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The origin of life and thinking from the viewpoint of modern physics

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Contents

Abstract. Attempts at a physical picture of how living creatures emerge from nonliving matter are beset with difficulties due to a low probability of some of the stages of the process. It is shown that these difficulties arise from the misconstruction of the term 'coding' and that they are overcome by assuming that the polynucleotide catalized rather than 'coded' the formation of protein in primary organisms (hypercycles). A realistic scenario including the emergence of a unified code is considered for such a process. A physical mechanism of thinking and the basis of a necessary evolutionary change are discussed, for which purpose the concepts of information, valuable information, and information generation are analyzed. It is shown that thinking reduces largely to pattern recognition. A possible molecular mechanism of recognition is considered which is shown to be quite likely to have appeared in the course of evolution.

1. Introduction

The problem of the origin of life is the subject of a special branch of biophysics, and still is considerably controversial. The existing views are expressed in monographs [1 – 3], collected papers [4, 5], and proceedings of conferences [6, 7]. One popular opinion is that contemporary physics is not capable of explaining or describing the beginning of life on the Earth. Such a view is based on the evaluated probabilities of this happening (which will be discussed later on).

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We do not share this opinion. Our vision of the problem and the ways for solving it make the topic of this publication (or, to be more precise, the first part).

Another issue relates to the mechanisms of thinking, especially its intuitive aspects. What are the mechanisms of perception, reasoning, and judgment, how did man acquire intellectual faculty? There is a view that contemporary physics cannot answer these questions, and this view is not even supported with any kind of estimates, which does not prevent it from being quite common.

We believe that the main difficulty lies not with the solution, but rather with the statement of the problem. No-one has so far clearly formulated what exactly is the phenomenon (or process) called 'thinking' that has to be understood (and/or described) in physical terms. As a matter of fact, we are talking of the mechanisms of generation of new valuable information and processing it.

Information is a relatively new concept that, in our opinion, has not yet been given an adequate definition. The same is even more true of the concept of 'valuable information'.

In the physics of inanimate nature these concepts are seldom used, and are actually not necessary.

By contrast, the concepts of 'information' and especially 'valuable information' are fundamental in biology, and it would be impossible to understand or describe the processes in animate nature without them. In fact, this is what distinguishes living matter as such. For this reason we have included a special section dealing with information and informatics (to use the British term for information science). In this section we discuss the issues of generation of information and the evolution of its value. We also answer the question why in animate nature (and in the objects brought into existence by living creatures) the concept of 'valuable information' is so important, while not being essential for the description of inanimate nature.

The problems of the origin of life and thought go beyond the scope of biology, and are of universal importance. In recent years they have attracted the interest of physicists, especially those concerned with nonlinear systems and self-organization (synergetics). These issues are discussed in publications by noted scientists [8 – 11] and *Phys. Usp.* reviews [12, 13]. In the paper by V L Ginzburg [14], the problems named in the title are rated as 'great'. They are part of the more general problem of 'physical reductionism'. The latter denotes the tendency to reduce the complicated phenomena of nature (and animate nature as well) to a sequence of elementary steps described by fundamental laws of physics. Whether this is possible and to what extent remains an open question. The issue becomes especially hot when the process described by the fundamental laws of physics loses stability. The loss of stability in developing systems (biological, in particular) is a necessary condition of development. Because of this, the concepts of stability and instability are of crucial importance for such systems. Such global matters, however, fall beyond the scope of this review, although they are closely related to the problems under discussion.

2. The problem of the origin of life

Let us make some preliminary remarks. We assume that the reader has some basic knowledge about biological macromolecules (proteins and polynucleotides).

In our biosphere, the carriers of information are polynucleotides, DNA (deoxyribonucleic acid) and RNA (ribonucleic acid). As a rule, DNA is responsible for storage of information and its transfer to descendants, whereas RNA takes part in the biosynthesis of proteins (translation and transcription). Which polynucleotides, DNA or RNA, have been implicated in the early processes of the emergence of life, is still a matter of debate [3].

The advantage of DNA is that these macromolecules are better suited for storage of genetic information and complementary autoreproduction. The advantage of RNA lies in its ability to perform certain catalyzing functions (although it is not so good at storing information and autoreproduction).

However, the functions of information storage and realization of information are considerably different and even complementary. The better the system is adapted for storing information, the harder it is to make it perform the task described by this information. Because of this, these two functions are assigned to two different subsystems. The former function is performed by DNA, the latter by proteins. RNA acts as messenger and performs neither of these functions. In principle, the role of messenger may be performed by the proteins connected with the subsystems (the so-called adapters).

Let us illustrate this point with an example from industry. Information about the manufacture of some product is contained in blueprints or diskettes, and is kept in an archive. This information is used in the workshop. One may try to imagine an arrangement in which one and the same facility would be used for both storage and realization of information. Any engineer will tell you, however, that this is difficult to do and (first and foremost) hardly worthwhile.

So we hereinafter assume that the primary polynucleotide was the molecule of DNA, and the primary 'working substance' was the protein molecule.

2.1 Early stages of biological evolution

In this process, three stages may be distinguished:

— formation of biologically important molecules (sugars, lipids, amino acids, and nucleotides) in the prebiological period;

— spontaneous aggregation of these molecules in space, and their condensation to form polymers (polypeptides and polynucleotides in a random sequence);

— formation of a biological information system and valuable information stored therein.

The third stage is associated with the selection of a genetic code common to all life on the planet, and the emergence of the simplest 'organisms' capable of complementary autoreproduction using this code. We put 'organisms' in quotes, because the first two stages have nothing to do with the genetic information. The processes that take place at these two stages correspond to the laws of physics and chemistry of open systems. Some self-organization of matter that occurs at the second stage is not yet sufficient for the code to arise. It is only at the end of the third stage that we can speak of the emergence of 'living matter', or 'organisms'. For the time being, we use these terms without giving a definition of what is 'life'. It will be appropriate to give this definition after discussing the third stage of evolution. Before that, however, we need to briefly discuss the first two.

Stage one — formation of biologically important molecules and their self-organization. Such organic substances as sugars, lipids, amino acids and nucleotides have an excess of free energy. Because of this, their concentration in a thermodynamically equilibrium system is very small. However, in an open system pumped with energy such substances may be synthesized in considerable quantities.

It has been demonstrated that most efficient synthesis of such substances may accompany volcanic eruptions [15], and can be stimulated by electric discharge (lightning), UV radiation, and cosmic rays. Certain polymers (like sugars) can be produced through polymerization of formaldehyde even in outer space [16, 17].

Under such conditions, however, the relative rates of formation and destruction of biologically important molecules are such that their concentration in the primeval ocean is very low. In other words, had they been evenly distributed in space, their further polymerization would have been practically impossible. Therefore, the second stage was necessary — the stage of self-organization.

Stage two — spontaneous aggregation of molecules. For the first time (as early as 1924) this possibility was noted by A I Oparin [18]. It was demonstrated that biologically important molecules may spontaneously form droplets or clusters called *coacervates*. Such a process by itself is not surprising, and is explainable from the standpoint of physical chemistry. In some aspects, coacervates resemble protozoic cells. Later similar structures were observed by S Fox [1], who called them *microspheres*. It was also demonstrated that under certain conditions (high temperature, presence of active phosphates, etc.) polypeptides with a random sequence of amino acids can be formed in the microspheres. Such polypeptides may show some hydrolytic activity, but otherwise are functionally inert.

As shown by F Egami [2], droplets similar to coacervates and microspheres can be formed in sea foam. He called them *marigrains*. In marigrains, the formation of polypeptides from phosphorylated amino acids is possible under relatively soft conditions.

The nonbiological synthesis of polynucleotides is also quite possible. Then the single-stranded polynucleotides are unstable and subject to hydrolysis. A stable polymer like the double helix of DNA is formed if the polymerization (termination of ester bonds) is accompanied by the formation of adenine – thymidine (AT) or guanine – cytosine (GC) pairs [1]. This requires a high enough concentration of active (phosphorylated) nucleotides. Of course, in the case of spontaneous polymerization the polynucleotides arrange themselves in a random sequence.

The second stage is important because self-organization in cell-like droplets (coacervates, microspheres and marigrains) paves the way for spontaneous formation of biopolymers.

Stage three — formation of an information system. An information system must possess certain special properties [19]. To carry information, the system must be a multistationary one, i.e. it may be found in two or more steady states. Memory requires that some of these steady states should be stable (which means that the information system must be a dissipative one).

Droplets consisting of randomly arranged polynucleotides and polypeptides possess the properties required. The number N_n of steady states of a polynucleotide consisting of n base units, each containing one of four nucleotides, is $N_n = 4^n$. The number of states of a polypeptide of m base units is $N_{\mathrm{p}} = 20^m$. Accordingly, the number of possible states of the 'droplet' is sufficiently large. The system is dissipative, because the formation of polymers takes up energy, which for the most part is converted into heat.

Storage of information in such a system calls for a special discourse; the main point here concerns the time of memorization.

In biological evolution, the characteristic time over which the memory is preserved about the selected variant (for example, code) is of the same order as the time of existence of the biosphere — that is, $\tau \sim 10^9$ years. Any heteropolymer, including DNA, remembers the imprinted information for the time of its existence τ_i, namely, for the time from its formation till hydrolysis. This time depends on many circumstances, but in any case is much less than τ. To preserve the memory for the time τ, it is necessary (and sufficient) from time to time (with the interval $\tau_0 \leqslant \tau_i$) to make several copies of the information (multiplication). One copy is not enough, because in the long run the likelihood of its loss is high. In biology, 'multiplication' means complementary autoreproduction of the polynucleotide.

Let us draw an analogy. Today we know several ways of long-term storage of information: writing on paper (a book), recording on magnetic tape, hard disk, etc. In all cases the time of storage is limited by the lifetime of the device (books molder, tapes perish, computers break down). To preserve information, it must be duplicated in an increasing number of copies. Otherwise this information is doomed to be lost.

In this way, the mechanism of complementary autoreproduction is necessary for the long-term storage of information.

2.2 Molecular aspects of the autoreproduction mechanism

The basic stage of autoreproduction is replication: rupture of hydrogen bonds between the complementary nucleotides, formation of new (complementary) pairs with free nucleotides from the environment, and subsequent closure of the ester phosphate bonds between adjacent nucleotides.

A protein-enzyme called *replicase* is needed to promote replication and protect DNA from hydrolysis.

Obviously, the primordial process of replication was simpler than today. Nevertheless, to understand the early molecular mechanism of replication, it would be worthwhile discussing its contemporary form, including the properties of protein-replicase and its biosynthesis.

Complementary autoreproduction of DNA in today's biosphere is promoted by special proteins called *replicases*. The main function of replicase is to facilitate the rupture of hydrogen bonds between purine and pyrimidine bases. Replicases have the shape of a horseshoe that attaches to DNA at the point of initiation and then can travel along the double spiral.

The mechanism of the act of catalysis is conveniently explained in terms of the 'protein – machine' concept [20, 21]. Figure 1a shows the cross section of a DNA – replicase complex.

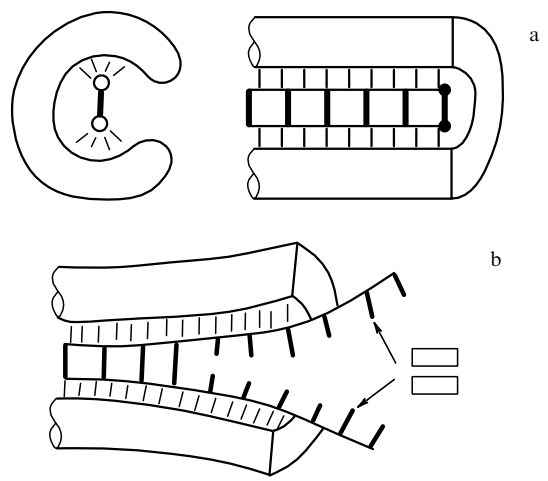

Figure 1. Schematic structure of the complex of protein-replicase with DNA (a), and scheme of functioning of the complex (b).

Bonds between nucleotides are represented by bold lines, thin lines denote bonds between the replicase and substratum. Rectangles depict nucleotides that attach to the free sections of DNA, thus forming a complementary replica of each strand of DNA. In order to form a complex, the replicase must be complementary to the outer surface of the DNA double helix. By 'complementary' we mean here not only geometric conformity, but also the availability of chemical groups interacting with DNA. However, the complementarity may be complete or partial. In the latter case, the free binding energy F is less than the maximum possible $F_{\max}$, which corresponds to complete complementarity. The difference $F_{\mathrm{ex}} = F_{\max} - F$ is represented in the form of stresses that are mainly concentrated on the hydrogen bonds between the nucleotides. The latter facilitates the rupture of hydrogen bonds — that is, the act of initiation.

Saturation of produced available bonds with nucleotides from the solution pushes the strands asunder and gives rise to mechanical forces that facilitate the movement of the replicase.

A similar mechanism of catalysis may also take place when the external conditions (temperature, pH, etc.) change periodically and cause the conformational transitions of the protein-replicase. Figure 1 shows two possible conformations

of the protein. In the first conformation, the complementarity is complete, and the binding energy is high, $F = F_{\max}$. Upon transition to the alternative (partially complementary) conformation, however, the complex is under stress, and so are the hydrogen bonds. The energy of stress in this case comes from the environment (or, more precisely, from the energy of the external source that causes the change of conditions). The conformational transition can also be caused by a chemical energy-rich agent as a result of its hydrolysis. Then the entire process will be energy-dependent. We see that the main catalysis determinants in this case are the shape of the protein (which is complementary to DNA but not completely), and its capability for conformational transitions.

We give much attention to the mechanism of catalysis of replication because we shall need it later for analyzing the possibility of spontaneous formation of the protein-replicase.

In today's biosphere the replicase is formed, like all other proteins, in the process of biosynthesis. Its shape is determined by the primary sequence, which in its turn is determined by the sequence of nucleotides in the corresponding segment of DNA (structural gene).The entire process is illustrated in Fig. 2. Here the last (closing) arrow corresponds to the case when the protein is a replicase that promotes the synthesis of DNA.

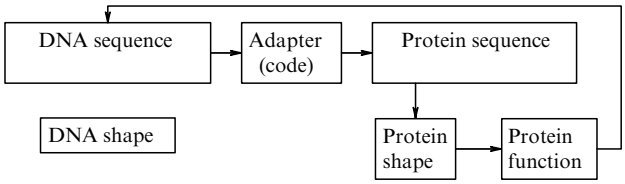

Figure 2. Scheme of protein synthesis in today's biosphere.

Let us briefly remember the contemporary mechanism of the *protein biosynthesis* (for more details see Ref. [22]). This process involves the following stages.

(1) Formation of a complementary replica of the so-called messenger RNA (*m*-RNA, also known as 'informational RNA') from the corresponding structural gene. This process is called *transcription*.

(2) Covalent bonding of transfer RNA (*t*-RNA) with the appropriate amino acids. This takes place in accordance with the genetic code [by *code* we mean the table of correspondence between nucleotides (codons) and amino acids]. This process involves the molecules of *t*-RNA and adapter proteins (known as *aminoacyladenylate synthetase*). Each *t*-RNA has a triplet of nucleotides (*codon*). Each adapter has, on one end, an appropriate anticodon (complementary to the codon), and on the other end a site complementary to the appropriate amino acid. The anticodons and the binding site are removed far enough from one another. Anticodons have a covalent bond with an adapter. The bond of the adapter with the respective amino acid is not a covalent bond: it is a common adsorption bond between substratum and enzyme due to ionic, van der Waals and similar forces. The transfer RNA has a codon and a group capable of forming an acyl bond with any amino acid. In the process of binding, the codon of *t*-RNA interacts with the anticodon of the adapter, and then the acyl bond is formed between the amino acid and *t*-RNA. Further desorption liberates *t*-RNA loaded with its 'own' amino acid.

