Let us set

$$u = u_0 + v + w, \quad v = P_N(u - u_0), w = Q_N(u - u_0).$$

Now Eq. (7.1) can be rewritten as a system, namely,

$$v_t = B_1 v + P_N G(v + w) + \sum_{k=1}^{m} \xi_k (P_N(F_k(u_0) + G_k(v + w))), \tag{7.10}$$

where

$$B_1 = A_1 + P_N DF(u_0),$$
$$||G(v + w)|| < c||v + w||_\alpha^2,$$
$$||G_k(v + w)|| < c||v + w||_\alpha^2,$$

and

$$w_t = A_2 w + Q_N(DF(u_0)(v + w) + G(v + w) + \sum_{k=1}^{m} (F_k(u_0) + G_k(v + w))\xi_k). \tag{7.11}$$

Denote by W_r the neighborhood $W_r = \{u : \ ||u - u_0||_\alpha < r\}$. If r is small enough, $W_r \subset B_R$. For integers $T = 0, 1, ...$, let us estimate the probability $P(N, h, T)$ that $u(h(T + 1)) \notin W_r$ under condition that $u(hT) \in W_r$. Due to Assumption 7.2 and since all ξ_k are Markov, one can, without loss of generality, set $T = 0$. First we find a priori estimate of $||v(t)||_\alpha$, $||w(t)||_\alpha(t)$ for $t \in [0, h]$ that holds with a probability close to 1. The second step is the need estimate of leaving of B_r at $t = h$.

Let us introduce auxiliary functions $V(t) = \sup_{\tau \in [0,t]} ||v(\tau)||_\alpha$, $W(t) = \sup_{\tau \in [0,t]} ||v(\tau)||_\alpha$. Using evolution operators one obtains

$$v(t) = R_1(v(\cdot), w(\cdot), t), \quad w(t) = R_2(v(\cdot), w(\cdot), t), \quad 0 < t < h, \tag{7.12}$$

where nonlinear operators R_i are defined on maps v, w of $t \in [0, h]$ such that the norms $|||v||| = \sup_{t\in[0,h]} ||v||_\alpha$ and $|||w||| = \sup_{t\in[0,h]} ||w||_\alpha$ are bounded. They have the form

$$R_2 = \exp(A_2 t)w(0) + \int_0^t \exp(A_2(t-\tau))Q_N(DF(u_0)(v+w) + G(v+w) + \sum_{k=1}^m \xi_k F_k(u_0+v+w))d\tau, \quad (7.13)$$

$$R_1 = \exp(Bt)v(0) + \int_0^t \exp(B(t-\tau))P_N(G(v+w) + \sum_{k=1}^m \xi_k(F_k(u_0+v+w)))d\tau. \quad (7.14)$$

Now we can estimate the norms $||R^w||_\alpha, ||R^v||_\alpha$ in a standard way [31]. By (7.4), one finds

$$|| \exp(-A_2 t)w(0)||_\alpha \leqslant r \exp(-\lambda_N h), \quad (7.15)$$

$$|| \exp(-Bt)v(0)||_\alpha \leqslant r \exp(-bh). \quad (7.16)$$

Furthermore,

$$\begin{aligned} &||G(v+w)|| < c(||v||_\alpha + ||w||_\alpha)^2, \\ &||(DF(u_0)(v+w)|| < c(||v|| + ||w||). \end{aligned} \quad (7.17)$$

