MODELLING OF CELLULAR FUNCTIONS BY MEANS OF TIMED MEMBRANE TRANSDUCERS

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INTRODUCTION

In theoretical computer science, automata theory is the study of abstract 'mathematical' machines or systems and the computational problems that can be solved using these machines (called automata). A finite state transducer (FST) is a finite state machine with two tapes: an input tape and an output tape [1]. This contrasts with an ordinary finite state automaton (or finite state acceptor), which has a single tape. On this view, a transducer is said to transduce (i.e., translate) the contents of its input tape to its output tape, by accepting a string on its input tape and generating another string on its output tape. It may do so nondeterministically and it may produce more than one output for each input string. A transducer may also produce no output for a given input string, in which case it is said to reject the input [2]. The concept of membrane transducers is an extension of concept of P transducers [3-5] - inspired by the structure and the functioning of the living cell. The concept of P transducers is the most powerful framework for unifying main aspects of biological systems at the main hierarchical levels: DNA level; cellular level; cell interaction with the environment [4].

In this paper we propose two new formalisms, named *deterministic finite timed transducer* and *timed membrane transducer.* In the framework of our approach the DNA (in genes) and ARN sequences were mapped by means of systems of 1D membranes. This approach allows to capture gene structure and all relevant functional aspects of time behavior of transcriptional and translational gene regulation. All rates (and characteristic constants) of protein interaction processes with DNA (inclusively, the rate of RNA polymerase moving along genes) are taken into account.

The aim of this paper is to model, using the concept of timed membrane transducers, the molecular machinery responsible for the main cellular functions (transcription and translation processes). Our model describes the functional organization of genes as well as how environmental factors act on them.

1. DETERMINISTIC FINITE TIMED TRANSDUCERS

Our aim is to model the input/output information processing by timed (one-dimensional) membrane transducers (TMT) to understand the functioning of the living cell in terms of genetic information processing. Cellular active elements, the proteins, such as regulatory enzymes, transcription factors, RNA polymerases, ribosomes, etc. are modeled using the concept of the finite timed membrane transducers. The structure-functional organization of single-stranded DNA (in a gene), and RNA segments (copies of genes) are viewed as one-dimensional (1D) membranes. The relevant features of 1D membrane structure are reflected by regulatory elements (specific nucleotide sequences) considered as input "signals" translated by TMTs into output signals.
On the other hand, a living cell reacts to external factors considered as input signals and in our TMT model it is taken into account the influence of environmental circumstances on the rates of regulatory enzymatic reactions.

A transducer is an abstract device that translates an input string $x=x_1 x_2 \ldots x_k$, consisting of the elements of the input symbol alphabet, into another output string $y= y_1 y_2 \ldots y_r$. consisting of the elements of the output symbol alphabet. We consider deterministic finite transducers [9]. The *deterministic finite transducer* is a structure:

$$DFT = (Q, \Sigma, \Gamma, \delta, q_0, F),$$

that consists of: $Q=\{q_0, q_1, \ldots, q_n\}$ – set of states; $\Sigma=\{a_1, a_2, \ldots, a_k\}$ – input symbol alphabet; $\Gamma=\{b_1, b_2, \ldots, b_s\}$ – output symbol alphabet; $\delta: Q\times(\Sigma\cup\{\varepsilon\})\times(\Gamma\cup\{\eta\}) \rightarrow Q\times(\Gamma\cup\{\eta\})$ – transition function determining the behavior of the device; ε, η – empty elements; $q_0 \in Q$ – initial state; F – set of final states, $F \subseteq Q$. $\Sigma^*=\Sigma\cup\{\varepsilon\}$, $\Gamma^*=\Gamma\cup\{\eta\}$.
The record $\delta(q_i, a_i, b_k)=(q_k, b_k)$ means that the *DFT,* being into the state $q_i \in Q$, *reads* $a_i \in \Sigma^*$ from *the input tape,* passes into the state $q_k \in Q$, and writes

