Biocomputing system of living cells

Aurelia Profir

Abstract

The aim of this paper is to show that the process of gene transcription can be represented as a finite automaton illustrating the processing of input/output signals in living cells at DNA level. It is proved that the expression regulation process of λ-phage genes CI and cro represents a molecular-genetic trigger (MGT) which is a self-organizing structure with two stable states. It is shown that MGT can be described as a finite automaton fulfilling logical function NOT AND. A living cell can be represented as DNA-based molecular-genetic machine which has the following characteristics: input, output, transition states, language of computation, predetermined genetic program, memory and energy source.

We propose a formal model of biocomputing system (having depth two) that consists of three *E.coli* bacterium cell cultures. This model corresponding to an elementary logical scheme can solve a class of formula in the conjunctive normal form (like formula (1)).

Introduction

The phenomenon of self-organization in physical, chemical and biological systems is intensively investigated during the last decades. This scientific direction named also “Synergetics” studies the processes of self-organizing of time, spatial, time-spatial and functional structures in cooperative systems [1, 2].

From synergetic point of view an information system must have some special properties. In order that the system contains the information it is necessary that it should be multistationary. It might exist

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in several stationary states, some of them being stable. At least an information system should be bistable, i.e. it should have two stable states (attractors) [2].

Each cell possesses a set of possible functioning alternative regimes (stable states). A cell functions only in one of them in every moment. The switching from one stable state to another one can hold as a response to internal and external factors: UV radiation, pH, temperature, concentrations of specific molecules, etc. These stimuli can be considered as input signals.

We note that the trigger models describe adequate one of significant properties of biological system – their ability to switch from one functioning regime to another one. The self-organizing bistable genetic structures, so-called molecular-genetic triggers (MGT), are investigated in molecular biology since the well-known work of Jacob and Monod [3]. In the paper [4] it is proved that the expression regulation process of λ-phage genes cI and cro represents a molecular-genetic trigger (MGT). Mathematical models of MGT are considered in details in the papers [4]–[7]. MGT represents a genetic system possessing two stable states (attractors) which can switch from one stable state (i.e. functioning regime) to another one. These two stable states of MGT correspond to the processes of transcription of two genes: cI and cro. The purpose of this paper is to show that MGT can be represented as a deterministic finite automaton fulfilling logical function NOT AND.

Thus, as cells react to environmental stimuli which in our case can play a role of input signals, we can control and direct intercellular processes (the process of gene expression) on the basis of mathematical and stochastic models [4]–[7]. Real values of molecule concentrations (input/output signals), the numerical evaluations of switching time of genes from active states to inactive ones (computation time) and the role of fluctuations in destruction process of dynamic memory (trigger effect) in MGT system are obtained on the basis of mathematical and stochastic models of MGT.

We propose a formal model of biocomputing system consisting of three E.coli bacterium cell cultures (infected by three strains of λ-phage, respectively). It corresponds to an elementary scheme (see
Fig. 5). It is shown that this biosystem is able to solve a class of formula in the conjunctive normal form (like formula (1)). The gene regulation processes of these cells correspond to three MGT-s (MGT1, MGT2, MGT3, i.e. finite automata). The cellular computing is a new research direction of DNA-based molecular computing. Some works in this direction were already carried out [8, 9].

This result was presented at the DNA8 conference held on June 10-13, 2002 in Sapporo, Japan, and it was published as an abstract in the conference pre-proceedings [14]. Here we present the full version of the paper.

1 λ-phage genome switching

Regulation process of gene expression is one of the main problems in molecular biology. A molecular mechanism of λ-phage genome switching is very well investigated and is based on a lot of experimental researches [10]. Prokaryotes are relative simple cells without nucleus. In prokaryotes (for example, bacteria) genes are active while the processes of gene transcription and mRNA formation are holding. In the opposite case genes are considered inactive. The genes are transcribed with formation of mRNA under the action of an enzyme named RNA polymerase. A promoter is a place where the process of gene transcription starts. RNA polymerase binding with a promoter starts to move along a gene synthesizing mRNA (gene transcript). As a result of mRNA translation process the protein molecules are synthesized by cell.