Observe that *t*-RNA does not have a section complementary to the amino acid: the amino acid is only attached to *t*-RNA by one covalent (acyl) bond.

(3) The synthesis of a protein sequence takes place in the ribosome. It involves *m*-RNA and *t*-RNA loaded with amino acids. In this case, the anticodons and *m*-RNA one by one interact with the codons of *t*-RNA, which ensures the formation of a *particular primary sequence of amino acids in the synthesized protein*.

The process by which messenger RNA directs the amino acid sequence of a growing polypeptide during protein synthesis is called *translation* — the information contained in the structural gene in the form of the sequence of nucleotides is translated into the information contained in the protein. From the above discussion it follows that the acts of translation take place in the system of adapters. The key role in this process belongs to the genetic *code*, by which we mean the correspondence between the triplets of nucleotides (codons) and amino acids.

All living organisms in today's biosphere use the same universal code represented in Table 1.

Let us point to the main *features* of the contemporary code.

(a) The genetic code is degenerate. This means that several different combinations (codons) encode one and the same amino acid (as shown in Table 1). Three codons (UAA, UAG and UGA) do not correspond to any amino acids (nonfunctional codons); they act as punctuation marks that denote the beginning and the end of a transcription. Owing to the code being degenerate, the number of different *t*-RNA is equal to the number of functional codons — that is, 61.

Table 1. Correspondence between amino acids and codons (genetic code)†.

No.	Amino acid	Codon (RNA triplet)	No.	Amino acid	Codon (RNA triplet)
1	Ala	GCA, GCC, GCG, GCU	11	Leu	CUA, CUC, CUG, CUU, UUA, UUG
2	Arg	AGA, AGG, CGA, CGC, CGG, CGU	12	Lys	AAA, AAG
3	Asn	AAC, AAU	13	Met	AUG
4	Asp	GAC, GAU	14	Pro	CCA, CCC, CCG, CCU
5	Val	GUA, GUC, GUG, GUU	15	Ser	AGC, AGU, UCA, UCC, UCG, UAU
6	His	CAC, CAU	16	Tyr	UAC, UAU
7	Gln	GGA, GGC, GGG, GGU	17	Thr	ACA, ACC, ACG, ACU
8	Gly	CAA, CAG	18	Try	UGG
9	Glu	AUA, AUC, AUU	19	Phe	UUC, UUU
10	Ile	AUA, AUC, AUU	20	Cys	UGC, UGU

† Abbreviations for nucleotides and amino acids: A — adenine, C — cytosine, G — guanine, U — uracil [whose counterpart in DNA is thymine (T)]; Ala — alanine, Arg — arginine, Asn — asparagine, Asp — aspartic acid, Val — valine, His — histidine, Gln — glutamine, Gly — glycine, Glu — glutamic acid, Ile — isoleucine, Leu — leucine, Lys — lysine, Met — methionine, Pro — proline, Ser — serine, Tyr — tyrosine, Thr — threonine, Try — tryptophan, Phe — phenylalanine, Cys — cysteine.

(b) Inverse degeneration — that is, a situation when one codon corresponds to several amino acids, is practically not encountered (with very rare exceptions, see Ref. [3]). This is important, because otherwise the translation would have not been one-to-one, and the biosynthesis of a protein would have been dependent on chance.

For a living organism, the ambiguous translation would be ruinous, because it would produce odd nonfunctional proteins instead of regular proteins with a specified sequence, shape and function. In other words, an inversely degenerate adapter in which, say, the GCA anticodon corresponded to histidine rather than alanine, would be a poison for modern organisms.

(c) The code is the same for the entire biosphere, from protozoa (*E.coli*) to the higher plants and animals.

(d) The contemporary code carries conditional information, because any other code obtained, for example, by permuting the amino acids in Table 1, would have been as good as the existing one in the current conditions. The number of different and almost equivalent versions of the code is equal to the number of permutations of amino acids, or 20!

2.3 Variants of primary biosynthesis

Now let us discuss the main issue: what was the beginning of the first organism that was capable of complementary autoreproduction — that is, the organism that contains DNA and proteins necessary for the synthesis of protein-replicase. In fact, we are talking about spontaneous creation of the information required for this purpose.

The concept of a hypercycle introduced by M Eigen [23] well applies to the cycle of biochemical processes in which proteins (P_i) catalyze the production of polynucleotides (I_i), while the latter 'encode' the biosynthesis of proteins ($i = 1, 2, \ldots, n$). The scheme of Eigen's hypercycle is shown in Fig. 3a. Thin lines correspond to catalysis, thick to 'encoding'. The simplest hypercycle involves just one protein (replicase) and one nucleotide ($i = 1$); its scheme is depicted in Fig. 3b. Contemporary biosynthesis is a quite complex hypercycle: it involves protein-replicase, messenger RNA, a set of adapters, a set of transfer RNAs (61 species), and a ribosome — in other words, the number of proteins and nucleotides involved is quite considerable.

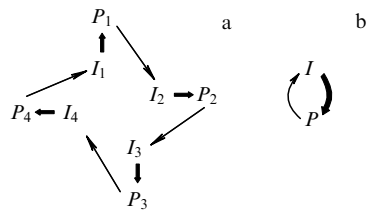

Figure 3. Scheme of hypercycle: complex (a), and simple (b).

Now the central question is, what was the primal hypercycle like, and what is the probability of its spontaneous (fortuitous) realization?

Probability estimates are always based on explicit or implicit assumptions which essentially reduce to the interpretation of the concept of 'encoding'.

I. Assume that the mechanism of encoding in the primal hypercycle was the same as today, involving more than 100 proteins. Each of these contains about 100 amino acids. Their encoding requires DNA containing 60,000 nucleotides. Given that all this information is valuable (that is, necessary for the synthesis), the probability that such DNA could have been produced by mere accident is

$$W_{\mathrm{I}} = 4^{-60000} = 10^{-40000}\,. \tag{1}$$

Obviously, this chance is ridiculously small.

II. Assume now that the primal mechanism of encoding was different from what it is today. Namely, it did not involve adapters, transfer RNA and other similar actors, and the encoding proceeded through direct recognition of codes and the respective amino acids. This hypothesis was proposed earlier in a number of works [24, 25]. In addition, it has been experimentally proved that the affinity of some codons to the 'kindred' amino acids is greater than for the 'alien' ones [26]. Then the primal hypercycle was as simple as can be, and involved one polynucleotide and one protein-replicase. The latter, however, should have been built of at least 200 amino acids (otherwise it would have been unable to perform its function). The 'encoding' DNA would then consist of 600 nucleotides in a specified order. The probability of spontaneous synthesis of such DNA is

$$W_{\mathrm{II}} = 4^{-600} = 10^{-400}\,, \tag{2}$$

which is greater than previous, but still too small.

These values correspond to the probability of synthesis of the required sequence in one try. They have to be compared with the number of attempts in the entire living space over the entire time of existence of the Earth. Assuming that V — the volume of the available hydrospace (pool, lagoon, etc.) — is $(5-10) \times 10^{10}$ cm^3, the volume required for the synthesis of one DNA is $v \cong 10^{-6}$ cm^3, the time of existence of the biosphere is $T_{\mathrm{bio}} = 10^9$ y, and the time of one attempt is of the order of one day, $t \approx 10^{-2}$ y, we get that the number of attempts is

$$N = \frac{V}{v}\,\frac{T}{t} = 10^{29}\,. \tag{3}$$

Similar estimates were obtained in Refs [27–30]. The accuracy of such estimates is plus or minus several units in the exponent, but much less than the exponent itself.

According to the first calculation, the probability of the origination of life is $w_{\mathrm{I}} = NW_{\mathrm{I}} = 10^{-39970}$, and $w_{\mathrm{II}} = NW_{\mathrm{II}} = 10^{-370}$ according to the second. Obviously, neither of these makes sense.

Results like W_{I} and W_{II} are the biggest single stumbling block in theories of the origin of life. It is these absurdly small probabilities that are used for justifying the conclusion that it is not possible to understand and describe the origin of life in the framework of contemporary science.

It is possible to 'stretch' these values. For example, one may assume that some amino acids in the protein can be replaced with different ones (and such is indeed the case).Then the encoding can be performed not by a unique sequence, but by a number (possibly quite large) of sequences. In this manner the probabilities can be raised by many orders of magnitude. It is still not possible, however, to push the probability to a sensible value of the order of 10^{-30}.

The heart of the problem lies in the meaning of the word 'encoding' — or, to be more precise, in the assumption that the sequence in the primal DNA must be special, not arbitrary. Then the probability is 'combinatorially' small —

when the number of elements is large, the number of selected combinations is always very small compared with the total number of variants.

The number of tries N is also large, but not combinatorially so. It is expressed in terms of physically realizable variables, and cannot be greater than a 'googol' (written out as the numeral 1 followed by 100 zeros, or 10^{100}). In reality it is smaller, and cannot compete with the combinatorially large numbers.

To overcome this difficulty, it is sufficient to relinquish the literal meaning of the word 'encoding', and accept that the DNA molecule in the primal hypercycle promoted the formation of the protein-replicase (catalyzed its synthesis) without the code. Such a scenario was considered in Refs [28 – 30]; let us discuss it in greater detail.

Recall that the function of the protein-replicase depends on its shape, which is complementary (perhaps not completely) to that of the DNA molecule. For the catalytic act as such, the sequence of DNA is not important. Generally speaking, a protein of the desired shape may form without the need for a code (that is, the DNA sequence) as a result of the following processes.

(1) Adsorption of amino acids by the DNA molecule (with any sequence).

(2) Condensation of amino acids — that is, formation of peptide bonds between their N and C atoms.

The resulting protein is a replica of the DNA molecule. Such a technique is well known in chemistry, and is commonly used for obtaining a polymer of the desired form. In the case under discussion, the protein, being a replica of the DNA, is capable of catalyzing the replication of DNA, like this is done today by the replicase. The process can be illustrated by the scheme in Fig. 4, where the shape of the protein is determined by the shape of the DNA, whereas their sequences are not important (although shown on the diagram).

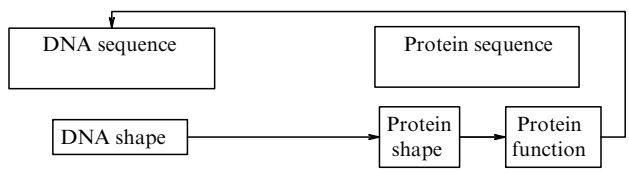

Figure 4. Scheme of primal synthesis of protein-replicase (without code).

The next step — the appearance of the proteins-adapters — can also be envisaged as a result of natural physicochemical processes (for more details see Refs [28 – 30]). The grooves of the DNA spiral may host short polynucleotides (oligomers) — in particular, codon triplets that form portions of the triple helix. Upon the formation of adsorbate and subsequent condensation, these codons may form covalent bonds with blocks of amino acids. In this way, among the oligomers there will be, on the one hand, polypeptides that contain codons, and on the other hand segments complementary to amino acid (or a block of amino acids). Such polypeptides have the property of adapters.

The correspondence between codon and amino acid in a given adapter this time depends on the sequence of nucleotides in the particular DNA molecule and the location of the amino acid in the given protein sheath. In other words, the adapters will be the same when they form on the same DNA (DNA molecules with the same sequence of nucleotides), and will be different otherwise. To reflect this circumstance, we shall hereinafter refer to the 'own' set of adapters for DNA with a given sequence, and the 'own' DNA for a particular set of adapters.

The maximum length of random DNA for which the formation of adapters does not yet lead to inverse degeneration was estimated in Refs [29, 30]. The number of nucleotides in such DNA had to be less than $n_{\max} < 96$. Obviously, DNA that short was not capable of 'encoding' (in the contemporary sense of the word) a protein-replicase of the appropriate length. On the other hand, the primal DNA could not be too short, because then it would not be able to catalyze the production of protein-replicase of the required shape. From these considerations, the length of DNA cannot be smaller than the size of the protein (50 – 100 A), and should contain some 30 nucleotides.

The availability of its own set of adapters greatly accelerates the synthesis of protein-replicase, because the adapters convey the appropriate amino acid to where it is needed, thus ensuring the formation of the primal sequence in the adsorbate, compatible with the functional form. At the same time, such a set will prevent the synthesis of protein on any other alien DNA. As a matter of fact, here we are dealing with the destructive role of inverse degeneration.

A hypercycle involving a polynucleotide (DNA), protein-replicase and a set of adapters is illustrated in Fig. 5, where the units shown in Fig. 4 are supplemented by the set of adapters. The scheme in Fig. 5 can describe the same processes as the scheme in Fig. 4 (as shown by arrows *1* and *2*), but also adds new possibilities owing to the availability of adapters. For example, arrows *3*, *4* and *5* indicate that there is a direct path from the sequence of DNA to the primary sequence of protein. In other words, the primary sequence of DNA starts to play an important role in the determination of the primary sequence of the protein. It is the adapters that promote the formation of the protein sequence that corresponds to the functional form of the protein. In this way, Fig. 5 describes a transitional stage which combines the 'codeless' processes of protein synthesis with the 'encoded' processes similar to biosynthesis of modern times. Because of this, a change in the DNA sequence (mutation) without a change in the set of adapters causes the synthesis of proteins with a modified sequence of amino acids — and hence with a modified form and function. This opens the possibility of further biological evolution.

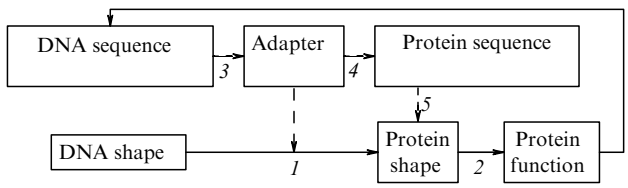

Figure 5. Scheme of intermediate variant of protein-replicase biosynthesis.

In this scenario the problem of the minute probability of occurring the primal hypercycle does not arise. Another question, however, has to be answered: how is it that our contemporary biosphere is completely dominated by one variant of code, with the absence of alternatives?

Two possible answers are discussed.

One hypothesis holds essentially that among different variants of the code one was better than the rest, and this best one was *selected* in the course of evolution [23].

The other hypothesis [28–30] assumes that all variants of the code were equivalent, but eventually a unified code was *chosen* (not selected) as a result of interaction between different populations. This hypothesis will be further discussed in greater detail.

Let us say a few words on the possibilities of experimental verification of such hypotheses.

Verification of the statement that one code was better (more stable against mutations) than others is difficult and time-consuming. Indeed, it requires creating a system based on a different code, and comparing it with the existing system employing another code. This has not been done.

Checking the hypothesis of direct selective interaction of codons (or anticodons) with amino acids requires finding the energies of their interactions. This is possible but has not been done.

The following is necessary to verify the hypothesis of heterogeneous catalysis: (i) to determine the conditions under which a dense adsorbate of amino acids is formed on the double helix of DNA (with arbitrary sequence); (ii) to accomplish condensation of amino acids on the complex produced; (iii) to test the efficiency of the resulting polypeptide as a replicase. Such experiments today are feasible, but have not yet been performed.