The typical integrals $I_f = \int_0^t f(t)\xi_k(t)dt$ can be estimated by the Hölder inequality

$$|I_f| \leqslant \Big(\int_0^t |f|^{q_1} dt\Big)^{1/q_1} \Big(\int_0^t |\xi_k|_2^q dt\Big)^{1/q_2},$$

where $1/q_1 + 1/q_2 = 1$. Let us set $q_1 = (1-\rho)\alpha^{-1}$, where ρ is small enough and $1-\rho-\alpha > 0$, $q_2 = (1-\rho-\alpha)^{-1}(1-\rho)$. Then one has

$$\Big\| \int_0^t \exp(A_2(t-\tau))Q_N \sum_k (F_k(u_0+v+w)\xi_k)d\tau \Big\|_\alpha \quad (7.18)$$

$$\leqslant \Big(\int_0^h |\xi_k(t)|^{q_2} dt \Big)^{1/q_2} \Big(\int_0^t || \exp(A_2(t-\tau)) Q_N \sum_k F_k(u_0+v+w)||_\alpha^{q_1} d\tau \Big)^{1/q_1}.$$

For $t > \tau$ estimate (7.4) gives

$$|| \exp(A_2(t-\tau)) Q_N F_k(u_0+v+w)||_\alpha < \beta_\alpha(\lambda_N, t-\tau) ||F_k(u_0+v(\tau)+w(\tau))||.$$

Therefore,

$$\Big\| \int_0^t \exp(A_2(t-\tau)) Q_N \sum_k \xi_k F_k(u_0+v+w) d\tau \Big\|_\alpha$$

$$\leqslant c\lambda_N^{-s} \phi(h, \xi(\cdot), q_2) \Big(\sum_k ||F_k(u_0)|| + C(V(t)+W(t)) \Big), \qquad (7.19)$$

where $s(q_1, \alpha) = (\alpha - 1)\alpha(1-\rho)^{-1} > 0$. To estimate

$$I_1 = \Big\| \int_0^t \exp(B(t-\tau)) P_N \sum_k \xi_k(\tau) F_k(u_0 + v(\tau) + w(\tau)) d\tau \Big\|_\alpha,$$

we use similar arguments. One has then

$$I_1 \leqslant \phi(h, \xi(\cdot), q_2) \Big(\int_0^t \beta_\alpha(b, t-\tau) d\tau \Big)^{1/q_1} (\delta_N + C(V(t)+W(t)). \quad (7.20)$$

In a similar way one can estimate all other contributions in the right hand sides of (7.12). One has (by summing the estimates obtained, $s' = 1-\alpha > 0$, $0 < t \leqslant h < 1$):

$$V(t) \leqslant r\exp(-bt) + c_0 \lambda_1^{-s'} \times (r^2 + (\delta_N + C_1(V(t)+W(t)))\phi(h, \xi(\cdot), q_2)), \quad (7.21)$$

$$W(t) \leqslant r\exp(-\lambda_N t) + c_1 \lambda_N^{-s'} (r^2 + C(V(t)+W(t)) + \phi(h, \xi(\cdot), q_2)(C_3 + C_1(V(t)+W(t)))). \quad (7.22)$$

Let us set $0 < r_0 < r < 1$, where r_0 is a constant uniform in δ_N, λ_N for small δ_N, λ_N^{-1}. Let

$$\phi(h, \xi, q_2) < c_3 \min\{\delta_N^{-1}, \lambda_N^{s'}\}, \quad c_3 > 0. \tag{7.23}$$

Then (7.21), (7.22) entail

$$V(t), W(t) < \overline{C}r, \quad 0 \leqslant t \leqslant h, \tag{7.24}$$

where $\overline{C}(r_0)$ is a constant such that $\overline{C}r > 2r + c_0\lambda_1^{-s'}\overline{C}r^2$ (clearly this constant can be taken uniform in δ_N, λ_N for small δ_N, λ_N^{-1}). Notice now that, according to Assumption 7.2, inequality (7.23) holds with a probability $p_N(\delta_N)$ that goes to 1 as $\delta_N \to 0$ and $N \to \infty$.