$b_k \in \Gamma^*$ into *the output tape* (for shortly, the notation $\delta(q_i, a_i) = (q_k, b_k)$ is used). The initial configuration is (q_0, x, η), where $q_0 \in Q$, $x \in \Sigma^*$. (q_i, x', y') *i*s an intermediate configuration of *DFT* where $q_i \in Q$, $x' \in \Sigma^*$, $y' \in \Gamma^*$. The final configuration is (q_f, ε, y), where $q_f \in F$, $y \in \Gamma^*$. For $\forall q_k \in Q$ *and* $\forall x = a_1 a_2 \ldots a_n$, $a_i \in \Sigma^*$, the following relation holds:
$\delta(q_i, a_1 a_2 \ldots a_n) = \delta(\delta(\ldots\delta(\delta(\delta(q_i, a_1), a_2), a_3)\ldots) a_n)$. The obtained result is $y = b_1, b_2, \ldots, b_s \in \Gamma^*$. Thus, *DFT* translates an input string $x \in \Sigma^*$ if and only if there is a *some* path $(q_0; a_1 a_2 \ldots a_n, \eta) \vdash (q_1; a_1 a_2 \ldots a_{n-1}, b_1) \vdash \ldots \vdash (q_i; a_i a_{i+1} \ldots a_i, b_1 b_2 \ldots b_{i-i\ldots} b_{n-1}) \vdash (q_f; \varepsilon, b_1 b_2 \ldots b_n)$ from the initial start state $q_0 \in Q$ (through $q_1, \ldots, q_i \in Q$ – intermediate states) to the final state $q_f \in$ F such that input x is translated into the output $y \in \Gamma^*$. To examine the translation of the input signals into output signals we extend *DTF* notion using the temporal characteristics. In biological processes $F = \varnothing$ because the functional mechanisms of proteins, described below, are cyclic.

We introduce a notion of *delay time*, denoted by τ_m, i.e., the time between the instant $t_i \in R_+$ in which the transducer is into a state $q_i \in Q$ $(i=0,\ldots,n)$, reading the input signal $a_i \in \Sigma^*$ and the instant t_{i+1}, in which the transducer passes into the state $q_k \in Q$ $(k=0,\ldots,n)$ and produces the output signal $b \in \Gamma^*$ in correspondence to the determined transition function δ. $\tau_m = t_{i+1} - t_i$. $T = \{\tau_m\} \subseteq R_+$.

The deterministic finite timed transducer can be defined in the following way:
DEFINITION 1. The *deterministic finite timed transducer* is a construct:

$$TT = (Q, \Sigma, \Gamma, \delta, q_0, T),$$

where Q, Σ, Γ, ε, η, q_0, T are similar to those elements mentioned above;
δ: $Q \times (\Sigma \cup \{\varepsilon\}) \times (\Gamma \cup \{\eta\}) \times T \rightarrow Q \times (\Gamma \cup \{\eta\})$ is a transition function that maps state-symbol-symbol-delay_time to the state–symbol . The record $\delta(q_i, a_i, b_k, \tau_m) = (q_k, b_k)$, (or $\delta(q_i, a_i, \tau_m) = (q_k, b_k)$) means that the *TT*, being into the state $q_i \in Q$ reads $a_i \in \Sigma^*$, passes into the state $q_k \in Q$ and writes $b_k \in \Gamma^*$.
In the next section we show how can be described by means TT the input/output signal processing by a cellular biosensor [4].

2. CELLULAR BIOSENSOR AS A TIMED TRANSDUCER

The input/output signal processing by a cellular biosensor can de described by a timed transducer:

$$TT_c = (Q^C, \Sigma^C, \Gamma^C, \delta^C, T^C, q_0^C),$$

where:
$Q^C = \{q_0^C, q_1^C\}$ is the finite set of states: q_0^C represents the "healthy" state of the cell; q_1^C – "*illness*" bacteria state of cell; $\Sigma^C = \{0,1\}$ – the finite input vocabulary; $\Gamma^C = \{G\}$ – the finite output vocabulary: G represents the fluorescent proteins;
δ^C: $Q^C H(\Sigma^C \chi \{\varepsilon\}) H(\Gamma^C \chi \{\eta\}) H T^C \rightarrow Q^C H(\Gamma^C \chi \{\eta\})$ – the transition function of TT_C:

$$\delta^C (q_0^C, 0, \tau_0^C) = (q_0^C, \eta),$$
$$\delta^C (q_0^C, 1, \tau_1^C) = (q_1^C, G),$$
$$\delta^C (q_1^C, 1, \tau_2^C) = (q_1^C, G),$$
$$\delta^C (q_1^C, 0, \tau_3^C) = (q_0^C, \eta);$$