2.4 Choice of the unified code

This stage took place after the formation of several different populations of hypercycles with various variants of the code. The description of this stage can be conveniently based on a mathematical model of the type

$$\frac{\mathrm{d}u_i}{\mathrm{d}t} = \frac{1}{\tau_i}\, u_i - b_i \sum_{j\neq i} u_i\, u_j - a_i\, u_i^2\,, \qquad a_i < b_i\,, \tag{4}$$

where u_i is the concentration of hypercycles in which the set of adapters corresponds to the ith variant of the code.

The term $(1/\tau_i)u_i$ describes autocatalytic reproduction with the characteristic time τ_i.

The term $b_i\, u_i\, u_j$ describes the interaction of hypercycles with different variants of the code. This term is negative because of the antagonistic (or competitive) nature of the interaction.

The term $a_i\, u_i^2$ stands for the effect of 'cramming' — annihilation (mutual destruction) of two similar hypercycles as they meet. This term is important when the concentration of hypercycles becomes large. The 'cramming' term in this case corresponds to the competition between the like hypercycles for the primal substrate. Such competition also exists between the unlike hypercycles. In addition, however, there is a purely antagonistic interaction between them. Its meaning in our case is simple: when two different hypercycles meet, their adapters mix, which leads to inverse degeneration. This is detrimental for both.

Now we assume that the parameters τ_i, b_i and a_i are the same and consequently do not depend on i, which allows us to drop the subscript i: τ, b and a. This assumption ensures equivalence of elements of different types.

Let us analyze the properties of model (4). It is convenient to express it in the dimensionless variables

$$t' = \frac{t}{\tau}\,, \qquad u_i' = b\tau u_i\,, \qquad a' = \frac{a}{b}\,. \tag{5}$$

Then the system (5) becomes

$$\frac{\mathrm{d}u_i'}{\mathrm{d}t'} = u_i' - \sum_{j\neq i} u_i'\, u_j' - a_i'\, u_i'^{\,2}\,. \tag{6}$$

Further we shall use the system (6); we assume that $a \ll 1$ and drop the primes.

The dimensionless system (6) contains a single parameter a which reflects the relative importance of antagonism: the smaller a, the stronger the antagonistic interaction. In our present case it is obviously much stronger than the non-antagonistic interaction, and the parameter a in Eqn (6) is considerably less than one.

System (6) features N stable steady states. Each only exhibits the elements of a certain type: for example, in the jth state we have $u_j = a^{-1}$, while all other $u_{j\neq i}$ are zero. In addition, there is the null steady state (all $u_i = 0$), which is unstable because all Lyapunov numbers are positive (and equal to one). The symmetric state in which all u_i are the same and equal to $\bar{u} = (N-1+a)^{-1}$ is also unstable (saddle); here, one Lyapunov number is negative, but all the rest λ are positive and equal to $\bar{\lambda} = (1-a)/(N-1+a)$.

The phase portrait of system (6) at $N = 2$ and $a = 1/3 < 1$ is shown in Fig. 6.

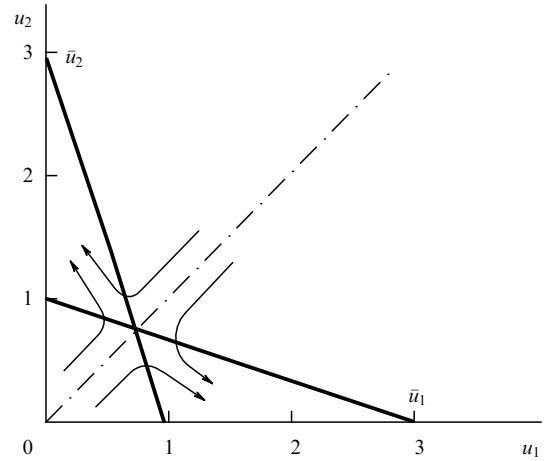

Figure 6. Phase portrait of symmetric system (6) with $a = 1/3$. Isoclines are represented by solid lines, the separatrix (and bisectrix) by a dot-and-dash line.

The process eventually leads to a 'pure' state — that is, one variant of the code is chosen. The same applies to the nonsymmetric model — the case when the variants are not the same. The winner is not the 'best' population, but rather the population that by some chance outnumbered the rest from the start. In other words, it is not the 'selection of the best' (in the traditional Darwinistic sense), but the choice of one among equivalent populations, which then ousts the rest.

One may say that this result is an illustration of the motto from Orwell's *Animal Farm*: "All animals are equal but some animals are more equal than others".

Let us end this section with several appropriate comments.

The evolution of the protein biosynthesis may be likened to the evolution of writing. The ancient form of writing is based on pictograms or hieroglyphs. Originally, each hieroglyph was a picture of the object, a kind of 'replica'. A

dwelling was represented by a triangle Δ adumbrative of a cabin, an ox by a head with horns ♉ (aleph). There was no need to use an alphabet (code). Hieroglyphic writing corresponds to the scheme of the primal synthesis of adapters in Fig. 4.

With time, some hieroglyphs lost direct connection with the entire object (and became much simpler), but acquired the new function of a letter. A letter is a part of a word — a fragment (one might say 'oligomer'), and does not mean anything by itself. It carries a meaning in combination with other letters, in accordance with the alphabet (code). Alphabetic writing developed in response to the increasing amount of information that had to be transferred. The reason is plain: with even a few symbols the number of combinations is factorially large compared with the number of symbols. The transition from hieroglyphs to letters was gradual. Firstly, the ideogram of an object (or operation) was augmented with a simpler symbol that served to define its meaning more exactly. Such a hybrid writing, retaining the hieroglyphs as ideograms, extended the capabilities of written communication. By and by, the hieroglyphs were replaced by letters. We would like to repeat that this was a gradual process, and the transformation of a hieroglyph into a letter did not compromise the intelligibility of the text. Both sides (the writers and the readers), through mutual teaching and learning, worked out the conventions of the code — that is, the alphabet. The simplified symbols — letters — evolved as fragments of the more intricate hieroglyphs. The Greek α (alpha) is a portion of the Hebrew 'aleph' — the horns being firstly fallen onto the side. The scheme of intermediate biosynthesis in Fig. 5 corresponds to the hybrid writing, when the adapters are on the one hand the fragments of the 'sheath' (hieroglyph), and on the other hand already the letters of the alphabet.

Let us point out an aspect of biological evolution. In the period under discussion, the hypercycle only involved a single protein-replicase with a single function. Even in the simplest populations of this kind a unified code was developed (chosen). We can say that 'in the beginning was the Word', and the word had one meaning: complementary reproduction — that is, life.

3. The problem of biological asymmetry

This problem is treated in review [31], which also lists the relevant bibliography. As it happens, the question remains open. Therefore, we shall just briefly formulate the problem and describe some possible ways of solving it.

Most of the organic molecules exhibit so-called chirality (right- or left-handedness), and have dextrorotatory (D) and levorotatory (L) isomers (enantiomers). Solutions and crystals of D isomers turn the plane of light polarization to the right or clockwise, and those of L isomers rotate it to the left or counterclockwise.

More complicated organic compounds may be made up of fragments of different chirality; then the net direction of rotation will depend on the optical properties of individual fragments.

In inanimate nature chiral molecules occur in a racemic mixture that contains equal quantities of dextrorotatory and levorotatory forms. In animate nature such symmetry does not exist.

All amino acids (with the exception of glycine which is nonchiral) are represented by their L forms. This implies that their main fragment coincides with the L form of glyceraldehyde, from which they all can be derived by the substitution of groups. Other fragments may have other chirality as well.

Pentose sugars-riboses which make up the main chain of the ribonucleic acids (DNA and RNA) occur in the D form.

Nucleotides that represent the side groups of ribopolymer mainly occur in the levorotatory form ('gauche' form).

We see that animate objects contain both right-handed and left-handed forms of different molecules, but they never occur in a racemic mixture.

Now we face the following questions:

— Why is it that the molecules in the living matter occur in a particular enantiomorphic form, and not in a racemic mixture?

— Why has Nature selected just this variant and not the opposite?

— Could asymmetric living objects arise from an inanimate environment which contained all the required components in a racemic mixture?

— Is it possible that the mirror symmetry was broken in the prebiological period?

The answer to the first question is simple. Chemical reactions in the organism are catalyzed by proteins-enzymes. Each such protein has an area (active site) complementary to the substrate. Catalysis of two optical isomers requires two enzymes. Catalytic processes in racemic mixtures would require a double set of enzymes. Such organisms would be bulky and poorly adapted to struggling for survival. It is not surprising then that 'racemic organisms' did not survive.

On top of this, the mirror-image of the enantio-specific enzyme is often an inhibitor of the process (a poison). As applied to the DNA reproduction, the effect of inhibition was theoretically considered in Ref. [31]. As demonstrated, a chirally pure DNA may form in a racemic mixture of mononucleotides, but only of a relatively short length ($N \approx 50-100$ base units). As the length increases, the probability of incorporation of antipodes grows factorially.

Recall that in the contemporary biosphere the segment of DNA that encodes one functional protein (about 200 amino acid residues) must contain at least 600 nucleotides. Because of this, 'levels of complexity' were introduced in Ref. [31]: biological ($N > 600$), and chemical ($N < 50$). Chirally pure DNA of biological complexity cannot reduplicate in a racemic mixture, but those of chemical complexity can.

The second question concerns the reasons of violation of chiral symmetry. In doing so two possibilities are discussed.

The first is related to the external asymmetrical factors. Such do exist, although they are by no means powerful. They include participation of chiral minerals (for example, quartz) in the DNA synthesis, the influence of circularly polarized light, and the possible role of external neutrinos and internal weak neutral currents. The latter hypothesis is especially popular, because it turns out that weak neutral currents promote the synthesis of D sugars and L amino acids (see Ref. [31]). The quantitative estimates show, however, that the effect of weak neutral currents is very small (of order 10^{-17}) [65]. Neutrino fluxes were analyzed in Refs [32, 33]. It was demonstrated that the biggest contribution could be associated with the neutrinos produced in the explosions of supernovae. Even in this case, however, the effects of a neutrino flux on biochemical processes are very small, and under equilibrium conditions this factor cannot lead to a considerable domination of one of the antipodes.

The second hypothesis assumes that under nonequilibrium conditions (in particular, biological or prebiological) the symmetry may be broken spontaneously owing to the instability of the racemic state. As a matter of fact, it is the same effect as that associated with the choice of the unified code. The description of the process may be based on a model of type (6) under the assumption that the number of variants is two $(i = 1, 2)$. Such model can also describe a purely chemical reaction of one-chirality molecular synthesis from a nonchiral precursor as long as the following conditions are met:

(a) the chiral molecular yield promotes the synthesis of molecules of like chirality (autocatalysis);

(b) upon encounter, two antipodes are removed from the reaction sphere (antagonistic interaction).

Such a possibility was first noted by Fisher; it is discussed in greater details in Ref. [31]. Depending on the reaction parameters, the racemic state can be either stable or unstable. In the latter case, molecules of one predominant chirality (depending on the random fluctuation) will be produced. In the neighborhood of the bifurcation point, the reaction kinetics can be described by a model based on just one equation

$$\frac{\mathrm{d}\eta}{\mathrm{d}t} = \varepsilon\eta - \eta^3 , \tag{7}$$

where η is the parameter of chirality:

$$\eta = \frac{C_+ - C_-}{C_+ + C_-} ;$$

C_+ and C_- are the concentrations of D and L enantiomers respectively; $\varepsilon \ll 1$ is the small bifurcation parameter such that at $\varepsilon < 0$ the racemic state $(\eta = 0)$ is stable, and at $\varepsilon > 0$ the racemic state itself is unstable, but the states $\eta = \pm\sqrt{\varepsilon}$ are stable.

However, a chirally pure product $(\eta = \pm 1)$ can only form when the parameter ε is of the order of unity, $\varepsilon \approx 1$. In practice this means that the nonautocatalyzed reaction channel with a racemic yield must be blocked. Such a situation is typical of biological systems, but can hardly be even theoretically expected of chemical systems.

Such is the essence of the problem.

The hottest issue today concerns the time of breakdown of chiral symmetry — whether this happened during the prebiological period, or at a later time. We believe that the answer is simple: chiral symmetry could be (and was) violated at the time of establishment of the primal hypercycles — neither sooner nor later.

Indeed, the DNA molecules in the primal hypercycles were not long (as mentioned earlier, their estimated length was $N \approx 30-50$ base units). They did not perform a biological function (encoding), but they fulfilled a chemical function (heterogeneous catalysis). Such molecules could well have been of one specific chirality. The presence of protein-replicase created steric obstacles for antipode introduction, which reduced the likelihood of errors in copying. This stage could take place in the racemic mixture of nucleotides; it did not require a chirally pure environment. On the other hand, nonautocatalyzed synthesis of DNA of such length is practically impossible.

Thus we see that the above scenario of formation of primal hypercycles may be regarded as an example of a chemical reaction that has the properties of being biologically specific (in the sense of Ref. [31]). The process took place on a level halfway between biological and chemical levels of complexity. In this case the process could lead with equal likelihood to chirally pure hypercycles of either forms (antipodes). In a scenario where the probability of establishment of a hypercycle is close to unity, the formation of antipodes is inevitable.

Subsequently, one of the variants (antipode) was completely eliminated for the same reasons as the alternative variants of the code. In this case the antagonistic interaction between the antipodes was even stronger than between the carriers of different codes. Upon the encounter of two antipodes one was eaten, and the other mortally poisoned by what he ate.

In today's biosphere, the nutrient medium of living organisms is built up of the products of their vital activity. Clearly these products do not occur in a racemic mixture — the mirror symmetry is broken in the same degree as in the living organisms themselves. The existence of total antipodes in such circumstances is not possible. Possible, however, is the existence of separate species that produce individual chiral isomers — and perhaps use them for defense.

It follows that biological asymmetry is caused by the instability of the symmetric state. In such a situation, there hardly is any reason to look for disturbing external factors.

Nevertheless, the search for such external factors continues.

The combined version is discussed, assuming both spontaneous breakdown of symmetry and the effects of neutrinos [34]. This is possible if the system evolves in such a way that ε slowly increases from negative to positive values, and the concentrations of antipodes are not small in the process. Then in the neighborhood of the bifurcation point (at $\varepsilon = 0$) the choice of the final state can be affected even by minor external causes.

In such a situation the Lyapunov numbers are small, the process evolves slowly even after bifurcation (when $\varepsilon > 0$), and the fast fluctuations are smoothed. Then a small permanent factor that breaks the chiral symmetry may be important. This factor is taken into account by introducing a constant term $\delta \ll 1$ to the right-hand side of Eqn (7):

$$\frac{\mathrm{d}\eta}{\mathrm{d}t} = \delta + \varepsilon\eta - \eta^3 . \tag{8}$$

The solution of Eqn (8) has a stable branch which exhibits no bifurcation at $\varepsilon = 0$. In addition to that, at $\varepsilon > 0$ there are two more solutions: one stable and one unstable (separatrix). At $\varepsilon = 0$ they lie very close (commensurate with $\sqrt[3]{\delta}$) to the stable branch.

In such circumstances, the external factor can formally be regarded as the primary cause of the phenomenon.

As applied to the process under discussion, however, this variant does not seem realistic.

More plausible is a different situation, in which the concentrations of hypercycles are small, whereas their relative fluctuations are large, and the antagonistic interaction is relatively strong $(a \ll 1)$. Then the symmetric state is highly unstable, the Lyapunov numbers are large, the process evolves quickly, and fluctuations of concentrations do not have time to smooth out. Then external factors like neutrinos are of little consequence, and the choice of the variant depends on the initial fluctuation — that is, at random.