Lemma 7.1. *Let us assume that r, $\overline{C}$ satisfy*

$$r > r\exp(-bh) + c_0\lambda_1^{-s'}\overline{C}r^2. \tag{7.25}$$

Then under condition (7.23) *and if δ_N, λ_N^{-1} are sufficiently small, one has $u(0) \in B_r$ implies $u(h) \in B_r$.*

To prove this lemma, we use (7.24), (7.21), and (7.22). This gives $V(h) \leqslant r\exp(-bh) + c_0\lambda_1^{-s'}\overline{C}r^2 + (\delta_N + c_4 r)\phi(h, \xi, q_2)$. If $V(h) > r$, we have a contradiction with (7.24) and (7.25). In a similar way,

$$W(h) \leqslant r\exp(-\lambda_N h) + c_1\lambda_N^{-s'}(\overline{C}r + c_5\phi(h, \xi, q_2)).$$

If $W(h) > r$ this inequality also leads to a contradiction with (7.24). □

Using this lemma, we obtain the following assertion.

Proposition 7.2. *Let us choose a $\overline{C}$, r satisfying* (7.25). *Suppose $B_{\overline{C}r} \subset \Pi$. Then if $u_0 \in B_r$, the probability P_d that $u(t) \notin \Pi$ for some $t \in [0, h]$, satisfy*

$$P_d < \text{Prob}\,\{\phi(h, \xi, q_2) > c_3 \min\{\delta_N^{-1}, \lambda_N^{s'}\}. \tag{7.26}$$

Now we shall use these estimates to investigate a biological mechanism of the stable evolution.

7.3. Stability of complex patterns

Let us consider Eq. (7.2). To understand the decentralization mechanism, let us remind the basic facts about biological systems. Cells are separated in compartments and biochemical reactions work in the corresponding compartments [43]. Moreover, we suppose that Π is a subdomain of H_α (for example, it is a ball of the radius R centered at u_0). To simplify the statement, we set $m = 1$.

We can describe this compartment structure by the following assumptions:

A1. *The function f_1 has the form*

$$f_1 = \sum_{l=1}^{L} \chi_l(u, x, \mathbf{s}),$$

χ_l are smooth functions of u and x with mutually disjoint supports Ω_l in x, where $c_0 r < diam(\Omega_l) < c_1 r$, r is a parameters, c_0, c_1 are independent of r as $r \to \infty$.

A2. *Equation* (7.2) *without noises (i.e., for $f_1 = 0$) has a stable stationary solution u_0 such that Eq.* (7.6) *holds, $u_0 \in \Pi$ and*

$$\mathrm{dist}\{u_0, \partial\Pi\} > R_0.$$

Let us denote

$$a_{ln}(\mathbf{s}) = \int_{\Omega_l} \chi_l(u_0(x), x, \mathbf{s})\psi_n(x)dx, \tag{7.27}$$

where ψ_n are eigenfunctions of the operator $A = -\Delta$ (see (7.3)). Under **A1** inequality (7.8) can be then rewritten as follows

$$Z(s) = \sup_{n=1,\dots,N} \Big| \sum_{l=1}^{L} a_l(\mathbf{s}) \Big| < \delta_N. \tag{7.28}$$

Even for a simple case, when a_{ln} are linear functions of s, for example,

$$a_{ln} = b_{ln} s_{i(l)} + c_{ln}, \tag{7.29}$$

an attempt to satisfy (7.28) leads to a linear boolean programming problem, which, in general, is an NP-hard one. Here the output size for this problem is $N + M$, where $M = \max \text{length } (s)$. In general, it is impossible, within a time polynomial in $N + M$, to find s satisfying stability conditions (7.28).

Nonetheless, under some restrictions to $Z(s)$ one can show that there are possible polynomial algortihms and thus one can expect that there is a stable random evolution process allowing to find s satisfying (7.28). We apply here a powerful tool from the probability theory: concentration inequalities [11, 10, 57, 58] and an idea of the phase transitions in hard combinatorial problems [77, 13, 14].