$T^C = \{\tau_0^C, \tau_1^C, \tau_2^C, \tau_3^C\}$ is the set of delay times, where:
τ_0^C indicates the penetration time of cellular cytoplasm by environmental factors; τ_1^C – action time of endogenous factors on cytoplasm components; τ_2^C – biosynthesis time of G fluorescent proteins; τ_3^C – cytoplasm escape time of G fluorescent proteins; q_0^C – the initial state of TT_c; {0,1} input symbols describe the absence and presence of environmental mutagen factors, respectively; {η,G} output symbols describe the absence and presence of green fluorescent proteins;
Fig. 1 illustrates the functional mechanism of regulatory enzyme modeling by TT_c

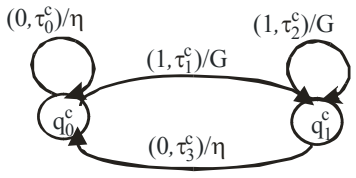

Figure 1. Input/output signal processing by the cellular biosensor modeled by TT_c.

3. TIMED MEMBRANE TRANSDUCERS

Now we define a *deterministic finite timed transducer with localization,* called *timed membrane transducer*.
DEFINITION 2. The deterministic finite timed transducer with localization, named *timed membrane transducer,* is a construct:

$$TMT = (Q, \Sigma, \Gamma, \delta, q_0, T, L),$$

where: Q, Σ, Γ, ε, η, q_0, T are similar to those components mentioned in Definition 1;
δ: $Q\times(\Sigma\cup\{\varepsilon\})\times(\Gamma\cup\{\eta\})\times T\times L \rightarrow Q\times(\Gamma\cup\{\eta\})\times L$ is a transition function that maps state-symbol-symbol-delay_time–localization to the states–symbol – localization.

The record $\delta(q_i, a_i, b_k, \tau_m l_j) = (q_k, b_k, l_k)$, (or $\delta(q_i, a_i \tau_m l_j) = (q_k, b_k, l_k)$) means that the *TMT* being into the state $q_i \in Q$ reads $a_i \in \Sigma^*$ being located in the region delimited by the l_k membrane (l_j – membrane label) or being located on the l_j membrane. So, l_j represents the location of TMT, $l_j \in L$. After that *TMT* passes into the state $q_k \in Q$ and writes $b_k \in \Gamma^*$, changing its localization: $l_k \in L$. $L \subseteq I_+$

Forwards, the functional mechanisms of the proteins, such as transcription factors, RNA polymerases, ribosomes, regulatory enzymes, etc. are modeled using the concept of *TMT*.

4. GENE TRANSCRIPTION MODELLING BY TIMED MEMBRANE TRANSDUCERS

Transcription is the mechanism by which a template strand of DNA is utilized by specific RNA polymerases to generate RNA copies of the gene [8]. All RNA polymerases are dependent upon a DNA template strand in order to synthesize *m*RNAs (copies of genes). The resultant RNA is, therefore, complimentary to the template strand of the DNA duplex and identical to the non-template strand. The non-template strand is called the coding strand because its' sequences are identical to those of the *mRNA*. However, in RNA, *U* is substituted for *T*.

In this section the functional mechanism of the RNA polymerases are modeled using the concept of deterministic finite timed transducers with localization (TMT). In living cells, the ability to express biologically active proteins comes under regulation at several points: the structure of DNA sequences can affect the ability of transcriptional regulatory proteins (termed transcription factors) and RNA polymerases to find access to genes and to activate transcription from them. Transcriptional initiation is the most important stage for control of gene expression. RNA synthesis requires accurate and efficient initiation, elongation proceeds in the 5' → 3' direction (i.e. the polymerase moves along the template strand of DNA in the 3' → 5' direction), and RNA synthesis requires distinct and accurate termination. Proteins (for instance, RNA polymerases) only recognize "signals" that physically (conformational) complement their surface features. A promoter region contains important sequences that are required for RNA polymerase to bind. Promoter sequences promote the ability of RNA polymerases to recognize the nucleotide at which initiation begins.