In Fig. 1 it is represented the structure of OR right operon which contains three operator sites OR3, OR2, OR1. Two promoters PRM and PR represent the places where the transcription process of genes cI and cro (in the opposite directions) begins. When RNA polymerase binds with the promoter PRM the transcription process of cI gene (on the left) starts, but when it interacts with the promoter PR the transcription process of cro gene (on the right) starts.

cI gene encodes λ-repressor molecules, cro gene encodes Cro protein molecules. λ-repressor dimer is denoted by R2. Activation and
Fig. 1. The scheme of structure of $O_R$ right operon which contains three operator sites $O_{R3}$, $O_{R2}$, $O_{R1}$. Two promoters $P_{RM}$, $P_R$ start RNA polymerase in the opposite directions.

repression of genes depend on the state of $O_{R3}$, $O_{R2}$, $O_{R1}$ operator sites of $O_R$ operon (Fig. 2). RNA polymerase binds with $P_{RM}$ promoter only in case if dimers are interacted by $O_{R2}$ and $O_{R1}$ sites. In this case $R_d$ dimers act on RNA polymerase as activators and the transcription process of $cI$ gene starts (feedback). At the same time $R_d$ dimers interacting with $O_{R1}$ block the transcription process of $cro$ gene ($cro$ gene is inactivated).

Because many of genes are under control of both of $P_{RM}$ and $P_R$ promoters we consider that $y$ gene is one of these genes. It is located on the left and on the right sides of $O_R$ right operon. The products of these genes (of molecular nature) are considered as output signals. Thus the output signals are produced by cells whenever $cro$ or $cI$ transcription process happens. Conversely, in case if both of genes are repressed the output signals are absent.

We examine 12 possible states of $O_R$ right operon (Fig. 2). We observe some distinct situations. In $O_2$, $O_5$, $O_7$, $O_9$ states RNA polymerase binding with one of two promoters transcribes $cro$ or $cI$ genes ($cI$ or $cro$ transcript held). Thus, in these states the output signals are synthesized by cells. In $O_{10}$, $O_{12}$ states both of genes are repressed and the output signals (molecules) are not produced in cellular computing system.

In Fig. 2 by $C$ is denoted a molecule of $Cro$ protein which is encoded by $cro$ gene; $R_d$ denotes a molecule of $\lambda$-repressor dimer which is encoded by $cI$ gene; $P$ denotes a molecule of RNA polymerase which starts the process of gene activation. These molecules reversible inter-
Fig. 2. Scheme of predetermined genetic regulatory system of λ-phage genome. It is represented the reversible interaction process of λ-repressor (R<sup>d</sup>), molecule Cro (C) and RNA polymerase (P) with O<sub>R3</sub>, O<sub>R2</sub>, O<sub>R1</sub> operator sites of O<sub>R</sub> right operon.

act with three operon sites in specific mode by predetermined genetic algorithm as it is illustrated in Fig. 2.

Let O<sub>1</sub> be the probability that sites O<sub>R3</sub>, O<sub>R2</sub>, O<sub>R1</sub> are free;

Let O<sub>2</sub> be the probability that RNA polymerase (P) interacts with O<sub>R1</sub> operator site and the transcription of cro gene process begins;

Let O<sub>3</sub> be the probability that R<sup>d</sup> repressor dimer reversibly interacts with O<sub>R1</sub> operator site and repress the transcription process of cro gene;

Let O<sub>4</sub> be the probability that R<sup>d</sup> dimers reversibly interact with O<sub>R2</sub> and O<sub>R1</sub> operator sites while the site O<sub>R3</sub> is free;

Let O<sub>5</sub> be the probability that RNA polymerase interacts with O<sub>R3</sub> operator site (cl gene is active), O<sub>R2</sub> and O<sub>R1</sub> sites are occupied by R<sup>d</sup> repressor dimers;

Let O<sub>6</sub> be the probability that Cro molecule interacts with O<sub>R3</sub> operator site. Sites O<sub>R2</sub> and O<sub>R1</sub> are free;

Let O<sub>7</sub> be the probability that Cro molecule and RNA polymerase
interact with $O_{R3}$ and $O_{R1}$ operator sites, respectively. $O_{R2}$ is free;

Let $O_8$ be the probability that $Cro$ molecules interact with $O_{R3}$ and $O_{R2}$ operator sites. $O_{R1}$ is free;

Let $O_9$ be the probability that $Cro$ molecules interact with $O_{R3}$ and $O_{R2}$ operator sites. RNA polymerase interacts with $O_{R1}$ operator site ($cro$ transcript);