Assumption A3. *Suppose that the function $Z(s)$ satisfies bounded differences inequality:*

$$|Z(s_1, s_2, ...s_{i-1}, s_i, s_{i+1}, ..., s_M) \\ -Z(s_1, s_2, ..., s_{i-1}, s_i', s_{i+1}, ..., s_M)| < \mu_i, \quad 1 \leqslant i \leqslant M, \tag{7.30}$$

and, moreover, μ_i satisfy

$$D_Z = \sum_{i=1}^{M} \mu_i^2 < \kappa(M), \tag{7.31}$$

where $\kappa(M) \to 0$ as $M \to \infty$ for fixed L, m, N.

Consider some examples when (7.31) holds. Let us consider the case when $L = o(M^{1/2})$, i.e., the domain number is much less than the gene number. If (7.29) are fulfilled and indices $i(l)$ are chosen randomly among the set $\{1, 2, ..., M\}$ of all possible indices (that is natural from the biological point of view) then for a random map $l \to i(l)$ one has $\mu_i <$ const LM^{-1} that gives even a stronger asymptotics $D_Z <$ const L^2M^{-1}.

A more intricated case occurs if each a_{ln} depends on genes $s_{i_1(l)}, s_{i_2(l)}$, ..., $s_{i_K(l)}$, where K is a natural number that determines how much genes are involved in genetic controls of reactions in a compartment. There occur maps $l \to i_j(l)$. We can suppose that they are random and then one has $D_Z <$ const $K^2L^2M^{-1}$. If K is bounded as $M \to \infty$ one obtains that (7.31) again holds.

Now we use the following fundamental theorem, so-called concentration inequality (see [10]). We formulate it below for our particular case.

Theorem. *Suppose that $X_1, X_2, ..., X_M$ are independent random boolean variable, X_i takes the value 1 with a probability p_i and 0 with the probability $1 - p_i$. The random variable $Z = Z(X_1, ..., X_M)$ satisfies*

$$\mathrm{Prob}\,\{|Z - \mathbf{E}Z| > t\} \leqslant 2\exp(-t^2/D_Z). \tag{7.32}$$

Let us fix numbers N, m. Let us consider the following problem associated with (7.28).

Problem 7.1. *To find the probabilities $0 \leqslant p_i \leqslant 1$ such that the average EZ satisfies*

$$2|EZ| < \delta_N. \tag{7.33}$$

The next assertion shows that if a solution of this problem on real p_i exists, the solution of boolean problem (7.28) can be found in a polynomial (in M, L) time. Notice that the real problem for averages can be much simpler than this boolean one.

Proposition 7.3. *Suppose*

$$\delta_N > 4(D_Z)^{1/2} \tag{7.34}$$

and problem (7.1) *has a solution. Then there exists a solution s_* of boolean problem* (7.28).

The proof is trivial: probability (7.32) is less than 1, thus a solution exists.

As an example, let us consider the case (7.29). Then the associated problem is a linear programming one: to satisfy inequalities

$$-\delta_N < \sum_{l=1}^{L}(b_{ln}p_{i(l)} + c_{ln}) < \delta_N, \tag{7.35a}$$

for $n = 1, 2, ..., N$ and

$$0 \leqslant p_j \leqslant 1, \quad 1 \leqslant j \leqslant M. \tag{7.35b}$$

Suppose that N, L are fixed and the number of genes $M \to \infty$. We can verify existence of solution of (7.35) in a time polynomial in M.

This fact and Proposition 7.2 allows us to propose the following algorithm of the evolution. We increase the genome, i.e., the gene number M, the number N and construct more and more refined decompositions of Ω in smaller and smaller domains in order to satisfy (7.33), (7.34). If the growth M, N satisfies restrictions $N = o(M)$, $\delta_N \to 0$ as $N \to \infty$, then for large N one can expect that Problem 7.1 has a solution such that (7.34) holds and this solution can be found within an average time polynomial in N (see [13, 14, 77]). Indeed, roughly M is the number of variables and N is a number of conditions to satisfy. In such a situation even NP- hard problems (like to K-SAT problem) can be resolved in an average polynomial time by greedy or local search algorithms.