4. The problem of tempo in biological evolution

In several billion years the biosphere evolved from protozoa to homo sapiens. One opinion holds that this is too fast, and such a tempo cannot be explained by modern science. The opposite view also exists, so there is room for debate (see Refs [35, 36]). Let us explain the point.

According to the traditional view (the so-called Darwinistic approach), evolution occurs through point mutations and subsequent selection of the better adapted individuals. In this process, the surplus genetic information that gives no advantage in the struggle for existence must be eliminated. This theory gives a satisfactory description of those stages of evolution when the established species occupy their ecological niches and adapt to them. In the course of evolution, however, there were other stages which saw the advent of new species with totally new functions. Such stages are known as *big leaps* or *aromorphoses* [1].

Let us give some especially vivid examples of such leaps in evolution.

At the early stages of evolution, living creatures fed on the organic matter accumulated over the prebiological period (or devoured each other). At that time the Earth's atmosphere contained no oxygen, and the main process that supplied energy for the synthesis of adenosine triphosphate (ATP) was glycolysis. With time, however, the supplies finally ran out, and a food crisis arose. The way out was found by creatures that learned to use the energy of light and decompose water (photosynthesis). This gave them a huge evolutionary advantage, and soon the photosynthetics conquered the ocean, and then the land too. This led to an ecological catastrophe: the photosynthetics decomposed water and evolved oxygen, which was poison for the anaerobes. The atmosphere became 'poisoned' with oxygen. Nature came to the rescue again: organisms developed that were able to synthesize ATP by oxidizing sugars with oxygen. This was the advent of breathing organisms.

Each instance of the emergence of fundamentally new organisms was a big leap, and there were many such leaps in evolution.

The problem is that traditional Darwinism cannot explain the occurrence of leaps. Let us illustrate this with the example of photosynthetics.

The process of light utilization includes several stages: absorption of light, conversion of its energy into a different form, and finally the synthesis of ATP. Each stage is effected by a special protein, and the entire process is controlled by a protein system. The origination of each separate protein does not give any evolutionary advantage, and is just an additional burden on the organism. The advantages (quite big) arise only when the entire system is in place.

The problem is essentially the same as that associated with the origin of life, but there are also some differences.

In the epoch under consideration, the apparatus of biosynthesis was already in place. Therefore, the protein was not created from scratch, but the encoding segment of DNA — that is, new information. The amount of new information depends on the size of the novel proteins, and the size in turn depends on the function. A photosynthetic system must contain at least two proteins (chromophore and ATP synthetase), each containing no less than 200 amino acids. The system-encoding segment of DNA must contain 1200 nucleotides. The amount of information in such a segment is $J = \log_2 4^{1200} = 2400$ bit. The probability that such segment will arise from point mutations in one act is $W_{\min} = 2^{-J} = 2^{-2400}$, which is absurdly small. This probability is calculated just for illustration, and is greatly underestimated. A more realistic evaluation of the amount of valuable information in a protein-chromophore (bacteriorhodopsin) was performed in Ref. [37]: $J_{\mathrm{b}} = 100$ bit. Then the amount of valuable information in the photosynthetic system is about 200 bit, and the probability that such system will arise because of point mutations is $W_{\max} = 2^{-200}$. This is most likely an overestimate, but is still ridiculously small compared with the number of tries, $N = 10^{30}$.

It is these estimates that lead to the belief that the actual tempo in evolution has no rational explanation.

To resolve this problem one must, like in the previous case, go beyond the limitations of the traditional approach and assume a different mechanism of big leaps, and a different type of mutations that exhibit the following properties.

(a) The amount of new (generated) information must be as small as possible; most of the required information must be sourced from the reserve. Information required for a life-support system under the old conditions must be preserved, and mutations should only affect the reserve information. This requires the existence of an 'archive' of neutral information (that is not used immediately and does not give any evolutionary advantage). This contradicts the dogma of elimination of redundant genetic information but, as we shall see, agrees with reality.

(b) Along with point mutations, block mutations must exist, in which the new information is combined with the reserve information.

Let us illustrate this point with an example taken from technological evolution. Inventing the steam engine — a machine with a fundamentally new function — James Watt did not invent all the parts (cylinder, piston, levers, etc.), but used instead the existing appropriate information that was contained in the description of the machines already available (mills, pumps, etc.) — that is, information from the archives. The basic novelty consisted in the arrangement of the old parts in the new design. The number of possible combinations of parts is not too large, and the selection of a suitable arrangement takes a reasonable time.

The analog of the archive in biology is the reserve of neutral genetic information. The analog of enumeration of variants is block mutation. While a point mutation consists in the replacement of a nucleotide with a different one, in a block mutation the genome is broken into parts (blocks) which are then arranged in a different sequence. According to estimates made in Ref. [38], the time required for the selection of a protein system with fundamentally new functions is quite reasonable.

The reserve of neutral genetic information has been found experimentally, and its existence has become a central concept in the 'neutralist' theory of evolution [39]. The mechanisms of genome splitting into blocks which are subsequently linked together in a new order were also discovered, and are currently under active investigation [40]. Thus, the feasibility of block mutations that have the properties (a) and (b) is no longer doubtful.

[1] Term introduced by Russian biologist A N Severtsov back in the 1930s. He distinguished aromorphosis which is the development of a new level of integration, idioadaptation which is a specific adaptation, and degeneration. (*Translator's note*.)

Observe that in the big leaps it is not the best fitted individuals who develop the new function that gives them a huge evolutionary advantage. By contrast, it is the feature of marginals who carry a lot of neutral information. The act of aromorphosis is not the selection of the best fitted, but rather the choice of a suitable variant. The selection starts at the next stage, when the novel organisms begin to adapt to the environment.

To summarize: the problems formulated above have not yet been finally solved; experimental and theoretical studies must be continued. However, possible solutions do exist. In any case, the claims that these problems are beyond the grasp of modern science are unfounded.

For solving these problems it is necessary (and sufficient) to shake off the dogmas and preconceptions and take a look at the problem with eyes wide open. For example, in the problem of the origin of life one needs to go from the literal meaning of the words 'DNA encodes the protein-replicase' to the broader sense of 'DNA catalyzes the formation of the protein-replicase'.

In the problem of tempo in evolution one has to reject the dogmatic 'point mutations and selection' and admit the possibility of block mutations and choice.

5. Information and informatics

5.1 Information and its properties

The term 'information' is used very often and with different meanings; perhaps even more often in vain — that is, without any real meaning at all.

For illustration, let us quote a collection of definitions borrowed from Refs [41, 42] (see also the references cited therein).

In the humanities, this term is used in the sense of 'knowledge of...' (and nobody seems to worry about the tautology of this definition).

• Information is knowledge received from someone else or derived from one's own learning or study.

• Information is knowledge contained in a given message and regarded as the object of transfer, storage and processing.

• Information in the common sense is knowledge, news; in scientific and technological applications information is something that is carried by a signal.

• Information is the designation of content received from the external world in the course of our adaptation to such, and the adaptation to such of our senses.

• Information is one of the properties of objects, phenomena, processes of objective reality, and of man-made controlling machines, which consists in the ability to perceive the internal status and the impact of the environment and to store the results for a certain time, to transfer the knowledge of the internal state and the accumulated data to other objects, phenomena, and processes.

• Information is the objective content of the linkage between interacting material objects, which is manifested in the change of states of these objects.

Along with these and similar definitions, there is a tendency to relate information to the degree of order of the system that receives this information.

• Information is order, communication is the creation of order from disorder, or at least the increase of the degree of order that existed prior to the receipt of the message.

The definitions that follow are to a certain degree repetitive.

• Information is current data about variables in a certain branch of activity, systematized notions about the main causal links that are contained in the knowledge as the concept of the more general class, with respect to which the information is subordinate.

• Information is knowledge about a distinctive event, occasion or something like this.

• All those data on the outer world which we gain both through a direct action of surrounding objects and phenomena on our organs of senses and by indirect way via perception of books, newspapers and stories of other people, are named information.

• In problems of communication 'information' means any message or transmission of news about something that had not been known in advance.

In philosophy, popular are definitions which contain a metaphoric term 'reflection'.

• Information in the most general case is a polymorphism which one object contains about another, it is mutual, relative polymorphism. In the context of the theory of reflection, information can be interpreted as a reflected polymorphism, as a polymorphism that the reflecting object contains about the reflected object.

• Information is the mental reflection of the objective causal links in the surrounding real world.

• Information is the content of the reflection processes.

• Information is not identical with reflection, it only is its invariant part admitting of definition, objectivization, and transmission.

• Information is a philosophical category considered alongside of such concepts as space, time, and matter. In the most general sense information may be regarded as a message — that is, a form of linkage 'between the transmitter that transmits the message and the receiver that receives the message'.

A special place in our collection of definitions belongs to the statements that information is an algorithm.

• Information ... is a plan of construction of the cell, and hence of the entire organism.

In other modifications of this definition, the word 'plan' is replaced with the word 'instruction'[2], 'algorithm', or 'operator'.

• The set of techniques, rules or data required for the construction of an operator will be referred to as information.

The abundance of definitions means that none has been universally recognized. This is not surprising, because information science (informatics) is quite young and is rapidly developing.

As indicated earlier, the concept of 'information' is constructive and substantive in sciences concerned with animate nature. Used in this field is the following definition coined by Henry Quastler [27]:

• Information is the *remembered* choice of one option out of several possible and equitable.

Hereinafter we shall use this definition, which will be referred to as 'Definition Q'.

Here we have emphasized the word 'remembered' because of its importance for the future discussion. This word relates

[2] Jantsch T *The Self-Organizing Universe: Scientific and Human Implications of Emerging Paradigm of Evolution* (Oxford: Pergamon Press, 1980) pp. 99 – 102. (*Translator's note*.)

to the fixation of information. Generally speaking, a choice may be not remembered (that is, forgotten at once). Such a choice is known as *microinformation*. The remembered choice, to be distinguished from the nonremembered, is referred to as *macroinformation*.

The words 'possible and equitable' mean that the options belong to the same set, and the *a priori* distinctions between them are not big. Ideally, the options can be totally equivalent and equiprobable (like heads or tails); they may also, however, be different. In such a case the word 'equitable' implies that the *a priori* probabilities of different options are of the same order of magnitude.

Definition Q differs from the foregoing definitions in the following:

In the first place, it is very clear-cut and comprehensible, and is widely used in the exact sciences [19, 27, 43, 44]. It has proved its constructivity in many real tasks. When dealing with specific problems, this definition does not conflict with the foregoing ones. For example, the definition of information as instruction or operator in particular applications implies the indication as to which possible action must be selected in one case or another.

Secondly, this definition treats information as something tangible and down-to-earth, nothing lofty or sublime about it. Supernatural awe is not there, which may be regarded by some as a drawback because this is what inspires many people to glorious exploits (scientific, parascientific or charlatanic). Nevertheless, just this definition facilitates scientific understanding of such subtle phenomena as the origin of life and the mechanisms of thinking — in other words, to build a bridge between the exact sciences and the liberal arts.

Thirdly, Definition Q allows introducing a quantitative measure of information.

Let us point to yet another feature of Definition Q.

The word 'choice' belongs to the verbal nouns and can be interpreted both as the process and as the result of a process. The difference is similar to that of the court proceeding and the verdict. Definition Q interprets 'choice' as the result, not as the process itself. It is in this sense (in the meaning of the 'verdict') that it is constructive, and it is in this sense that it is applied to real problems.

However, information as the result of a choice between options is impossible without the process of making this choice, as a verdict is impossible without a hearing. Not every process leads to a choice: this only happens in processes of a certain class. Therefore it is worthwhile introducing the concept of an 'information process' whose properties will be discussed later.

The quantity of information is also important. In those cases when all options are equiprobable, the quantity of information I is defined as

$$I = \log_2 n \,. \tag{9}$$

The logarithm is taken for convenience, because the number of options n is often combinatorially large, as large as $n \sim 10^{100} - 10^{1000}$. For example, when the number of elements (amino acid residues) is only 20, the number of options (permutations) is 20!, or 10^{27}.

The unit of information is known as a *bit* — one bit is the amount of information corresponding to the selection of one option out of the two. Because of this, the choice of logarithm base 2 is the most convenient.

If the *a priori* probabilities p_i of the election of the ith option are not equal ($p_1 \neq p_2 \neq \ldots \neq p_i$) although comparable, then one obtains

$$I = -\sum_i p_i \log_2 p_i \,, \qquad i = 1, 2, \ldots, n \tag{10}$$

[with $p_1 = p_2 = \ldots = p_n = 1/n$, Eqn (10) becomes Eqn (9)]. If one option is much preferable to the rest ($p_i \gg p_{i \neq j}$, $p_i \approx 1$, $p_j \ll 1$), we have

$$I = \log_2 1 + O(p_j) = 0 \,. \tag{11}$$

The concept of the quantity of information was introduced by Claude Shannon [45] long before there was a definition of information itself; as indicated above, a universally accepted definition has yet to be developed. For this reason the concept of information is often supplanted with the quantity of information. This leads to confusion, because there is information and information — that is, information has a number of important features which are not reflected in its quantitative measure.

We have already mentioned the difference between micro- and macroinformation. Other important qualities are: conditional (unconditional), new (not new), valuable (not valuable), coded and semantic (for the time being, we appeal to the reader's intuition). These qualities are often overlooked — for example, it is assumed sometimes that nonvaluable information is not information at all. This leads to misapprehension.

Let us discuss these properties of information.

(i) *Macroinformation* is the remembered choice of one option out of several possibilities; 'remembered' means that the choice made is preserved for some time which is greater than the characteristic time of using this information. The latter may vary from years (information written in a book, computer, diskette, etc.) to seconds.

(ii) *Microinformation* is the choice of one option out of several possibilities that is not remembered. This means that the choice is preserved for a few picoseconds, and is immediately forgotten. An example of microinformation is the definite set of molecular coordinates and velocities in ideal gas at a given instant. Owing to the instability of motion of molecules, this choice is destroyed (forgotten) after a few collisions — that is, under normal conditions within

$$\tau_{\text{micro}} \sim \frac{h}{\kappa T} \sim 10^{-13}\ \text{s} \quad \text{at} \quad T = 300\ \text{K} \,.$$

This time is not sufficient for processing this information or using it to make forecasts. Observe that microinformation is related to physical entropy. This linkage is based on the fact that the concept of physical entropy is only valid when the system is ergodic — that is, when the system quickly forgets its instantaneous state, and resides in all possible states with equal probability.

Generally speaking, macroinformation is not related to physical entropy. A change in the macroinformation (either an increase or decrease) in any process is always accompanied with an increase in physical entropy, which is much greater than the change in macroinformation.

Equations (9) and (10) are equally valid for macro- and microinformation. At the same time, the quantitative distinction between macro- and microinformation is quite considerable.

In the case of macroinformation, n is the number of stable states of the system. In the case of microinformation, n is the

total number of states of the system, not necessarily stable — this means that this is a microscopic concept. Let us give an example. The entropy of one mole of ideal gas in the state of thermodynamic equilibrium is

$$S = \frac{3}{2} k N_{\mathrm{A}} ,$$

where $N_{\mathrm{A}} = 6.02 \times 10^{23}$ mol^{-1} is the Avogadro constant, and $k = 1.38 \times 10^{-16}$ erg K^{-1} is the Boltzmann constant. The entropy is linked to the number of microstates n by the Boltzmann relation

$$S = k \ln n .$$

Hence we find

$$n = \exp\left(\frac{S}{k}\right) = \exp\left(\frac{3}{2} N_{\mathrm{A}}\right) ,$$

which is very large.