Transcription proceeds in an ordered process. RNA polymerase (in the prokaryotic cell) is composed of 5 distinct polypeptide chains. Association of several of these generates the RNA polymerase holoenzyme. The holoenzyme (Core + σ) has a much higher affinity for promoter sequences. Thus σ-subunit confers sequence specificity onto the Core enzyme and ensures that transcription only starts from promoter sequences. When the RNA chain is about 10 nucleotides long, σ-subunit dissociates, leaving Core. The loss of σ-subunit allows Core to leave (unbind) the promoter and bind DNA less specifically. Now Core can elongate RNA processively (utilizing its affinity for nonspecific DNA).

The RNA polymerase is directed to the start point of the gene, the sigma factor is released and the RNA polymerase carries out the process of transcription. Similarly, there are other base sequences at the end of a gene, denoted as stop signals {TAA,TAG,TGA}. The START and STOP signals are recognized by RNA polymerases. We consider that gene coding regions comprises for prokaryotic genes – polycistrons, for eukaryotic genes – interrupted amino acid coding sequences, i.e., sequence of exons and introns. Following termination the Core polymerase dissociates from the DNA template strand. The Core and σ subunit can then reassociate forming the holoenzyme again ready to initiate another round of transcription (cyclic process).

Let us describe the functional mechanism of RNA polymerase by means the timed membrane transducer TMT_1:

$$TMT_1 = (Q^1, \Sigma^1, \Gamma^1, \delta^1, q_0^1, T^1, L^1),$$

where $Q^1 = \{q_0^1, q_1^1, q_2^1, q_3^1, q_4^1\}$ is the finite set of RNA polymerase states, which indicate: q_0^1 – free RNA polymerase (holoenzyme (Core + σ)), the initial state of TMT_1, q_1^1 – RNA polymerase recognizes the *promoter signal* and binds to the DNA (RNA Polymerase-Promoter Complex); q_2^1 – RNA polymerase recognizes the *start signal* and begins to move along DNA template strand (releasing the σ factor), transcribing the gene; q_3^1 – RNA polymerase, reading the *stop signal*, ends the gene transcription process and releases the DNA; $\Sigma^1 = \{\gamma, \sigma, s, \alpha, t\}$ is the finite vocabulary of the input signals recognized by RNA polymerase: γ –

promoter signal; σ – sigma factor; *s* – start point of the gene; α – nucleotides, α ∈ {*A, T , C, G*); *t* – stop signal, i.e., transcriptional termination site of the gene; Γ^1 ={*s', θ, t'*} the finite vocabulary of the output signals: *s'* – start point of RNA copy of gene, t'– stop point of RNA copy of gene, θ – nucleotides, θ ∈ {*U, A, G, C*); δ^1: $Q^1 H(\Sigma^1 \chi \{\varepsilon\}) H(\Gamma^1 \chi \{\eta\}) H T^1 H L^1 \rightarrow Q^1 H(\Gamma^1 \chi \{\eta\} H L^1)$ – transition function of TMT_1 that determines the order of events in transcription:

$$\delta^1(q_0^1, \varepsilon, \tau_0^1, l_0) = (q_0^1, \eta, l_0),$$
$$\delta^1(q_0^1, \gamma, \tau_1^1, l_0) = (q_1^1, \eta, l_1),$$
$$\delta^1(q_1^1, s, \tau_2^1, l_1) = (q_2^1, s', l_1),$$
$$\delta^1(q_2^1, \alpha, \tau_3^1, l_1) = (q_2^1, \theta, l_1),$$
$$\delta^1(q_2^1, t, \tau_4^1, l_1) = (q_3^1, t', l_1),$$
$$\delta^1(q_3^1, \sigma, \tau_5^1, l_1) = (q_0^1, \eta, l_0);$$