8. Conclusion

Here we discuss physical and biological interpretations and consequences, connections with experiments. There exists a number of approaches, theories and speculations about biological evolution (see an overview of some of them in [51]). We proposed a mathematical approach, having a goal to confirm the one of them, so-called Red Queen hypothesis proposed by the famous biologist L. van Valen and formulated more mathematically by M. Gromov and A. Carbone.

In previous works [67, 64, 65] we have considered circuit models important in biology, chemistry, economics, and physics. We first find some properties of stable evolution algorithms for these circuits. This question is connected with the graph evolution theory pioneered by Erdös and Rényi [18] since circuits can be associated, in a natural way, with directed weighted graphs. Then an evolution adds edges and vertices to a graph. An evolution algorithm is a program to add these edges and vertices. It is interesting to note that the Erdös and Rényi evolution leads to so-called universal graphs (about them [74]).

For circuits and for simple viable domains Π (time fixed rectangles) one can show that the Erdös–Rényi evolution is unstable but the Albert–Barabasi preferential attachment algorithm [6], may be stable. We showed that the larger valency of some key nodes the stabler circuit and the valency have a tendency to increase (cannot be bounded by a constant within all times). These results are in a good accordance (qualitatively) with experimental facts [35, 37]. Indeed, in Nature we observe so-called free scale graphs that can be obtained by the preferential attachement.

In this paper, we gave the first example of the stable circuit growth performed under some rigid restrictions (at each step one can add at most one edge and one node). The networks, obtained in such a way, also occur in biological applications (O. Radulescu, private communication).

The result on increasing of the Kolmogorov complexity and the length of genetical code is confirmed by experimental data, in general times. Actually, the code length also had a tendence to increase during evolution process (although this increasing was nonmonotone).

This approach also leads to the concept of a genetically programmed death (developed, in particular, by V. M. Dilman [15]).

At last, results on spatially extended systems (obtained here and earlier, see [66, 64, 65]) also are in a good accordance with biological facts. Here we showed that if a system generate typical patterns observed in biological applications (see [62, 45, 48, 50]) and if these patterns in an evolution process become more and more complicated, then such an evolution process may be stable. Results of Sec. 7 lead to relations that can be checked experimentally.