Let $O_{10}$ be the probability that $Cro$ molecules interact with $O_{R3}$ and $O_{R2}$ operator sites. The molecule of $\lambda$-repressor ($R_d^\dagger$) interacts with $O_{R1}$ operator site. In this case the genes $cro$ and $cI$ are repressed;

Let $O_{11}$ be the probability that the molecule $Cro$ interacts with the operator site $O_{R3}$. The molecule of $\lambda$-repressor ($R_d^\dagger$) interacts with operator site $O_{R1}$;

Let $O_{12}$ be the probability that the molecule $Cro$ interacts with $O_{R3}$ operator site. Molecules of $\lambda$-repressor ($R_d^\dagger$) interact with $O_{R2}$ and $O_{R1}$ operator sites. In this case $cro$ and $cI$ genes are repressed.

The sum of probabilities [4] is

$$O_1 + O_2 + O_3 + O_4 + O_5 + O_6 + O_7 + O_8 + O_9 + O_{10} + O_{11} + O_{12} = 1.$$ 

Other possible states are neglected because their probabilities are minor.

2 Living cell as a deterministic finite automaton

In this section it is described the mechanism of genetic $\lambda$-phage switching using the concept of a deterministic finite automaton [11]. A finite automaton is determined as a quintuple

$$M = (Q, \Sigma, \delta, q_1, F),$$

where $Q = \{q_1, q_2, q_3, q_4, q_5, q_6, q_7, q_8, q_9, q_{10}, q_{11}, q_{12}\}$ is the set of automaton states; $\Sigma = \{\varepsilon, r, p, c, 1, 0\}$ is the alphabet of terminals. Denote by symbol $\varepsilon$ an empty state of automaton tape cell, by $r$ a dimer of $\lambda$-repressor, by symbol $p$ an enzyme molecule of RNA polymerase
and by $c$ a molecule of protein $Cro$; 1 and 0 denote the values $true$ and $false$, respectively, for the output signals produced by cells as a result of the input signals processing at DNA level (see Fig. 2-4); $\delta$ is the function of transitions (Table 1); $q_1$ is the initial state of the finite automaton $M$; $F$ is the set of final automaton states $(q_2^0, q_5^0, q_7^0, q_9^0, q_{10}^0, q_{12}^0)$;

<table>
<thead>
<tr>
<th>$\delta$</th>
<th>$\varepsilon$</th>
<th>$r$</th>
<th>$p$</th>
<th>$c$</th>
<th>1(true)</th>
<th>0(false)</th>
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<tr>
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<tr>
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<td>$q_4^0$</td>
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<td>$q_3$</td>
<td>$\emptyset$</td>
<td>$q_5^0$</td>
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<td>$q_{12}^0$</td>
<td>$\emptyset$</td>
<td>$\emptyset$</td>
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<tr>
<td>$q_{12}^0$</td>
<td>$q_{11}$</td>
<td>$\emptyset$</td>
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</tr>
</tbody>
</table>

Table 1.

If $\delta(q_i, \sigma) = \emptyset$, where $\emptyset$ is empty set, for some $q_i \in Q, \sigma \in \Sigma$, then it means that the transition function is not defined.

The initial state $q_1$ of finite automaton corresponds to the case when all three operator sites of $O_R$ right operon are free (contains the empty symbols) (Fig. 3); the final states $q_2^0, q_7^0$ and $q_9^0$ correspond to the states when RNA polymerase transcribes $cro$ gene; the final state $q_5^0$ corresponds to the state when RNA polymerase transcribes $cI$ gene. Thus, the final states $q_2^0, q_5^0, q_7^0$ and $q_9^0$ correspond to automaton state 1(true) when at least one of genes ($cI$ or $cro$) is active and living cells produce the output signals of molecular nature. The final states $q_{10}^0, q_{12}^0$ correspond to automaton state 0(false) when both of genes are repressed and the output signals are not produced by cells.
The finite automaton tape consists of three cells which correspond to \( O_R3, O_R2, O_R1 \) operator sites of \( O_R \) right operon of \( \lambda \)-phage (Fig. 2, 3). Each cell of the automaton tape can be in one of the finite set states: \( \varepsilon, r, p, c \). The process of reversible molecule interaction with three operator sites corresponds to a writing operation of a symbol in an automaton tape cell.