If at a given instant the velocities and coordinates of all particles of the gas are known (that is, one definite microstate is selected), then the quantity of microinformation is

$$I = \log_2 n = \frac{S}{k} \log_2 \mathrm{e} = 1.44 \frac{S}{k} . \tag{12}$$

Equation (12) is known as the relation between microinformation and entropy.

Now let us estimate the amount of macroinformation in a gas-filled vessel. This system has only one stable steady state — the state of thermodynamic equilibrium ($n = 1$). Accordingly, the amount of macroinformation in this system is $I_{\mathrm{macro}} = \log_2 n = 0$. Hence we see how different are macro- and microinformation not only in quantity, but also in quality.

All real information processes use remembered macroinformation. Microinformation is used mostly in theoretical speculations on 'Maxwell's demon'.

So in future we shall only deal with remembered information, and the prefix 'macro' will be dropped.

(iii) *Conditional* and *unconditional* (objective) information. An example of conditional information is information about the language — alphabet, vocabulary, grammar, etc. Indeed, this information is required for communication within a social community that uses the particular language, and has resulted from a convention between its members. The conventional nature of such information is emphasized by the fact that in another social community a different language may be used, which in principle is neither better nor worse than the first.

Scientific terminology is another example of conditional information. Assume that an astronomer discovered a new star, calculated its distance from the Earth, measured its luminosity, etc. but did not give it a name. This information is objective (unconditional). Another astronomer discovered nothing but suggested a name for the new star (conditional information). The name was accepted, and the fame of discoverer went to the one who has proposed the name. Which proves that the role of conditional information is by no means minor even in the exact sciences.

It is not always simple to distinguish between conditional and unconditional information. The following circumstances are important in this respect.

Firstly, conditional information has a tendency towards unification. This is natural, because this adds to its value.

Secondly, the unified conditional information is often regarded as unconditional. For example, mathematics unified at the lower level, which includes arithmetic, gives the impression that 'it cannot be otherwise'. The unification of mathematical apparatus, however, is a result of evolution. At earlier stages the notation was different from what it is today.

At higher levels there are several options of describing one and the same object: continual description, dynamic equations, probabilistic models, cellular automata, etc. In many cases the advantage of one description over the rest is not obvious. Because of this, the choice of a particular mathematical apparatus is an act of generation of valuable conditional information.

Thirdly, a very interesting and acute issue concerns the conditional (or unconditional) nature of information in the exact sciences. The common view is that in the course of development of natural sciences we receive unconditional objective information. This is really so when we are dealing with experimental qualitative examinations. For example, the observation that 'like charges repel, unlike charges attract' is an objective fact. However, the interpretation of this fact and even its representation in the form of Coulomb law contain an element of convention. Indeed, here one is already using a specific mathematical language (algebra). The same law could have been expressed in a different language (algorithmic language, computer code, etc.). Of course, the results should be the same, similarly to the content of a statement expressed in different languages.

(iv) Often distinguished are *code* information and *semantic* information. To construct a meaningful sentence, for example, one needs an alphabet, vocabulary, syntax and so forth (that is, a code), although the code by itself does not carry any meaning. In other words, the code information is needed for receiving, generating and sending semantic information — that is, the code provides the basis for the sense. The term *thesaurus* denotes the basic information without which is it not possible to perceive the semantic information.

In biology, the semantic information refers, for example, to the protein's capability of selectively catalyzing some reaction or other. This capability depends on the primary sequence, which in particular determines the ability to interact with the cofactor, inhibitor, etc.

It is obvious, however, that without the code and the system of protein biosynthesis the construction of the contemporary system of functional (meaningful) proteins would have been impossible even given the availability of the relevant information in DNA.

(v) *New* information is the selection of one option out of many, that has not been made before. This information may be either unconditional or conditional. In both the cases, the term 'new' is perceived intuitively. We hear that the new is the well forgotten old, and this statement makes sense. More precisely, the new as a rule emerges at the interface of sciences that use different languages (codes).

For example, the word 'mother' in the English language has a definite meaning, and is not new. By contrast, the word 'Mutter' (which is the German for 'mother') is new for most speakers of English.

Similar examples can be found in the exact sciences. For instance, the method of stationary concentrations has been long known (and used) in chemistry. In mathematics,

however, the idea of this method was regarded as new, because it was expressed in the language of chemists rather than the language of mathematicians. So this method was legalized in mathematics only after the relevant theorems had been proved by A N Tikhonov and L S Pontryagin, and came to be known as Tikhonov's theorem.

5.2 Value of information

The *value* of information depends on the *purpose* with which this information is used. We emphasize the word purpose here because it calls for special attention.

Several measures of the value of information have been suggested. The first belongs to M M Bongart and A A Kharkevich [46, 47]. It is convenient when the *a priori* probability of attaining the goal P^{in} (that is, the probability of achieving the goal without receiving — and/or generating — the information) is very small ($P^{\text{in}} \ll 1$). Then the value of information of the ith type is

$$V_i = \log_2 \frac{P_i^{\text{fin}}}{P^{\text{in}}}\,, \tag{13}$$

where P^{fin} is the probability of achieving the goal after receiving (and/or generating) the information of the ith type. The logarithmic measure is convenient here as well, because $P^{\text{in}} \ll 1$, while P^{fin} may be close to unity.

The value of information may be positive when $P^{\text{fin}} > P^{\text{in}}$, or negative when $P^{\text{fin}} < P^{\text{in}}$. In the latter case it is referred to as *misinformation*.

Finally, every man receives information that is totally unrelated to his purpose, and therefore has zero value. The amount of such information is not small.

There is information that at first sight is never going to become valuable for anyone. For example, the composer has jumbled all the characters in a text, so that the text has lost any sense. The amount of information remains the same, but its value is zero for anyone.

So we come to deal with the concept of *meaning*. As opposed to *value*, this concept has claims to objectivity, based on the following consideration: one can select a certain amount of information that will be never used by anyone for any purpose. Then this information is called *meaningless*. The objectivity of this criterion is based on the words 'never', 'anyone', 'for any purpose'.

This statement is strong, absolute — and therefore wrong. In our example one could say that the gibberish created by the composer contains valuable information for the psychiatrist, whose purpose is to diagnose the composer's state of mind. So the assertion 'by anyone' ought to be interpreted as 'by anyone concerned with the meaning of the text and nothing else'. Even then, however, the meaning of text depends on the thesaurus. For most readers the word 'abracadabra' means nothing, but knowledgeable people know it can be used to work miracles.

Another way of measuring the value of information was proposed by R L Stratonovich [48]. According to him, the value of information is measured by the cost of 'penalties' (or expenses) paid for achieving the goal by the selected path. This method is convenient if the goal can be achieved with certainty even without reception or generation of information, but the cost of achieving it (in terms of time, labor and money) depends on the selected path towards the goal.

Of special interest in biology are those cases whose *a priori* realization is associated with a very small probability. Such is the situation with the origin of life, with the problem of biological evolution, etc. So in future we shall measure the value of information according to Eqn (13).

Purpose is an accustomed concept as applied to human society. The authors of Refs [46, 47] assumed that the purpose was defined from the outside, and its source was not discussed. Such a situation is encountered rather often. For example, an engineer is working on a new machine and has to choose among the possible designs. The purpose is to make the machine perform the desired function, and the value of the selection depends on this purpose. If there are several equally acceptable options, then the selection of one of them results in neutral (nonvaluable) information. The same applies to the information contained in the segment of DNA that encodes a protein sequence. Here the objective in recruiting a protein is to provide its functioning. If the replacement of some of the amino acid residues with different ones does not prevent the performance of the function, then the selection of one particular option generates nonvaluable information. It is in this sense that the words 'valuable information' were used above in Sections 2 and 4.

As a matter of fact, a man can set a goal for himself. As a rule, the main goal is achieved through a sequence of intermediate goals. In other words, there is a system of hierarchic levels, of which each is associated with a particular goal.

Let us illustrate this with the following example. A child learning to speak receives information about the language from the environment. Having mastered the language, the young man faces the choice of his future profession. The choice made and the studies completed, the man will more than once in his life choose where to apply his efforts. The new choices, however, will depend on those made earlier. One can say that every time the man sets a new goal before himself. All these goals, however, serve his main purpose: to survive and to give life to offspring. Human behavioral reactions (conditioned reflexes and unconditioned responses) and desires associated with them also serve the same purpose. We are not going to discuss those exceptions when a man sets for himself unseemly and unnatural goals, although such exceptions unfortunately are not rare.

Now the question is whether other living organisms (even the prokariotes) have a purpose in life. The answer is known: the main purpose — survival — is common to all living beings. In humans it is, as a rule, conscious, in prokariotes unconscious, but it is still there.

It is therefore clear that the value of information is a concept rich in content, which is necessary for describing animate nature. It is related to the important feature of the animate nature: the ability of living organisms to set goals.

Now does nonliving nature have a goal? There are several views on this matter.

According to one standpoint, inanimate nature has no purpose or design; it developed according to the laws of nature, and this is sufficient for describing the processes.

Another view is that nonliving nature and even each part of it (subsystem) has a goal, and this goal is to reach a particular attractor — a steady final end.

The first view is rather common among natural scientists. They believe that information in the processes of evolution of inanimate nature was generated and accumulated, but its value was zero because there was no purpose. In other words, there is no valuable information in nonliving nature. This is the reason why the concept of information was not much used

(and still rarely is) in the description of processes taking place in nonliving nature. This concept is simply not necessary, and not constructive.

At first sight, the second view also has the right to exist. Moreover, in the early days of modern science the laws of nature were formulated teleonomially, as a working of some ultimate purpose or design. For example, the principle of least action formulated in mechanics is equivalent to the laws of dynamics of Hamiltonian systems. The second law of thermodynamics was formulated as the tendency of the entropy of closed systems to reach a maximum. More generally, the motion of a dynamic system towards the attractor was interpreted as its purpose.

Such approaches were (and still are) constructive when the set of dynamic equations admits a unique solution (under given conditions) — that is, when there is one particular predestinated attractor.

If the motion is not stable, and there are several final states (attractors), then the statement that 'the purpose consists in reaching the appropriate attractor' does not make sense, because it is not known in advance which attractor is 'appropriate'.

For example, one might say that the purpose of the Tungus meteorite was to hit the Tungus taiga (indeed, what other purpose could be pursued by a meteorite called Tungus!). Or, when the roulette ball hits the red slot, one could say that such was the ball's purpose. But obviously all this is nothing more than an amusing play around words.

Thus, it is possible to formulate a dynamic problem in terms of achievement of a particular purpose by the entire system, but only if there is one attractor that will be reached sooner or later. It is exactly in such a case, however, that information is not generated. In other words, the situation in inanimate nature is the following: if there is a purpose, there is no information; if information is generated, then there is no purpose.

Now one could ask whether there was a purpose (and what kind of purpose) associated with the objects that stood halfway between living and nonliving (i.e. with the hypercycles discussed in Section 2), and how they developed the ability to set a purpose. The answer follows from the arguments developed above: systems that satisfy some special criteria may arise in nonliving nature. In such systems, the concepts of 'information', 'purpose', and 'valuable information' become constructive and meaningful. An example of such a system is an ensemble of hypercycles. When such a system arises, however, it immediately passes into a living organism.

What the relevant criteria are in the general case, we shall discuss in the next section.

5.3 Informatics, its subject and fundamental problems

Informatics is the science concerned with the processes of transmission, generation (loss), reception, storage and processing of information. Three branches may be distinguished in informatics.

The technical aspect: transmission, encoding, and reception of information.

The applied aspect: the design of computers, development of software, etc. — what is known as 'computer science'.

The fundamental aspect: generation of valuable information, evolution of valuable information, extraction of valuable information (processing of information), and realization of valuable information.

We are going to discuss the fundamental problems of informatics. Let us recall the main points.

A choice made by somebody else and imposed on the system from the outside is known as *reception* of information.

A choice made by chance (or involving an element of chance) is called *generation* of information. In life we often face the necessity to make decisions in the conditions characterized by insufficient definiteness. The same applies to gambling games (like roulette). The problem of random choice is also important for such fundamental issues as the origin of life (emergence of genetic information), biological evolution, etc. In point of fact every creative act is an example of unpredictable choice.

Generation of information is not possible in any physical system by far. For this, the system must possess certain properties. Let us describe these properties using the language of the theory of dynamic systems.

(1) The system must be *multistable* (at least bistable). This means that the system must have $n \geqslant 2$ stable states, any one of which can be chosen.

(2) The elected state may be considered as *remembered* if it is preserved for a sufficiently long time. This requires that the state should be absolutely stable (the real parts of all Lyapunov numbers are negative). Such systems are dissipative.

(3) The system must contain an *intermixing layer*.

The intermixing layer in a dynamic system is defined as the region of phase space that exhibits the following properties [19, 49]:

(1) all paths leaving the specified range of the initial conditions fall into the intermixing layer;

(2) the behavior of paths within the intermixing layer is chaotic. This means that the Kolmogorov entropy is large enough, and the system is globally unstable;

(3) all paths that have entered the intermixing layer will leave it and get into the dynamic multistationary layer, which has at least two stable steady states.

Property (3) distinguishes the intermixing layer from a strange attractor.

There are two concepts that can be defined for systems with an intermixing layer: the horizons of forecast in time and space. The time horizon of forecast is widely used in the treatment of stochastic processes; it is the time interval Δt within which one can predict with probability close to unity the state of the system at the time $t + \Delta t$ if the state at the time t is known. By order of magnitude, Δt is equal to $1/\lambda$, where λ is the largest Lyapunov number.

The spatial horizon of forecast δx is only relevant for the intermixing layer. It is defined as the interval δx in the initial conditions from which the system with a high probability arrives at the same final state.

If the intermixing layer is wide enough, and the Kolmogorov entropy in this layer is sufficiently large, then the spatial horizon of forecast is very narrow. Hence it follows that knowing the initial conditions with accuracy Δx (such that $\Delta x \gg \delta x$), it is practically impossible to predict the final state that will be achieved by the system.

An example of a system with an intermixing layer is pinball — a game played on a table in which the player operates a plunger to shoot a ball along a slanted surface having pins and pockets at two corners ('red' and 'black', see Fig. 7). Motion of the ball is described by Newton's equations with due regard for friction. At first (before the first collision with a pin — region a) the behavior of the ball is dynamic

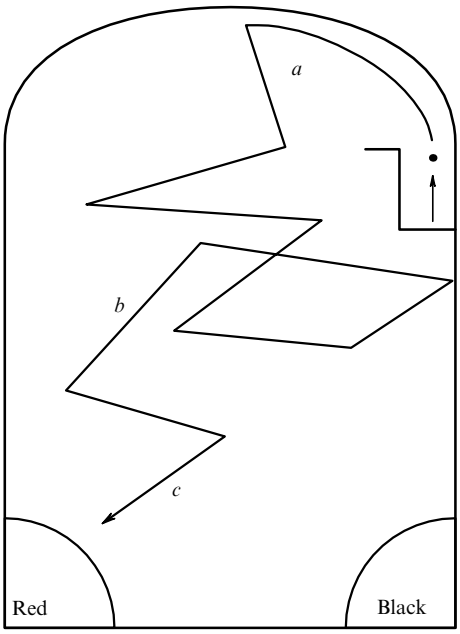

Figure 7. Pinball game (the simplest roulette): *a* — input dynamic layer; *b* — intermixing layer; *c* — output dynamic layer.