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References

1. B. Alberts, D. Bray, J. Lewis, M. Raff, K. Roberts, P. Walter, *Molecular Biology of the Cell*. 4nd ed. Garland Publishing, Inc., New York, 2002.
2. J.-P. Aubin, A. Bayen, N. Bonneuil, P. Saint-Pierre, *Viability, control and games: regulation of complex evolutionary systems under uncertainty and viability constraints*. Springer-Verlag, 2005.
3. J.-P. Aubin, *Mutational and morphological analysis: tools for shape regulation and morphogenesis*. Birkhauser, (2000).
4. J.-P. Aubin, *Dynamic economic theory: a viability approach*, Springer-Verlag, 1997.
5. J.-P. Aubin, *Neural networks and qualitative physics: a viability approach*. Cambridge University Press, 1996.
6. R. Albert, A. L. Barabási, *Statistical mechanics of complex networks*. — Rev. Modern Physics **74** (2002), 47–97.
7. A. Barron, *Universal Approximation Bounds for superpositions of a sigmoidal functions*. — IEEE Trans. Inf. Theory **39** (1993), 930–945.
8. R. Bhattacharya, M. Majumdar, *Random Dynamical Systems. Theory and Applcations*, Cambridge, 2007.
9. M. Benaim, N. El Karoui, *Promenade aleatoire (Chaines de Markov et simulations; martingales et strategies)*. — Les editions de l'école polytechnique (2004).
10. S. Boucheron, O. Bousquet, G. Lucosi, *Theory of classification: survey of some recent advances*. — ESAIM: Probability and Statistics **9** (2005), pp. 323–375.
11. B. S. CirelTson, I. A. Ibragimov, V. N. Sudakov, *Norm of Gaussian sample function*. — In: Proceedings of the 3rd Japan–U.S.S.R. Symposium on Probability Theory, Lect. Notes Math. 550 20-41 Springer-Verlag, Berlin (1976).
12. T. H. Cormen, Charles E. Leiserson, L. Ronald, *Rivest, and Cliff Stein, Introduction to Algorithms*. (Second Edition), MIT Press.
13. C. Deroulers, R. Monasson, *Criticality and universality in the unit-propagation search rule*. — Eur. Phys. J. **B49** (2006), 339.
14. C. Deroulers, R. Monasson, *Critical behaviour of combinatorial search algorithms, and the unitary-propagation universality class*. — Europhys. Lett. **68** (2004), 153.
15. V. M. Dilman, *Aging, Rate of Aging, and Cancer*. — A Search for Preventive Treatment Annals of the New York Academy of Sciences **719 (1)** (1994), 454–455. doi:10.1111/j.1749-6632.1994.tb56849.x.
16. R. Edwards, T. H. Siegelmann, K. Aziza, L. Glass, *Symbolic dynamics and computation in model gene networks*. — Chaos **11** , (2001) 160–169.
17. M. Eigen, P. Schuster, *The Hypercycle: A Principle of Natural Self-Organization*. Springer, Berlin, 1979.
18. P. Erdos, A. Rényi, *On the evolution of random graphs*. — Publ. Math. Inst. Hungarian Academy of Sciences **5** (1960), 17–61.
19. K. Funahashi, Y. Nakamura, *Approximation of Dynamical Systems by Continuous Time Recurrent Neural Networks*. — Neural Networks **6** (1993), 801–806.

20. A. Gabrielov, N. Vorobjov, it Complexity of computations with Pfaffian and Noetherian functions. — In: Normal Forms, Bifurcations and Finiteness Problems in Differential Equations, Kluwer (2004), pp. 211–250.
21. L. Glass, S. Kauffman, it The logical analysis of continuous, nonlinear biochemical control networks. — J. Theor. Biology **34** (1973), 103–129.
22. D. Grigoriev, N. Vorobjov, *Complexity Lower Bounds for Computation Trees with Elementary Transcendental Functions Gates.* — Theoret. Comput. Sci. **157** (1996), 185–214.
23. D. Grigoriev, *Deviation theorems for solutions of linear ordinary differential equations and applications to parallel complexity of sigmoids.* — St.Petersburg Math. J. **6** (1995), 89–106.
24. D. Grigoriev, it Deviation theorems for Pfaffian sigmoids. — St.Petersburg Math. J. **6** (1995), 107–112.
25. D. Grigoriev, it Approximation and complexity: Liouvillean type theorems for linear differential equations on an interval. — Found. Computat. Math. **1** (2001), 289–295.
26. D. Grigoriev, it Approximation and complexity II: iterated integration. — Found. Computat. Math. **2** (2002), 295–304.
27. M. Gromov, A. Carbone, it Mathematical slices of molecular biology. Preprint IHES/M/01/03, 2001.
28. J. K. Hale, J.K. La Salle, M. Slemrod, it Theory of a general class of dissipative process. — J. Math. Anal. Appl. **39** (1972), 177–191.
29. L. H. Hartwell, J. J. Hopfield, S. Leibler, A. W. Murray, *From molecular to modular cell biology.* — Nature (London) **402** (1999), C47–C52.
30. R. Hecht-Nielsen, *Kolmogorov's mapping neural network existence theorem.* — IEEE International Conference on Neural Networks, San Diego: SOS Printing (1987), 11–14.
31. D. Henry, *Geometric Theory of Semilinear Parabolic Equations.* — Lect. Notes Math. **840**, Springer, New York, Heidleberg, Berlin, 1981.
32. M. W. Hirsch, *Differential topology.* New-York, Heidelberg, Berlin, 1976.
33. J. J. Hopfield, *Neural networks and physical systems with emergent collective computational abilities.* — Proc. Natl. Acad. USA **79** (1982), 2554–2558.
34. K. Hornik, M. Stinchcombe, H. White, *Multilayer feedforward networks are universal approximators.* — Neural Networks **2** (1989), 359–366.
35. H. Jeong, B. Tombor, R. Albert, Z. N. Otvai, A.L. Barabási, *The large-scale organisation of metabolic networks.* — Nature (London) **407** (2000), 651–654.
36. Yu. Ilyashenko, Li Weigu, *Nonlocal bifurcations.* — Amer. Math. Soc. (1999).
37. H. Jeong, S. P. Mason, A. L. Barabási, Z. N. Otvai, *Lethality and centrality in protein networks.* — Nature (London) **411** (2000), 41–42.
38. A. Khovanskii, *Fewnomials, Translations of Mathem.* Monographs, Amer. Math. Soc. **88** (1991).
39. P. Koiran, C. Moore, *Closed-form analytic maps in one and two dimensions can simulate Turing machines.* DIMACS Technical Report 96-25. Theoretical Computer Science **210(1)** (1999), 217–223
40. O. A. Ladyzenskaya, *On a dynamical system generated by Navier–Stokes equations.* — Zap. Nauchn. Semin. LOMI **27** (1972), 97–114.