Fig. 3. 12 genetic predetermined automaton states and 12 states of automaton tape cells, respectively.

Now let us examine the sequences of machine words corresponding to lysogenic and lytic paths of development of \( \lambda \)-phage. These are the following:

1. Lysogen way (\( cI \) gene is active and \( cro \) gene is inactive). By virtue of its structure the automaton \( M \) will consecutively pass from the initial state \( q_1 \) up to the final state \( q_3^0 \):

\[
q_1 \varepsilon \models q_3 \varepsilon \models q_3 r \models q_4 \varepsilon r \models q_4^0 \varepsilon r \models q_5^0 \varepsilon r r.
\]

2. The lytic path (\( cro \) gene is active, \( cI \) gene is inactive).

   a) The first variant. The finite automaton work begins from the initial state \( q_1 \):

\[
q_1 \models q_2^0 p
\]
and in the converse case
\[ q_2^0 p \models q_1 \varepsilon. \]

b) The second variant. Switching of \( cI, cro \) genes. The finite automaton \( M \) begins the work from the state \( q_0^0 \) (\( cI \) is active) into the state \( q_2^0 \) (\( cro \) gene is active). The automaton consecutively takes the following states:

\[ q_0^0 \varepsilon r \models q_4^0 r \models q_4^0 r \models q_3^0 r \models q_3^0 r \models q_2^0 p. \]

For convenience it is described only the process of reversible interaction of \( \lambda \)-repressors and RNA polymerase with three operator sites. Similarly can be written sequences of automaton words that correspond to reversible interaction process of protein \( Cro \) molecules with three operator sites (automaton tape cells).

Thus, the switching of genetic system of \( \lambda \)-phage is described as the finite deterministic automaton \( M \) that executes a computation by a predetermined genetic algorithm. Succession of regulatory events of each path of development of \( \lambda \)-phage (lysogenic state, lytic growth) represents the cascade mechanism when genes \( cI \) and \( cro \) are activated or are inactivated according to the predetermined genetic program (Fig. 4).

In Fig. 4 it is represented the diagram of the finite automaton \( M \):

\[
M = (\{q_1, q_2, q_3, q_4, q_5, q_6, q_7, q_8, q_9, q_{10}, q_{11}, q_{12}\}, \varepsilon, r, \rho, c, 1, 0, \delta, q_1, \{q_2, q_3, q_4, q_5, q_6, q_7, q_8, q_9, q_{10}, q_{11}, q_{12}\}).
\]

In dependence of the molecule concentration of \( \lambda \)-repressor or \( Cro \) protein the certain branches of gene switching cascade mechanism are realized. The high value of molecule concentration is represented below by 1 and low value — by 0. Because \( MGT \) mathematical model of \( \lambda \)-phage gene switching is two-dimensional we have two input signals: \( x_1, x_2 \). The input signals corresponding to \( x_1, x_2 \) variables must regulate the transcription process of genes \( cI \) and \( cro \) and control the level of molecules concentration of \( \lambda \)-repressors (\( R^d \)) and \( Cro \). Also,
Fig. 4. The diagram of the finite automaton $M$. Arrows indicate reversible molecules interaction processes with three operon sites at DNA level.

they regulate the process of synthesizing by cells of the output signals (Fig. 4). For convenience, we consider that $x_1$ and $x_2$ correspond to concentration molecules of $\lambda$-repressor ($r$) and Cro protein ($c$), respectively. Boolean values true of the output signal will be denoted by 1, and values false – by 0. For instance, the state $q_0^0$ is realized whenever Cro protein and $\lambda$-repressor are absent, i.e. the respective molecule concentrations are low (i.e. are 0). In this case cro gene is activated and the output signal 1(true) of molecular nature (molecules encoding by y gene (Fig. 1)) is produced by cells. The state $q_0^0$ is realized, i.e. CI gene is activated, whenever the molecule concentration of $\lambda$-repressor will be high (i.e. is 1). The output signal synthesized by cell also is 1(true). If both of input signals are equal to 1 ($x_1 = 1, x_2 = 1$), then both of genes are repressed and the output signal is 0(false) (see Table 2).
Table 2. (LOGICAL FUNCTION NOT AND). Table of the output signals $y$ depending on the input signals $x_1$ and $x_2$.