$T^1 = \{\tau_0^1, \tau_1^1, \tau_2^1, \tau_3^1, \tau_4^1, \tau_5^1\}$ is the set of delay times, where: τ_0^1 – time-interval when the holoenzyme is localized in the cytoplasm; τ_1^1 – concentration of DNA breaks that correlates with the transcription initiation probability; τ_2^1 – promoter escape time; τ_3^1 – time of nucleotide synthesizing; τ_4^1 – DNA escape time; τ_5^1 – σ factor reassociation time. $L^1 = \{l_0, l_1\}$ – locations for RNA polymerase: l_0 – map the cell cytoplasm; the 1D membrane l_1 maps the gene with its regulatory region. The functional mechanism of the RNA polymerase modeling by TMT1 is pictured in Fig. 2.

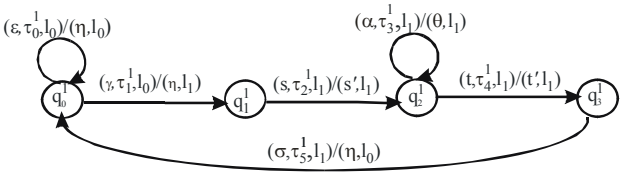

Figure 2. The functional mechanism of RNA polymerase modeling by TMT_1.

5. TRANSLATION PROCESS MODELLING BY TIMED MEMBRANE TRANSDUCERS

The translation process is the RNA directed synthesis of polypeptides (proteins). The processes leading to the ability to form a peptide bond are very complex. The template for correct addition of individual amino acids is the *mRNA*, yet both *tRNAs* and *rRNAs* are involved in the process. The *tRNAs* carry activated amino acids into the ribosome which is composed of *rRNA* and ribosomal proteins. The ribosome is associated with the *mRNA* gene copies ensuring correct access of activated *tRNAs* and containing the necessary enzymatic activities to catalyze peptide bond formation [7].

The ability to identify the roles of the various ribosomal proteins in the processes of ribosome assembly and translation was aided by the discovery that the ribosomal subunits will self assemble *in vitro* from their constituent parts.

Following assembly of both the small and large subunits onto the *mRNA*, and given the presence of charged *tRNAs*, protein synthesis can take place. To reiterate the process of protein synthesis: synthesis proceeds from the *N*-terminus to the *C*-terminus of the protein; the ribosomes "read" the *mRNA* in the 5' to 3' direction; active translation occurs on polyribosomes (also termed polysomes). This means that more than one ribosome can be bound to and translate a given *mRNA* at any one time. The chain elongation occurs by sequential addition of amino acids to the *C*-terminal end of the ribosome bound polypeptide. Translation proceeds in an ordered process. First accurate and efficient initiation occurs, then chain elongation and finally accurate and efficient termination must occur. All three of these processes require specific proteins, some of which are ribosome associated and some of which are separate from the ribosome, but may be temporarily associated with it. RNA polymerase produces a transcription unit that extends from the promoter to the termination sequences. The gene is defined in reference to the start site – those sequences before the start site are called the upstream sequences, those after the start site are called downstream sequences. The immediate product is the primary transcript. Transcriptional unit comprises: start codon {*AUG*} → Met (not fMet), interrupted amino acid coding sequences, stop codons.

The initiation of translation requires the (*AUG*) recognition by ribosomes. The ribosomes are known to scan *mRNA* from left to right (5' to 3') and to initiate translation usually at the first-encountered *AUG* triplet (*start signal*). The ribosome binds directly to the Shine-Dalgarno sequence, and translation is initiated at an *AUG* triplet located several bases downstream of the sequence. The code is composed of a triplet of nucleotides. That all 64 possible combinations of

the 3 nucleotides code for amino acids, i.e. the code is degenerate since there are only 20 amino acids. Elongation of polypeptides occurs in a cyclic manner. Like initiation and elongation, translational termination requires specific protein factors identified as releasing factors. The signals for termination are the same in both prokaryotes and eukaryotes. These *signals* are termination codons present in the *mRNA*. There are 3 termination codons: *UAG*, *UAA* and *UGA*. The inactive ribosome then releases its *mRNA* and the 80S complex dissociates into the 40S and 60S subunits ready for another round of translation. The cycle can now begin again.