41. C. Lobry, *Une proprieté generique des couples de champs de vecteurs.* — Chechoslovak Math. J. **22 (97)** (1972), 230–237.
42. Ming Li, P. Vitanyi, *An Introduction to Kolmogorov Complexity and Its Applications.* Second Edition Springer Verlag, 1997; xx+637pp.
43. A. L. Lehninger, D. L. Nelson, M. M. Cox, *Principles of Biochemistry.* 2nd. ed. Worth, New York, 1993.
44. A. Lesne, *Complex networks: from graph theory to biology.* — Lett. Math. Phys. **78** (2006), 235–262.
45. H. Meinhardt, *Mathematical Models for Biological Pattern Formation*, edited by P. K. Maini, H. G. Othmer, IMA Volumes in Mathematics and its Applications, **121**, Springer, New York, Berlin, Heidelberg, 2000.
46. L. Mendoza, E. R. Alvarez-Buylla, *Dynamics of Genetic Regulatory Networks for Arabodopsis thaliana Flower Morphogenesis.* — J. Theor. Biol. **193** (1998), 307–319.
47. E. Mjolness, D. H. Sharp, J. Reinitz, *A connectionist Model of Development.* — J. Theor. Biol. **152** (1991), 429–453.
48. J. D. Murray, *Mathematical Biology.* Springer, New York, Berlin, Heidelberg, 1993.
49. C. H. Papadimitriou, K. Steglitz, *Combinatorial optimization, Algorithms and Complexity.* Prentice Hall, Inc. Englewood Cliffs, New Jersey, 1982.
50. J. Reinitz, D. H. Sharp, *Mechanism of formation of eve stripes.* — Mechanisms of Development **49** (1995), 133–158.
51. M. Ridley, *Evolution.* 2nd ed. Blokwell Scientific Publications Ltd, Oxford, 1996.
52. D. Ruelle, *Elements of differentiable dynamics and bifurcation theory.* Acad. Press, Boston, 1989.
53. I. Salazar-Ciudad, J. Garcia-Fernadez, R. V. Solé, *Gene Networks Capable of Pattern Formation: From Induction to Reaction-Diffusion.* — J. Theor Biology **205** (2000), 587–603.
54. S. Smale, *Mathematics of Time.* Springer, New York, 1980.
55. P. Smolen, D. Baxter, J. H. Byrne, *Mathematical modelling of gene networks.* — Review Neuron **25** (2000), 247–292.
56. H. J. Sussmann, *A general theorem on local contollability.* — SIAM J. Control and Optimization **25**, No. 1 (????), 158–194.
57. M. Talagrand, *Concentration of measure and isoperimetric inequalities in product spaces.* — Publications Mathematiques de lTI.H.E.S. **81** (1995), 73–205.
58. M. Talagrand, *New concentration inequalities in product spaces.* — Invent. Math. **126** (1996), 505–563.
59. R. Temam, *Infinite dimensional system in mechanics and physics.* New York: Springer-Verlag, 1998.
60. D. Thieffry, R. Thomas, *Dynamical behaviour of biological regulatory networks. II. Immunity control in bacteriophage lambda.* — Bull. Math. Biology **57** (1995), 277–295.
61. R. Thom, *Stabilité structurelle et morphogénèse.* New York, Benjamin, 1972.
62. A. M. Turing, *The chemical basis of morphogenesis.* — Phil. Trans. Roy. Sco. B **237** (1952), 37–72.
63. S. Vakulenko, S. Genieys, *Patterning by genetic networks.* — Mathematical Methods in Applied Sciences **29** (2005), 173–190.