(input dynamic layer). When the ball bounces off the pins, which play the role of the convex reflecting wall in Sinai's billiards (region *b*), its motion is chaotic — this is just the intermixing layer. When the motion of the ball slows down, it enters the sphere of attraction of one of the pockets (region *c*) and rolls into the hole. In this region the behavior of the ball is again dynamic and predictable (output dynamic layer). The roulette used in gambling games offers similar properties.

Let us use the example of roulette to analyze the process of generation of information, and to demonstrate that the value of generated information varies with time.

Assume that the player initially makes a bet (that is, a choice) on *red* (which means that he generates information) and fixes his gaze on the ball. Assume that the player knows the equations of motion, so he can determine the coordinates and velocity of the ball with finite accuracy at any intermediate instant t. Then he is able to estimate at any instant the probability of reaching the goal $P_{\rm red}^{\rm fin}(t)$, compare it with the *a priori* probability $P^{\rm in} = 1/2$, and calculate the value of his information. At the initial moment $t = 0$ it is impossible to predict the result, so $P_{\rm red}^{\rm fin}(t=0) = P_{\rm bl}^{\rm fin}(t=0) = 1/2$. The value of any information at this instant is zero:

$$V_{\rm red}(t=0) = V_{\rm bl}(t=0) = \log_2 \frac{P^{\rm fin}}{P^{\rm in}} = 0\,,$$

that is, at the initial moment generated is only the non-valuable information.

At the final moment $t > t_d$, when the ball has already fallen into the sphere of attraction of the pocket (the red hole, for example), we have

$$P_{\rm red}^{\rm fin}(t) = 1\,, \qquad P_{\rm bl}^{\rm fin}(t) = 0\,.$$

Then

$$V_{\rm red}(t > t_d) = \log_2 2 = 1 = V_{\max}\,,$$

$$V_{\rm bl}(t > t_d) = \log 0 = -\infty\,.$$

At some intermediate instant $t < t_d$, when the ball is close to leaving the intermixing layer, the result can be predicted with a probability that is not equal to zero, one, or one-half. For example, one finds

$$\frac{1}{2} < P_{\rm red}^{\rm fin}(t) < 1\,, \qquad 0 < P_{\rm bl}^{\rm fin} < \frac{1}{2}\,.$$

Then the values are

$$V_{\rm red}(t \leqslant t_d) = \log_2 2 \cdot P_{\rm red}^{\rm fin}(t \leqslant t_d) > 0\,,$$

$$V_{\rm bl}(t \leqslant t_d) = \log_2 2 \cdot P_{\rm bl}^{\rm fin}(t \leqslant t_d) < 0\,.$$

This implies that the value of information depends on the time. At first it is zero, and then increases or decreases until the ball leaves the intermixing layer.

Bets may be placed (and information is generated) not only at the start, but also when the ball is already running, up to the moment $t_{\rm cr}$ when the croupier announces that the bets are made. An experienced croupier will select the time $t_{\rm cr}$ close to the end of the intermixing layer — that is, $t_{\rm cr} \leqslant t_d$. However, if the croupier is slow or drunk, he may stop betting at the time when the ball has left the intermixing layer and is landing on the hole (that is, at $t_{\rm cr} > t_d$). Then the player can make a bet and win for sure. This, however, is not generation of valuable information, but the reception of information from the gambling system.

If the player is able to measure the coordinates and velocity of the ball fast enough, and quickly calculates its path, then he can make a bet at $t \leqslant t_{\rm cr}$ and increase the probability of winning. In this case we can say that valuable information is partly received and partly generated.

Of course, it is impossible to make such coordinate measurements and calculations with the required speed and accuracy. Nevertheless, experience and intuition (or 'inner voice') are often helpful. It is this circumstance that makes gambling so addictive.

One could even go so far as to say that playing roulette is not simply gambling, but also exercising in the generation of valuable information. This exercise involves two important elements: choice of the optimal time for generation, and gathering and processing (at least on the intuitive level) of information required. The latter decreases the amount of generated information, but increases its value.

We have used the examples of mixing and an intermixing layer from mechanics because they are clear and well studied there.

In living nature the 'game of roulette' is quite common. It can even be said that the presence of the intermixing layer is a prerequisite for any living system capable of generating valuable information.

In our example the purpose was set from the outside (by the gambler), it did not arise by itself in the system (the roulette wheel). The latter is possible in dynamic systems that meet the following requirements.

(i) The system must consist of elements, each of which has the properties (1)–(3) listed above. This means that each element occurs in one specific state (out of several possible) which was chosen at random and remembered. In other words, each element contains its own ('proper') information.

(ii) The elements must possess the property of self-reproduction (autocatalysis). This property is required to ensure remembering the choice made for a time that is considerably longer than the lifetime of each element.

(iii) Interaction between elements with different information must be antagonistic.

For such systems we can introduce the concept of 'purpose' and define it as follows [19]:

the purpose of each element is to preserve its own information.

This statement is a generalization of the principle of the struggle for existence, but it can be extended to intermediate systems that satisfy the criteria (i) – (iii) above. The system of primal hypercycles discussed earlier possesses these properties.

In inanimate nature we find examples of systems that satisfy some of the above criteria, but not all at once. Each criterion can be expressed in the physico-chemical language, as has been done above for the example of hypercycle occurrence.

Having formulated the purpose, one can follow the evolution of the value of the emerging information. Let us do this for the example of choice of the unified code.

The random synthesis of the DNA–replicase complex and the pertinent adapters is the realization of one of the variants of the code — that is, generation of information. Each such complex is a carrier of its own information. In the course of interaction, each population tends to preserve its information, which constitutes its purpose (but not the purpose of the entire system).

On the one hand, this is nothing more than the brief description of physico-chemical processes bringing about the antagonistic interaction. On the other hand, it is a generalization of the principle of the struggle for existence. Indeed, the principle that 'the purpose consists in the preservation of one's own information' can be applied not only to the living organisms, but also to inanimate objects that possess some special properties and can become the living ones (to hypercycles, for example).

Such a definition of purpose can also be extended to human social behavior. Then by one's own information we should mean not only the inherited information, but also the information acquired and generated by a person during his life. Then the purpose will include not only his will to survive and produce offspring, but also the desire to learn and create.

Let us use the example of hypercycle interaction to illustrate the evolution of value of information. At first, when all populations are represented equally, the value of any information is zero, because the *a posteriori* probability of survival P^{fin} (after the formation of the population — that is, after the choice of a code) is equal to the *a priori* probability P^{in}.

As one particular population forces out the rest, the probability increases that the information specific to this population will be preserved. Its information becomes more valuable. At the end of the process, when only one pure state remains, the information specific to this population becomes the most valuable.

At this time one may claim that the purpose of the entire system coincides with the purpose of its elements. The meaning of this statement, however, is about the same as saying that the purpose of the Tungus meteorite was to hit the Tungus taiga.

6. The problem of the origin of thinking

This problem is different from those discussed so far. Earlier we were dealing with concrete processes and phenomena. The difficulty was that seemingly justified estimates led to absurd results. The way out was found by considering alternative approaches that lead to reasonable estimates.

The crux of the problem of thought is different. In the first place we have to formulate what exactly we want to describe in the language of physics, what is the phenomenon that appears mysterious and inexplicable. It is this problem that is treated in the above-mentioned monographs [8 – 11] and reviews [12, 13]. The problem has not yet been solved, and we shall discuss the possible ways of solving it. After that it will be worthwhile discussing the origin of thought apparatus.

We do not aspire to give a definition of 'thought'; however, we shall enumerate its basic features, and demonstrate that each of them (and even all together) can be reduced to a chain of physico-chemical processes. Moreover, we shall show that mathematical models of such processes have already been developed and work well. With this purpose we shall make an excursion to the theory of pattern recognition and theory of neural networks (neurocomputing).

6.1 Main features of the process of thinking

(i) The process of thinking takes place in the neural networks of higher animals, and man above all. The disciplines concerned with real neural networks — neurophysiology and neurochemistry — are highly advanced: we know how the nervous impulses form and propagate, how they are conducted from one neuron to another, etc. All this is described in textbooks and specialized monographs [50] but these sciences do not answer the question of how man thinks (especially intuitively).

(ii) Thinking is associated with the processing of information (stored and received from the outside). The result of processing is a forecast of the behavior of surrounding objects (whether animate or inanimate).

(iii) The final result of thinking is decision-making — that is, choice of one out of several possible variants of further action (in other words, information). The value of this information depends on the purpose. The latter can either be set externally, or formulated by the man himself. By this means thinking is the property of systems capable of self-setting the goal.

(iv) Each stage of thinking is associated with reception of information and generation of new information. The latter is related to creativity; therefore, creativity is a part of thinking.

(v) It is customary to distinguish between logical thinking and intuitive thinking. Logical thinking uses an unambiguous algorithm, which is possible when the available information is sufficient for making an unequivocal (the only right) decision. Creativity in this case reduces to choosing the optimal way towards achieving the result, which is actually fixed. The result is already contained in the algorithm (i.e. in axiomatics) and initial conditions.

Intuitive thinking relies on associations, analogies and precedents. It is used when the available information is not sufficient for making a decision, or when the algorithm itself is branched and therefore ambiguous. This is related to the instability of the decision-making process.

Intuitive forecasts come true with a high probability, but not with certainty. Their reliability (or convincingness) depends on many details (signs) that often escape notice. The construction of a convincing intuitive inference is an art in itself.

Intuitive reasoning prevails in everyday life, in humanities, and in art. It is significant that in natural and exact sciences the role of intuitive reasoning is by no means small [51].

The common belief is that only man is capable of logical thinking, and not the animals. Both men and animals are capable of intuitive thinking so long as the latter must also arrive at decisions. Because of this, logical reasoning is often held above intuitive reasoning, and considered more abstract and advanced.

(vi) Thinking, especially intuitive thinking, is individual. We know that different people use different approaches to recognition and forecasting tasks. At the same time, the results can (and should) be the same (which is not always the case). But the paths towards the result are different, which reflects the individuality of reasoning.

The description of these phenomena in the language of physics is based on the theory of pattern recognition and neurocomputing.

6.2 Excursion to the theory of recognition

The foundations of recognition theory were laid in the works of M M Bongart [46], A Kronrod, P Kunin and I M Gel'fand (see Refs [52, 53]). They discussed a problem formulated not quite scientifically: how does a mouse recognize a cat? Later on the recognition theory found many applications — in particular, in military science, character recognition [54], and especially in medical diagnostics [53, 55].

The goal of the theory of pattern recognition is similar to that of all other theories — to predict the behavior of the object of study. Otherwise, however, it is a very specific theory. In place of axioms and deduction it uses precedents. The theory is based on the following statement:

If the object under study looks like a known one, its behavior is likely to be similar to that of the prototype.

So the theory is concerned with the meaning of 'likeness' and how it can be measured.

This theory does not also require proofs of statements. Proofs are replaced with criteria of similarity, which never allow making unambiguous inferences. In spite of this, recognition theory is regarded today as a branch of mathematics. It has its specific concepts and terms; let us discuss what they mean.

Learning set — a collection of already known precedents.

Examined set — a collection of objects (or phenomena) that are compared with the known precedents.

Attributes — qualitative and quantitative characteristics of the objects from the learning set that may assume continuous or discrete values. In the latter case, the dichotomic system is often used, where the attribute may take on either of two values: yes or no (or 0, 1; or -1, $+1$).

Examples of attributes from medical diagnostics are temperature, biochemical analyses, etc. (continuous attributes), as well as blood group, eye color, etc. (discrete attributes).

Space of attributes is a graph where the magnitude of each attribute is measured on a separate axis. The axes as a rule (but not always) are orthogonal. Each element of the set is represented by a point in the space of attributes.

Clusterization and classification. As a rule, the points in the space of attributes are distributed not homogeneously, but tend to form groups (clusters) separated by regions where the concentration of points is low.

Distinct groups are called *classes*; the above representation is known as a *graphic* (visual) *method of classification*. Other methods (analytical) are essentially similar to the graphic method.

Conjunctions. Often the classes and the separating regions lie not on the axes, but in the depth. Then one can transform the space — that is, introduce the new variables which are combinations (linear or nonlinear) of the old attributes. Such combinations are called conjunctions. In medical diagnostics the distinguishing features are called symptoms, and the conjunctions are known as syndromes.

Decision rule — an algorithm that allows assignment of the object under examination to one of the classes. If the rule is formulated, and the number of conjunctions is not big, the task of recognition is simplified and can be accomplished quickly.

Learning — the procedure that leads to formulation of the decision rule.

If the space of attributes is constructed in advance, and the learning set is built up of elements belonging to different classes, the process of learning becomes simpler. However, the problem of constructing the conjunctions and formulating the decision rule still remains. Such is the situation with the hands-on seminars on medical diagnostics or systematics (of plants and/or animals). This method is known as learning with a teacher (supervisor).

If nothing is known in advance, one has to follow the entire procedure; this is *learning without a teacher*. Such is the situation with the study of new flora and/or fauna, and with the diagnostics of new diseases.

Validation is necessary when the result of recognition is crucial. In such a case the recognition routine (with a given decision rule) is performed a number of times. Then the results are compared, and submitted as final if they are the same. Otherwise it is necessary to do additional learning and reformulate (refine) the decision rule.

Attention — a relatively new (in theory) term, which acquires mathematical meaning in addition to its everyday sense. As indicated, the choice of attributes, evaluation of their importance, choice of conjunctions and their weights are often based on guesswork, to be later checked by trial and error. This process often involves the use (conscious or unconscious) of information known previously or received from the outside. Attention is the choice of the above variables based on the information received (and/or known) (which in fact amounts to the reception of information).

This definition does not contradict the habitual sense of the word. For example, advice to 'pay attention to such-and-such an attribute' implies that its weight in the conjunction must be increased.

By virtue of 'attention', the process of recognition can be accelerated considerably. There is, however, the other side of the coin: if the attention is directed in the wrong way, this may lead to the wrong result or to a failure of the recognition system.