The TMT_2 describes the functional mechanism of ribosomes:

$$TMT_2 = (Q^2, \Sigma^2, \Gamma^2, \delta^2, q_0^2, \mathrm{T}^2, L^2),$$

where: $Q^2 = \{q_0^2,\ q_1^2,\ q_2^2\}$ is the finite set of the ribosomes states, which indicate: q_0^2 – diassociated ribosome (with ribosome recycling factor); translation is initiated at an *AUG* triplet (denoted by *s'*) and binds directly to the *mRNA* gene copy; the initial state of TMT_2, q_1^2 – ribosome scans *mRNA* gene copy, translating triplets of the *mRNA* gene copy into amino acids (synthesized polypeptidic chain); q_2^2 – ribosome ending the translation of *mRNA* gene copy and releasing the *mRNA* (the newly-synthesized polypeptide is released from the ribosome); Σ^2 = {ω, *s'*, *b*, *t'*, ρ} – the finite input vocabulary (signals recognized by ribosomes): ω – Shine-Dalgarno sequence; *s'* – start signal (*AUG*) of translation; *b* – triplet of the *mRNA* chain; *t'* – stop signal of translation; ρ – ribosome recycling factor; $\Gamma^2 = \{\pi, \mu\}$ – finite output vocabulary: π – amino acid *Met*; μ – one of 20 types of amino acides; δ^2: $Q^2\ H(\Sigma^2 \chi \{\varepsilon\})\ H(\Gamma^2 \chi \{\eta\})\ H T^2\ H L^2 \rightarrow \mathrm{Q^2\ H\ (\Gamma^2 \chi\ \{\eta\}\ H\ L^2)}$ – the transition function of $\mathrm{TMT_2}$ that describes the order in translation:

$$\delta^2(q_0^2, \omega, \tau_0^{2`}, l_0) = (q_0^2, \eta, l_2),$$
$$\delta^2(q_0^2, s', \tau_1^{2`}, l_2) = (q_1^2, \mu, l_2),$$
$$\delta^2(q_1^2, b, \tau_2^2, l_2) = (q_1^2, \pi, l_2),$$
$$\delta^2(q_1^2, t', \tau_3^2, l_2) = (q_2^2, \eta, l_2),$$
$$\delta^2(q_2^2, \rho, \tau_4^2, l_2) = (q_0^2, \eta, l_0);$$

$\mathrm{T}^2 = \{\tau_0^2,\ \tau_1^2,\ \tau_2^2,\ \tau_3^2,\ \tau_4^2\}$ is the set of delay times, where: τ_0^2 indicates the ribosome assembling time; τ_1^2 – synthesizing time of amino acid of *Met*; τ_2^2 –synthesizing time of amino acid of polypeptidic chain; τ_3^2 – RNA escape time; τ_4^2 – recycling factor association time with ribosome; $L^2 = \{l_0, l_2\}$ are locations of the ribosomes: l_0 and l_2 mapping the cell cytoplasm and the RNA strand, respectively. In Fig. 3 it is represented the functional mechanism of ribosomes by TMT_2.

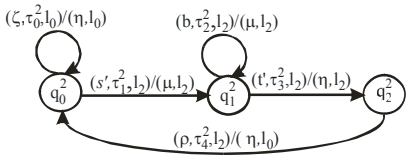

Figure 3. The functional mechanism of ribosomes modeling by TMT_2.

6. FUNCTIONAL MECHANISM OF THE REGULATORY ENZYME

It is known that a living cell reacts to internal and external factors, considered as input signals. They are denoted by *x*, $x \in \{0,1\}$. The low and high concentrations (intensities) of the input signals are denoted by 0 and 1, respectively. As a result of input signals action on regulatory enzymes two states of enzymatic activities can be obtained: E^+ (activated state) and E^- (inactivated state), respectively. E^+ enzyme molecules destroy repressor molecules *R* and E^- can not destroy repressor molecules [5].