64. S. Vakulenko, D. Grigoriev, *Algorithms and complexity in biological pattern formation problems.* — Annales of Pure and Applied Logic **141** (2006), 421–428.
65. S. Vakulenko, D. Grigoriev,]it Evolution in random environment and structural stability. — J. Math. Sci. **138** (2006), 5644–5662.
66. S. Vakulenko, D. Grigoriev, *Stable growth of complex systems.* — In: Proceeding of Fifth Workshop on Simulation, St.Petersburg (2005), pp. 705–709.
67. S. Vakulenko, D. Grigoriev, *Complexity of gene circuits, Pfaffian functions and the morphogenesis problem.* — C. R. Acad. Sci, Ser I. **337** (2003), 721–724.
68. S. Vakulenko, S. Genieys, *Pattern programming by genetic networks, Patterns and Waves.* — Collection of papers, eds. A. Abramian, S. Vakulenko, and V. Volpert, St.-Petersburg (2003), pp. 346–366.
69. S. A. Vakulenko, *Dissipative systems generating any structurally stable chaos.* — Adv. Diff. Eqs. **5** (2000), 1139–1178.
70. L. Van Valen, *A new evolutionary law.* — Evolutionary Theory **1** (1973), 1–30.
71. L Valiant, *Evolvibility.* — Lect. Notes Comput. Sci. **4708** (2007), 22–43.
72. L. G. Valiant, *A theory of learnable.* — Comm. ACM **27** (1984), 1134–1142.
73. A. D. Ventsel, M. I. Freidlin, *Random Perturbations of Dynamic systems.* Springer, New York, 1984.
74. A. M. Vershik, F. V. Petrov, *Invariant measures on the set of graphs and homogeneous uncountable universal graphs.* PDMI preprint 08/2008 (2008).
75. B. L. van der Waerden, *Modern Algebra.* Vol. 1, Ungar, New York, 1953.
76. M. Blum, *A machine-independent theory of the complexity of recursive functions.* — J. Assoc. Comput. Machin. **14** (1967), 322–336.
77. E. Friedgut, *Sharp thresholds of graph properties, and the k-SAT problem.* — J. Amer. Math. Soc. **12**, No. 4 (1999), 1017–1054.
78. L. Wolpert, R. Beddington, T. Jessell, P. Lawrence, E. Meyerowitz, J. Smith, *Principles of Development.* Oxford University Press, 2002.
79. M. K. S. Yeung, J. Tegner, J. J. Collins, *Reverse engineering gene networks using singular decomposition and robust regression.* — In: Proceeding of Nat. Acad. Sci. **99** (2002), pp. 6163–6168.
80. A. K. Zvonkin, L. A. Levin, *The complexity of finite objects and the development of the concepts of information and randomness by means of the theory of algorithms.* — Russ. Math. Surv. **25**, No. 6 (1970), 83–124.

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