<table>
<thead>
<tr>
<th>INPUT</th>
<th>OUTPUT</th>
</tr>
</thead>
<tbody>
<tr>
<td>$x_1$</td>
<td>$x_2$</td>
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<tr>
<td>0</td>
<td>0</td>
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<tr>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>1</td>
<td>1</td>
</tr>
</tbody>
</table>

A language defined by automaton $M$ (denoted by $L(M)$) [11] is a set of input chains which is recognized by automaton $M$. For instance, for the input chain $prr$ there exists the unique configuration sequence of the automaton $M$, namely:

$$(q_0^0, prr) \models (q_4, err)$$

$$\models (q_4, rr)$$

$$\models (q_3, er)$$

$$\models (q_3, r)$$

$$\models (q_1, e)$$

Thus, the chain $prr$ belongs to language $L(M)$ ($prr \in L(M)$), where $e$ is the empty chain. Thus, the formal language $L(M)$ consists, for example, of the following chains: $eee, eep, eer, err, prr, eee, eep, eee$, etc. Our deterministic finite automaton can read chains as well from left to right as from right to left. For instance, if chains $ccp, eee$ are recognized by $M$ reading them from left to right, then these chains belong to $L(M)$. If the chain $prr$ is recognized by $M$ reading it from right to left, then it also belongs to $L(M)$.

Obviously, in this case we can say that *E.coli* bacterium cell (infected by strain of $\lambda$-phage) can be represented as a deterministic finite automaton having two inputs and one output. It fulfills logical function $NOTAND$. It is an example of DNA–based molecular-genetic machine which has the following characteristics: input, output, transition states, language of computation, predetermined genetic program, memory and energy source.
3 Self-organizing biocomputing model solving a logical problem

We propose a formal model of cellular computing system that consists of three living E.coli bacterium cell cultures (infected by three strains of λ-phage) which can be represented as finite automata fulfilling logical function NOTAND. The gene regulation processes of these three cell cultures correspond to three MGT: MGT1, MGT2, MGT3. They correspond to three finite deterministic automata (A1, A2, A3) fulfilling logical functions NOTAND (Fig. 5).

In this paper we show that the self-organizing system of finite automata can solve the concrete example of logical problem in the conjunctive normal form like this one:

$$\beta = (x_1 \lor x_2) \land (\neg x_1 \lor \neg x_2)$$  \hspace{1cm} (1)

We have two variables $x_1$, $x_2$ and two clauses. It is satisfying when any of the following truth-assignments make formula (1) true:

$$(x_1 = false, x_2 = true), (\neg x_1 = true, \neg x_2 = false), \quad (2)$$

$$(x_1 = true, x_2 = false), (\neg x_1 = false, \neg x_2 = true). \quad (3)$$

We use three connectives: or, and, negation.

It is known that a living cell (bacterium) reacts to internal and external factors considered as input signals. In dependence of genetic construction of promoter regulatory sites of genes we can organize the input of initial data for biosystem using signals of wave or molecular nature. Values 1 and 0 are continuous values of molecule concentrations or intensities. The high (1) and low (0) concentrations of specific molecules (for example, activators, repressors, hormones, toxins, etc.) can be used as signals of molecular nature and binding with promoter regulatory sites they control the transcription processes of genes. In case of light-induced gene [12] the input signals of wave nature may be utilized.

There are $2^n$ ($n$ is the number of variables in (1), $n = 2$) different sets of initial values. All possible combinations of two input signals are:
00, 01, 10, 11. The input signals corresponding to \( x_1, x_2 \) variables must regulate the transcription process of genes \( cI \) and \( cro \) and control the level of molecules concentration of \( \lambda \)-repressors \( (R^\lambda) \) and \( Cro \). Also, they regulate the process of synthesizing by cells of output signals.

![Diagram](image)

Fig. 5. The elementary scheme of two levels cellular computing system consisting of three finite automata which can solve a class of propositional formula in the conjunctive normal form (like formula 1).

The living cells that form a biosystem communicate among themselves by means of intercellular signals. Cells (emitters) secrete output signals of molecular nature. The molecules diffuse in the surrounding medium of cellular computing system and the signals are transferred from emitter cells to receptor cells. For the trigger switch the concentrations of molecules or light intensities have to be higher than a critical value \([4]-[7]\). We remark that the computation process based on \( MGT \), i.e. finite automata for solving formula (1) can be associated with a binary tree structure consisting of 2 levels. The number of levels (the depth) determines the formula (1) calculation time. The first level cells receive in parallel the initial input signals and produce output signals that are input signals for the second level cells. Cells, whose gene transcription process correspond to \( A1 \) and \( A2 \) belong to the first level cells. They receive in parallel input signals \( x_1, x_2 \) and \( \neg x_1, \neg x_2 \), respectively. Their output signals \( y_1, y_2 \) are the input signals for cells, whose gene regulation processes correspond to \( A3 \) and belong to the second level cells.