This can be illustrated with the diagram in Fig. 8 (borrowed from Ref. [55]). This example will help us to discuss the importance of intuition and logic in pattern recognition. The right-hand side of the diagram is based on human intuition, and will not work without human participation. There are many attributes to start with, and the number of their combinations (conjunctions) is factorially large. With the logical approach, it is necessary to enumerate all the

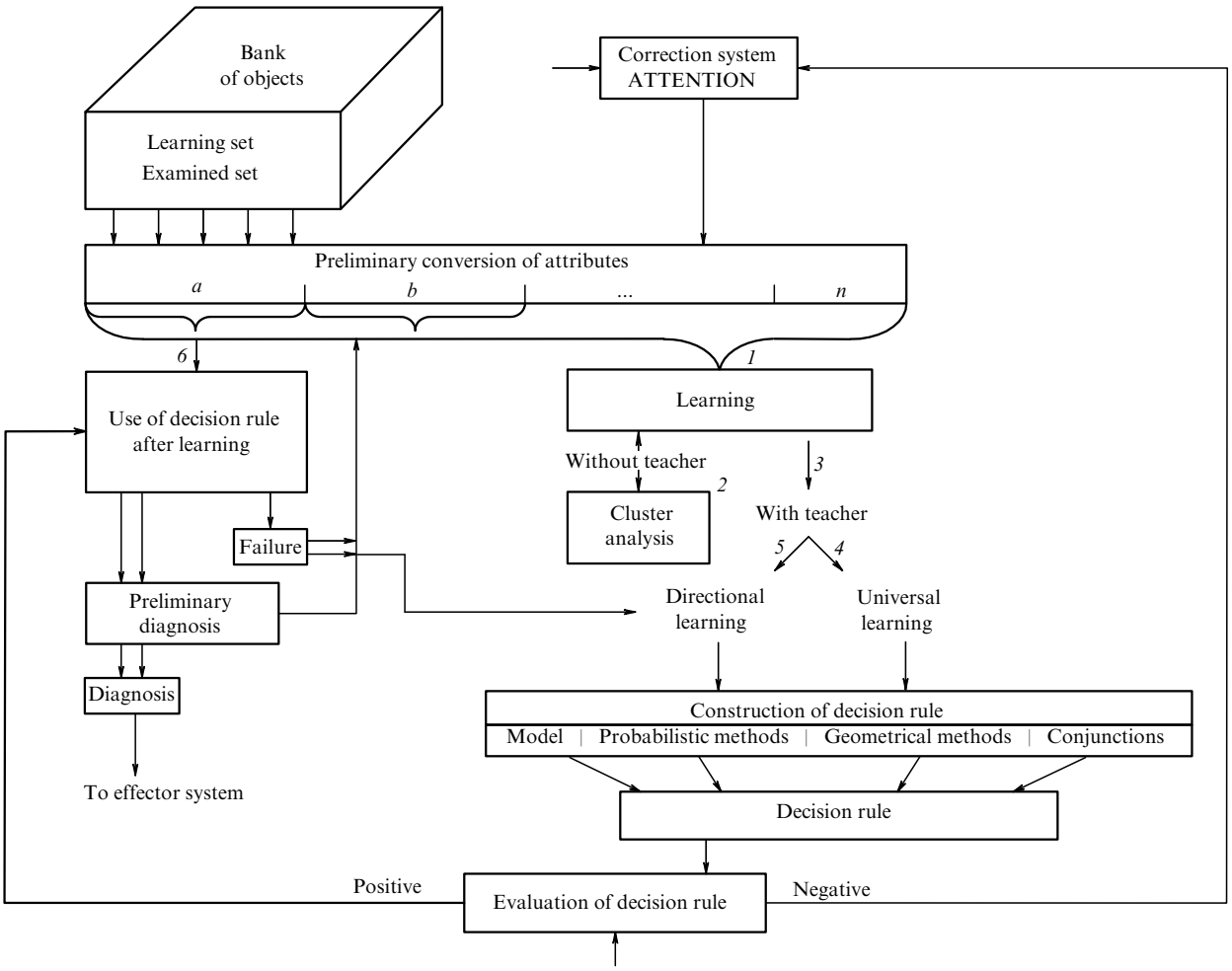

Figure 8. Block diagram of pattern recognition (medical diagnostics).

conjunctions, which is beyond the capacity of man or computer. In reality, the choice of significant attributes and their conjunctions is performed by the diagnostician, who will use his experience and intuition — that is, through direct assessment of the truth. Formulation of the decision rule also requires the diagnostician's intuition and programmer's thesaurus — that is, the knowledge of the language used to formulate the final algorithm.

The left-hand side of the diagram — recognition based on an unambiguous algorithm — may be regarded as a logical operation.

Logical recognition has its own advantages and shortcomings.

Firstly, there is no need to enumerate all possibilities, which greatly accelerates the process.

Secondly, the decision rule allows making interpolation within the learning set. Then the discrete set of attributes, objects and diagnoses becomes a continuous set.

Thirdly, there is a possibility to extrapolate the decision rule beyond the learning set. Extrapolation always involves a hypothetical element. Sometimes it is justified, and then logical recognition has a great advantage. Sometimes it is not justified, and then logical recognition leads to an error. In case of intuitive recognition of elements outside of the given set, man will turn to other learning sets and check whether the same decision rule works there as well. This approach is longer but more reliable.

Fourthly, logical recognition permits duplication — the decision rule can be transferred to other users, skipping the stage of learning. An example is given by textbooks on medical diagnostics.

Fifthly, after formulation of the decision rule, the amount of information decreases (because the details are dropped), while the valuable information is preserved. A smaller memory capacity is required to store this information. One may say that the decision rule appears as an abstraction compared with intuitive recognition. This is important when one has to deal with several learning sets at once. It is practically impossible to remember the procedures of recognition for all of them at once, but it is not that difficult to remember the decision rules. What is more, in this case the set of decision rules may be regarded as a kind of superset, which allows formulating the decision rule which will play the role of unified theory embracing all learning sets.

Observe that in the case of logical recognition new valuable information is not generated. What takes place is the processing of the received information and extraction of valuable information from it. Generation of valuable information proceeds on the right-hand (intuitive) side of the diagram in Fig. 8.

Recognition — that is, attribution of the examined object to a particular class — makes sense when the class number is discrete and finite, and when each class differs from the rest.

For example, the classes in medical diagnostics are different conditions of the organism.

In the language of dynamic systems, the objects of the same set must be described by a single multistationary model. Then the space of attributes corresponds to the phase space, and the classes to the different stationary states. The dynamic model itself plays here the role of the decision rule.

Let us illustrate this with an example from physics — the formulation of Coulomb's law. In this case the learning set comprises the discrete assembly of pairs of charges q_{i1}, q_{i2} at a distance $\mathbf{R}_i$ from each other. Initially, the space of attributes included the magnitudes of charges, the distance $\mathbf{R}$, the size of the charge-carrying objects r, etc. The 'diagnosis' consisted in finding the force $\mathbf{F}_i$ acting between the charges.

Two classes were elected in the learning set: $|\mathbf{R}_i| \gg r$ and $|\mathbf{R}_i| < r$. On the intuitive level, chosen in the first class were the significant attributes q_{i1}, q_{i2} and $\mathbf{R}_i$, the main conjunction $q_{i1}q_{i2}/|\mathbf{R}_i^2|$, which allowed formulating the decision rule — that is, Coulomb's law

$$\mathbf{F}_i = \frac{q_{i1}q_{i2}}{|\mathbf{R}_i^2|}\,\frac{\mathbf{R}}{|\mathbf{R}|}\,.$$

The formulation required using the thesaurus of vector algebra. Then this rule was interpolated, and the discrete set of observations transformed into the continuous set of solutions. Extrapolation of this rule to large (astronomical) distances proved true. The hypothesis of additivity of forces in systems of many charges permitted a purely logical derivation of the decision rule for the interaction of electrical multipoles — this rule also held good.

Extrapolation to small (atomic) distances did not work. So it was necessary to use a different learning set, work through the complete routine of intuitive recognition, and formulate a new decision rule — the Schrödinger equation.

We have gone into so much detail in order to demonstrate how the intuitive and logical approaches mix and complement each other in the theory of recognition.

The process of recognition can be automated with modern general-purpose computers.

Specialized computers — so-called neurocomputers — are a recent development, and they deserve separate treatment.

6.3 Neurocomputing

Neurocomputing, or the theory of neural networks, is a new rapidly developing branch of mathematics and computer science. It started as an attempt at mathematical simulation of real neural networks. The neuron was represented by the simplest bistable element, and the main focus was on the links between the elements. This model immediately found many useful applications, and went on to develop on its own. Neurophysiology was soon forgotten, although the terminology (neuroprocessor, neuron) remained; today they are only historically justified. On the other hand, many neurophysiologists were upset by such simplification of the neuron, because a real neuron is much more complicated than a bistable element. As a result, neurocomputing and neurophysiology today are different disciplines, and the advances in one are often overlooked in the other. At the same time, certain results obtained in the theory of neural networks are fundamental for both neurophysiology and informatics in general. In this section we shall briefly describe the main principles of neurocomputing. For the state of the art in this field one may refer to Refs [56–61].

The simplest neuroprocessor is a plate that carries active elements (conventionally referred to as neurons). In the simplest case they are bistable automata which may occur in either of two states. For example, it may be lamps that are either on (state one) or off (state two). Active elements are connected with links (wires). If linked elements are in the same state there is no current in the link. If linked elements are in opposite states, each tends to switch the other into the same state as its own. Then the link carries a current.

In the limiting case, each element is connected with all the rest. In reality the number of links may be smaller, but it still must be large enough. Thus the final state of each element depends on the algebraic sum of signals coming from the other elements: if the majority of them are excited, then the element becomes excited; if most other elements are not excited, then the element goes to the unexcited state.

The scheme of such a processor is shown in Fig. 9.

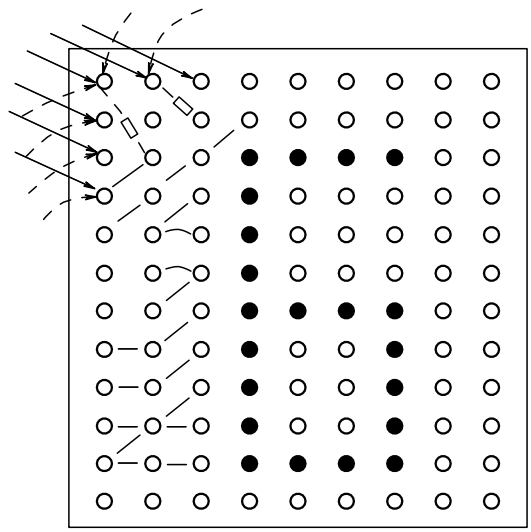

Figure 9. Scheme of Hopfield's recognition neuroprocessor.

Each link has the following important property: the passing current irreversibly changes the strength of the link. This is achieved by using special devices (represented by rectangles on the diagram) which increase the resistance of the wire (that is, reduce the strength of the link) when a current is passed through the link.

Presentation of the pattern — or, which is the same, input of the primary set of attributes — is performed in the following manner. At the initial instant, the external links (shown by solid arrows in the diagram) are used to send signals that switch certain elements into the active state (for example, certain lamps are turned on). The pattern is applied for some time, during which the links are 'taught' (the conductivity of links that carry a current decreases).

If the initial set of attributes is represented in a numerical form, we have to agree which arrangement of lamps corresponds to a particular pattern — that is, create the encoding table. If the input data are in a graphic form (a picture, diagram, portrait), its representation with illuminating lamps can be straightforward.

The processor thus constructed has the following properties.

First, it is capable of learning. Teaching consists in presenting the processor with a standard pattern (in the

form of lighted lamps) — for example, the character Б shown in Fig. 9 — and keeping it for a sufficiently long time. Then the links between the 'on' and 'off' lamps weaken, and remain so after the external signal is removed.

The procedure can be repeated with standard patterns from different classes (for example, the characters 'A', 'B', etc.).

After teaching, the processor will be able to recognize the presented (examined) objects, relating them to one of the classes (from those that it has been taught). For example, teaching can be based on portraits of different people. After teaching, the processor is presented with a portrait that is incomplete and noisy, namely, has some missing details (lamps off), and some extra features (lamps on). After some effort, the processor will produce a complete and clean portrait — that is, will recognize the pattern.

The workings are simple, and can be described in plain English.

Assume that after teaching the processor is confronted with a noisy image of the character, in which some relevant neurons are off, and some spurious neurons are on. The processor will work in such a way as to excite the neurons that belong to the image of character, because their links with the excited neurons are strong enough, and the links with the unexcited neurons are weakened. The spurious excited neurons will be switched off, because their links with the excited neurons are weak, and the links with the unexcited neurons are sufficiently strong.

The problem of attention in neurocomputers is solved in the following way. A wire from the outside comes to each element (shown in Fig. 9 by dashed arrows). The signal is applied not to the input of the element, but to some other point that controls the excitation threshold. In this way it is possible to make the system more sensitive to one part of the image (or images), and less sensitive to other parts.

This very simple construction is known as the *Hopfield processor* [56]. It has a number of shortcomings: for example, it is difficult to implement 'validation' and to organize directional flows of information (because the links are symmetric — the current may flow through the wire in either direction). More advanced processors use directional links (that only transmit the current in one direction), and several plates.

The process of learning with directional links is a little harder than in the Hopfield processor, but the principle remains the same: the passage of current modifies the link.

Validation and repetition can be implemented in a processor that contains at least two plates. Such a processor is known as a *back propagation* device. The pattern is recognized by the first plate and sent to the second, where the process of recognition is repeated using additional information, and the result is returned to the first plate. This cycle is repeated several times, until the recognized patterns coincide.

The links between the plates must be sufficiently strong, and directed both ways.

The *Grossberg neurocomputer* [57] contains at least two plates. The first contains the taught links, and performs the recognition itself. Information is transmitted to the second plate through the interplate links (not necessarily taught). In the second plate, the elements and links between them are organized in the following way. Each element has a link connected to itself, which performs self-activation of the element. In addition, there are teachable suppressive links directed towards other elements. With such an arrangement, the recognized pattern is represented in the second plate by one element in the active state (that is, one switched-on lamp).

In other words, the pattern is autolocalized in the plate. This gives the following advantages. Firstly, the number of recognized patterns is increased. Secondly, the likelihood of false recognition decreases. Thirdly, it is easier to focus attention on a particular pattern by virtue of its localization in space.

These processes can be described by mathematical models.

The model of the already taught Hopfield processor is given by

$$\frac{\mathrm{d}u_i}{\mathrm{d}t} = f(u_i) + \sum_{j \neq i} w_{ij}\, u_j\,, \tag{14}$$

where $f(u)$ describes the properties of the neuron. In the simplest case, the neuron is a bistable symmetrical element; then

$$f(u_i) = u_i - u_i^3\,. \tag{15}$$

In the steady states, $u = \pm 1$ (where $u = +1$ corresponds to the active state — lamp on, and $u = -1$ to the passive state). External signals required for switching from one state to the other (that is, switching thresholds) are the same.

When the thresholds are not the same, we have

$$f_i(u_i) = u_i + b_i\, u_i^2 - u_i^3\,, \tag{16}$$

where the parameter b_i controls the switching threshold of the ith element. By adjusting b_i, it is possible to 'draw attention' to one pattern or another. This is accomplished by lowering the switching thresholds for those neurons that are active in the preferred pattern.

The quantities w_{ij} represent the strengths of links between neurons. In the Hopfield processor they are symmetric, whence $w_{ij} = w_{ji}$. In the simplest case all w_{ij} are positive but differ in magnitude. Then each neuron will tend to switch other connected neuron into its own state.

In general, model (14) is close in structure to the model of choice (6) discussed earlier. The difference is that the coefficients w_{ij} are not the same; they are formed in the course of learning.

The model of the learning process is

$$\frac{\mathrm{d}w_{ij}}{\mathrm{d}t} = w^0 \left(1 - \frac{1}{2}\int_0^{\tau} (1 - u_i\, u_j)\, \varphi(t)\, \mathrm{d}t\right), \tag{17}$$

where $\varphi(t)$ is a positive monotonically decreasing function such that

$$\int_0^{\infty} \varphi(t)\, \mathrm{d}t \leqslant 1\,, \tag{18}$$

where τ is the time of learning, and w_{ij}^0 are the initial values of the coupling coefficients, assumed to be equal to one another.

If at the time of learning neurons i and j are in the same state $(u_i\, u_j = +1)$, the coupling coefficient w_{ij} remains the same. The links between the neurons that at the time of learning occur in the opposite states $(u_i\, u_j = -1)$ are weakened.