If input signals are \( x_1 = 1, x_2 = 1 \) (state \( q^0_{10} \) or \( q^0_{12} \), Fig. 3, Table 2), then output signal \( y_1 \) is weak and we can neglect with him \( (y_1 = 0(false)) \). In this case the process of gene transcription does not hold
because the genes \((cI \text{ and } cro)\) are repressed (are inactive). Let the input signals be \(x_1 = 0, x_2 = 0\) (i.e. molecules of \(\lambda\)-repressors and protein \(Cro\) are absent), then the output signal \(y_1\) is \(1\) (true) (Table 3), i.e. the genes are active (the process of gene transcription happens). The cells, corresponding to \(A1, A2, A3\), adjusted by methods of genetic engineering will receive only a concrete set of input signals (and will not react to other signals do not belonging to the given set). At the same time these cells secrete only specific output signals of molecular nature.

From genetics point of view, logical element \(NOT\) can be associated with the transcription process of a gene which is under control of some promoter with a negative type of gene regulation. In Fig. 5 logical element \(NOT\) is designed by a circle. The repressor molecules may serve as input signals for logical element \(NOT\), and binding with the promoter they stop the gene transcription process (gene is repressed). The gene is active whenever the repressor molecules (input signals) are absent.

In Table 3 the evolution process of input/output signals at \(DNA\) level and the communication process of cellular computing system components (living cells) are represented.

<table>
<thead>
<tr>
<th></th>
<th>(x_1)</th>
<th>(x_2)</th>
<th>(\neg x_1)</th>
<th>(\neg x_2)</th>
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<th>(y_2)</th>
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</table>

Table 3. Dependence of \(\beta\) output signal of the cellular computing system on the input signals \(x_1, x_2\).

The presence of output signals \(\beta\) secreted by cells, whose gene transcription regulation processes correspond to \(A3 (MGT3)\), designs that the first level cells of cellular computing system receive a combination of the input signals which satisfy equation (1). Note that the computation process of cellular computing model for solving formula (1) can be
associated with a binary tree structure consisting of 2 levels. The number of levels (the depth) determines formula (1) calculation time. The mathematical and stochastic models permit us to effectuate numerical evaluation of genes switching time (computation time). We can calculate the necessary computation time (as a function of environmental stimuli), i.e. duration in which $1(true)$ output signal (molecules $\beta$) has to appear in cellular computing system. We consider that the output signals are $0(false)$ if $1(true)$ signals do not appear in the evaluated computation time. The proposed cellular computing model (having depth 2) can calculate a class of propositional formula in the conjunctive normal form (like formula (1)) with two variables ($n=2$) and two clauses in two parallel-consecutive steps with parallel gates fulfilling logical functions NOT AND.

Final remarks

In this paper it is assumed that $MGT$, i.e. the regulation process of gene transcription in living cells may be represented as a deterministic finite automaton. A living cell is an example of DNA-based molecular-genetic machine fulfilling logical function NOT AND. It is shown that the cellular computing model (having depth 2) can calculate a class of formula in the conjunctive normal form (like formula (1)) in parallel-consecutive mode (in two steps). We consider that the cellular computing system is able to solve P-complete problems in polynomial time due to high degree of computation parallelism (for instance, the well-known $n-SAT$ problem).

$MGT$ (i.e. finite automaton) being an analogous of transistors can be of several types in dependence of genetic construction of cells. A simplest types of $MGT$ may be represented as a deterministic finite automata with 3 automaton states having alphabets of 5 symbols. Variables $true$ and $false$ correspond to active and inactive states of gene, respectively. There are different types of $MGT$ both with positive and negative type of gene transcription regulation process. They can fulfill logical functions $OR$, $XOR$, NOT $AND$, $AND$ [4–7], [13]. Theoretically, it is possible to form a biosystem of living cells (fulfilling
logical functions) that correspond to any logical scheme.

References


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