The model of a taught Hopfield processor has an important property: owing to the symmetry of the coeffi-

cients ($w_{ij} = w_{ji}$) it can be represented in the potential form

$$\frac{\mathrm{d}u_i}{\mathrm{d}t} = -\frac{\partial U(u_1, u_2, \ldots, u_N)}{\partial u_i}\,, \qquad i = 1, 2, \ldots, N\,, \tag{19}$$

where N is the number of elements, and the potential $U(u_1, u_2, \ldots, u_N)$ takes the form

$$U = -\left[\sum_i \left(\frac{1}{2}\,u_i^2 - \frac{1}{4}\,u_i^4\right) + \sum_{i,j\neq i} w_{ij}\,u_i\,u_j\right]. \tag{20}$$

Equation (19) has a mechanical analogy: it describes the motion of a sphere of unit mass in viscous liquid in the potential field U. This analogy allows one to use familiar concepts and patterns and apply them to the problem of pattern recognition.

Let us illustrate this for the example of two-dimensional space ($i = 1, 2$). Imagine an uneven surface with holes and watersheds — it is the potential function $U(u_1, u_2)$. Presentation of the input pattern corresponds to placing the ball at some point on the surface. Recognition corresponds to the motion of ball to the nearest hole, where it lands. 'Elevated attention' implies that the hole is made deeper; less attention means that the hole is shallower. Adjacent holes may form a chain or channel, so that the ball can easily be moved with a slight push from one hole to the next. This means that the objects represented by the holes in the same channel are somehow similar or associated.

The change of attention corresponds to varying the depth of holes and channels, and varying the height of the dividing watersheds. In the language of mechanical analogy one may say that the change of attention corresponds to adding (or removing) a heavy liquid in the channels or holes. If liquid is added to the hole, the ball level in the hole is elevated and the barrier that the ball has to overcome to get to the next hole becomes lower — the attention to the pattern corresponding to this hole is lower. If liquid is removed from the hole, the corresponding amount of attention increases.

Please note that in the real processor there is no place for such images as holes, channels, barriers or watersheds — they are only present in the phase space of model (14). Nevertheless, they help to describe the process of recognition, because the appropriate equations are the same (which is, after all, the objective reality).

This example proves that the mathematical model allows the use of familiar concepts and ideas for describing a process, even though they actually do not belong to this process.

In more sophisticated processors, the coupling coefficients are not symmetric ($w_{ij} \neq w_{ji}$), and the model cannot be represented in the form (19). Nevertheless, the parallels (channels, watersheds, holes) can still be used: holes correspond to the stable steady states, and watersheds to separatrices. These concepts make sense in any model, not only in the potential one.

The *Boltzmann processor* (see Ref. [59]) may be regarded as a modification of the Hopfield processor. The process of recognition takes place in a noise field. The mathematical model is similar here to Eqn (14), but includes random fluctuations:

$$\frac{\mathrm{d}u_i}{\mathrm{d}t} = f(u_i) + \sum_{j\neq i} w_{ij}\,u_j + g(t)\xi(t)\,, \tag{21}$$

where $\xi(t)$ is the random function of time (noise), and g is the amplitude of the noise.

The noise is introduced for the following purposes.

(i) In the Hopfield processor, a false result is possible, especially if the holes are close to one another, and the initial conditions are defined on the watershed (separatrix). This means that the initial information is not sufficient for distinguishing between similar patterns. So it is necessary to request, receive or generate additional information.

The noise whose amplitude $g(t)$ is greater than the barrier between the holes allows the system to be kept in an ambiguous state (called *frustration*) pending the receipt (or generation) of additional information. The noise amplitude $g(t)$ may vary (decrease) with time, so that eventually the process becomes dynamic, and the noise no longer prevents recognition.

(ii) If there are two close holes in the path of the ball, the noise will help it to get into the deeper one (without the noise the ball could have stuck in the shallow hole). The depth of hole depends on learning and concentration of attention; therefore, the noise helps with the realization of attention.

In this way, the Boltzmann processor speeds up and facilitates the recognition of more familiar patterns (and phenomena), and/or those to which the attention is drawn.

(iii) The Boltzmann noise plays the role of an intermixing layer, which helps to generate valuable additional information, or to receive it from the flow of information coming from the outside. As a matter of fact, this process is close to that discussed in connection with the game of roulette.

The simplest mathematical model of autolocalization of the pattern, corresponding to the Grossberg principle, is defined as

$$\frac{\mathrm{d}u_i}{\mathrm{d}t} = f(u_i) + \alpha v_i - \sum_{j\neq i} w_{ij}\,u_j\,,$$
$$\frac{\mathrm{d}v_i}{\mathrm{d}t} = \frac{1}{\tau}(u_i - v_i)\,. \tag{22}$$

The last term in the first equation describes mutual suppression (similar to the antagonistic interaction in the model of interaction of species, discussed in the preceding sections). The coupling coefficients w_{ij} change in the course of learning in the same way as in the Hopfield processor. The second equation describes self-activation.

Autolocalization of the pattern has the following advantages.

In the Hopfield processor, the pattern is distributed. The image of the character 'Б', for example, is built up of many excited neurons. In the Grossberg processor, the image is compacted, and appears as one excited neuron — this is what is called autolocalization. Before learning, it is not known where the particular pattern is going to be localized. After learning, however, the site of localization is fixed, and is not subject to change. One can say that the initial (untaught) state of the Grossberg processor is unstable, and the site of localization is chosen at random.

The state in which the pattern is localized is stable, and this circumstance facilitates the adjustment of the level of attention. One only needs to change the excitation threshold of a single neuron (while in the Hopfield processor this has to be done to many neurons).

All these principles (paradigms) are used in the recognition neurocomputer; accordingly, the neurocomputer is built up of a number of plates with different properties and functions.

Notice that the use of two-dimensional plates is not accidental. The fact is that each plate performs a certain function. The network of links between the elements is designed to accomplish this function. At the same time, almost every element must be accessible for connection with the outside world or with other plates. A two-dimensional organization (plate structure) satisfies this requirement, whereas in the case of three dimensions (using, say, cylinders or spheres in place of plates) this would have been practically impossible.

In principle, the same ideas can be realized in a biochemical computer rather than with physical elements. Such attempts are currently under way (on the level of ideas and conceptual designs). The 'neurons' here are represented by immobilized proteins-enzymes which may occur in two (and more) distinct states (see Ref. [61]).

Using the models (14) – (18) and (21), (22), one can realize the principles of neurocomputing with ordinary (general-purpose) computers. Such an approach is today very common, and is usually referred to as *emulation*. The advantages of parallel processing are retained, but each teachable link has to be represented by a few lines of code. In a neuroprocessor, each link is an analogue element which saves material and space.

Now let us compare the processes in a neurocomputer with the recognition diagram shown in Fig. 8.

The processes on the right-hand (intuitive) side of the scheme — that is, learning, identification of significant attributes, and choice of conjunctions in a neuroprocessor — take place quickly thanks to the following circumstances. Firstly, they proceed concurrently and, secondly, there is almost no enumeration of conjunctions. The processor (like the diagnostician) chooses the appropriate conjunction through direct assessment of the truth.

Now can the processor (without human assistance) formulate the decision rule?

The answer is ambiguous. On the one hand, the decision rule appears in every neurocomputer as a result of learning, after which the recognition goes quickly. On the other hand, this decision rule is not formalized, and each computer has its own rule. The latter is inevitable, because the processes of learning and localization are unstable, the localization site is chosen at random, and is individual in every processor. The problem of exchanging the decision rule between processors remains open, although studies in this direction are under way (Yu Sandler, private communication).

In emulation programs, the decision rule is actually represented by a mathematical model (14) (with fixed links w_{ij}). Its formulation, however, requires a thesaurus — the language of differential equations, thus resulting in the participation of a person. The program of the taught computer can be copied; it will work for a particular set of objects, but will be not capable of learning and recognizing other objects.

Real neural networks are different from the neuroprocessors described above.

In the first place, the real nerve cell — the neuron — is more complicated than a bistable element. It can occur in several steady states, including autooscillatory and even pseudochaotic [13].

Secondly, the role of wires is played by the extensions of the nerve cell: dendrites (that conduct impulses from adjacent cells inward toward the cell body) and axons (nerve fibers that generally conduct impulses away from the body of the nerve cell). The links are based on gap junctions (called synapses). In synapses the impulse can be transmitted directly (by diffusion of ions) or indirectly (through formation and diffusion of special substances called neuromediators). The signal in synapses is transmitted mainly in one direction — from axon to dendrite.

Thirdly, axons are not passive conduits, but active media, and transmit signals in the form of autowaves.

Fourthly, the neural network as such is also an active medium. It can host autowaves which cause simultaneous excitation of many neurons at once [12]. Rhythmic processes and autowaves are actually observed in the brain, and are today under active investigation [see Refs [12, 13]). The question of their role in the process of thinking so far remains open.

All in all, the main properties — summation of the input impulses and generation of the output impulse — are the same for the model neuron and for the real one. A real neural network is capable of learning and attention. Moreover, the possibilities of realization of these properties are much extended. Learning may take place through reorientation of the axon – dendrite junctions; the focus of attention can be biased by varying the composition of the mediators. Autowaves may increase the contrast of the image, etc.

In our opinion, however, these distinctions of the real neural network are important but not fundamentally so. The recognition principles remain the same and they are only adapted for realization in biological objects.

This conclusion can be supported with an example. The authors of Refs [62, 63] studied the properties of self-diagnostic system in humans. It was found that the structure and functions of the so-called Rexed lamina, which constitute the gray matter of the spinal cord, correspond with marvelous precision (as far as this is possible in neurophysiology) to the construction of an optimal neurocomputer. There is a recognition plate (similar to the Hopfield processor), two back propagation plates, a plate where the pattern is localized (similar to the Grossberg processor), etc.

So it follows that each stage of the process of recognition in the neural networks of living organisms (including humans) can be understood and described from the standpoint of natural science, based on the advances in the field of neurocomputing. Moreover, there already are mathematical models like Eqns (14) – (22) that demonstrate such a possibility.

6.4 Thinking and pattern recognition

The analogy between these processes was discussed in Ref. [60]. From arguments developed above it also follows that the process of pattern recognition by neurocomputers has almost all the attributes of thinking.

Indeed,

— this process takes place in neural networks — natural in man, artificial in neurocomputers. The main operating principles in both may be considered the same;

— it is a data processing activity;

— decision-making in this case reduces to the choice of a class (from among those learned) to which the object belongs;

— decision-making with insufficient information is a creative act. A neurocomputer has all that is needed, including the means for reception of information, the intermixing layer (Boltzmann's noise), and storage of the result. The neuroprocessor is able to choose the right time for

making the decision. The decision is taken intuitively by the neurocomputer;

— each neurocomputer is individual. This is observed at different stages of learning. For example, the localization of the image in the Grossberg processor occurs in an element chosen at random. Even in originally identical processors these elements, as a rule, will not be the same. This does not interfere with the performance of the processor, but makes it different from others.

Still, the question remains to what extent thinking can be reduced to recognition.

To this question there is no universally accepted answer, so we can only give some pertinent considerations.

If the goal of thinking consists in predicting the behavior of surrounding objects, then thinking can be reduced to recognition. Even when a man encounters an unfamiliar object, he will try to attribute it to one of the known classes of the learning set (one of the familiar patterns). In the case of success, this is regarded as a creative act.

If the properties of the new object prevent it from attributing to one of the known classes, but contain the attributes of two classes at once, then we are dealing with 'prostration'. Then the recognition theory prescribes to expand the learning set, augment it with other familiar objects, and separate the appropriate class there (the recognition theory does not work with totally unfamiliar objects).

Let us illustrate this situation with an example from scientific research. Each discipline has its collection of patterns as its own learning set. Facing the need to recognize a new object, the scientists will first of all turn to this set. To expand this set means to augment it with patterns from another (related) discipline and to perform a classification of the expanded set. As a rule, it then becomes possible to attribute the object under study to one particular class. There are many successful examples of such an approach in modern science, especially in related disciplines.

A narrow specialist, however, often acts differently — keeping within the boundaries of his learning set, he will attribute the object to two classes at once and state the existence of dualism. Frustration remains, but people get used to it.

Thus, the process of thinking can to a large extent be reduced to pattern recognition.

Hence the next question is whether it is possible to build a neurocomputer capable of scientific and possibly artistic creativity. Or, to put it differently, is there any difference between the human intelligence and the reasoning of a neurocomputer, and can the latter replace the man?

Of course, there is a difference. It is quantitative, and quite considerable.

Neurocomputers are specialized — each has its own learning set, corresponding to its particular purpose. A neurocomputer cannot expand its learning set, even when it gets into 'prostration'. In principle, a neuroprocessor can be taught with two different learning sets — for example, the set of handwritten documents and the set of digestive disorders. Then it may happen that in a difficult case of making a diagnosis the processor will come up with the conclusion that 'the object under study equally resembles diarrhea and constipation, but most likely is the handwriting of a schizophrenic'. Quite absurd of course, but the reader will agree that this conclusion has an intuitive and human touch to it.

Of necessity, every man learns on many different sets. In fact, the learning set is the entire surrounding world for all his life. The most intensive learning occurs in childhood and adolescence, and is based on personal experience — in other words, it is individual and takes place without a teacher.

Professional education takes place at a university (where the learning sets are specialized), 'with a teacher' who formulates the decision rules for recognition (preferably unambiguous). Then the recognition (thinking) becomes a logical process. This accelerates and facilitates the process of recognition, if the object under study is a member of the professional learning community. If this is not the case, one has to turn to a broader learning set (extending beyond the professional) and find there the pattern corresponding to the object studied. This is intuitive reasoning, and is perceived as a creative act.

This implies that a man-made neuroprocessor can replace a professional (a professor or a philosophy doctor), but cannot replace a scientist.

We did not touch upon such things as feelings and desires, the problems of creative art. Of course, they also are related to thinking and pattern recognition. We believe that these phenomena can also be treated from the standpoint of natural science. These problems, however, fall beyond the scope of this publication.

So a model of intuitive reasoning (in the sense described above) is already available; we know how it looks and works. One still has to figure out the details, which may turn out to be more important and interesting than we currently see them.

To conclude, let us discuss the problem of the origin of thought apparatus in the course of evolution. Even worms and primitive animals have nerve cells. The emergence of nerve cells was not an aromorphosis, because all cells and one-celled organisms can generate electric impulses. Nerve cells can do it better, owing perhaps to the gradual development of this capability. The formation of a neural network may be an aromorphosis, but not of high complexity, and reasonably probable.

The bigger brain of higher animals allowed the inclusion of a greater number of learning sets in the process of recognition. Each new set gave an evolutionary advantage. This stage of evolution was most likely gradual, and its description does not pose any problems. One can say that at this stage the living organisms developed the faculty of intuitive thinking. It is not possible to date this development, because the process was gradual.

The dramatic increase in the cranial volume (and the size of the brain) in humans can be regarded as an aromorphosis, but also not complex, and reasonably probable. The first creatures of this type emerged not among the best fitted, but more likely among the marginals. The disproportionately large head was hardly an advantage at the time. Therefore, such 'freaks' could hardly enjoy evolutionary benefits, although they had the improved ability of intuitive recognition. Nevertheless, they survived thanks to their ability to form a collective. In the book [64] it is demonstrated that the rate of the Earth's population growth is proportional to the square (not the first power) of the number of people. Such a law can be explained in terms of the collective behavior of human populace.

The faculty of logical thinking and the associated benefits appeared after the formation of the collective and the development of a common language for a given social

community. This opened the possibility to formulate and use decision rules.

Thus, the power of logical thinking is not the result of biological aromorphosis, but the result of development of social relations.

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