The functional mechanism of regulatory enzyme which react with the endogenous factors is described by TMT_3 :

$$TMT_3 = (Q^3,\ \Sigma^3,\ \Gamma^3,\ \delta^3, q_0^3, \mathrm{T}^3, L^3),$$

where $Q^3 = \{q_0^3,\ q_1^3\}$ is the finite set of state: q_0^3 and q_1^3 indicate that the regulatory enzyme is in inactive (E^-) and active (E^+) state, respectively, $q_0^3 \in Q^3$ – initial state of TMT_3; Σ^3 = {0,1} – the finite input vocabulary; $\Gamma^3 = \{\nu\}$ – the finite output vocabulary: ν represents the low concentration of repressor molecule; δ^3: $Q^3\ H(\Sigma^3 \chi \{\varepsilon\})\ H(\Gamma^3 \chi \{\eta\})\ H\ T^3\ H\ L^3 \rightarrow Q^3\ H(\Gamma^3 \chi \{\eta\}\ H\ L^3)$ – the transition function of TMT_3 :

$$\delta^3(q_0^3, 0, \tau_0^3, l_0) = (q_0^3, \eta, l_0),$$
$$\delta^3(q_0^3, 1, \tau_1^3, l_0) = (q_1^3, \eta, l_3),$$
$$\delta^3(q_1^3, 1, \tau_2^3, l_3) = (q_1^3, \eta, l_3),$$
$$\delta^3(q_1^3, 0, \tau_3^3\ l_3) = (q_0^3, \nu, l_0);$$

$\mathrm{T}^3 = \{\tau_0^3,\ \tau_1^3,\ \tau_2^3,\ \tau_3^3\}$ is the set of delay times, where: τ_0^3 indicates the allocation time of the

regulatory enzyme (*RecA)* in cytoplasm, τ_1^3 – interaction time of the regulatory enzyme and DNA breaks, τ_2^3 – repairing time of DNA break and the destroying a repressor molecule *R,* τ_3^3 – DNA escape time; $L^3 = \{l_0, l_3\}$ are locations of the regulatory enzymes: l_0 and l_3 mapping the cell cytoplasm and the DNA break, respectively.
Fig. 4 illustrates the functional mechanism of regulatory enzyme modeling by TMT_3

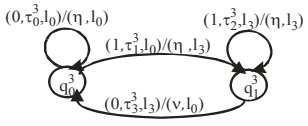

Figure 4. The functional mechanism of regulatiry enzyme modeling by *TMT3.*

7. FUNCTIONAL MECHANISM OF REPRESSOR MOLECULES

The functional mechanism of repressor molecule can be described by TMT_4 (Fig. 5):

$$TMT_4 = (Q^4, \Sigma^4, \Gamma^4, \delta^4, q_0^4, T^4, L^4),$$

where: $Q^4 = \{q_0^4, q_1^4\}$ is the finite set of state: q_0^4 – repressor is free, q_1^4 – repressor is binding to the operator; $\Sigma^4 = \{\varphi\}$ – finite input vocabulary, $\Gamma^4 = \{\beta, \beta'\}$: β – operator is repressed by repressor molecule; β' – operator is free; $\delta^4 : Q^4 H(\Sigma^4 \chi \{\varepsilon\}) H(\Gamma^4 \chi \{\eta\}) HT^4 HL^4 \rightarrow Q^4 H(\Gamma^4 \chi \{\eta\} HL^4)$ – the transition function:

$$\delta^4 (q_0^4, \varepsilon, \tau_0^4, l_0) = (q_0^4, \eta, l_0),$$
$$\delta^4 (q_0^4, \varphi, \tau_1^4, l_4) = (q_1^4, \beta, l_4),$$
$$\delta^4 (q_1^4, \varepsilon, \tau_2^4, l_4) = (q_1^4, \beta', l_4),$$
$$\delta^4 (q_1^4, \varphi, \tau_3^4, l_4) = (q_0^4, \beta', l_4);$$

$T^4 = \{\tau_0^4, \tau_1^4, \tau_2^4, \tau_3^4\}$ is the set of delay times, where: τ_0^4 indicates the allocation time of repressor molecule in cytoplasm, τ_1^4 – binding time of repressor molecule to operator site, τ_2^4 – repression time of operator site, τ_3^4 – operator escape time;

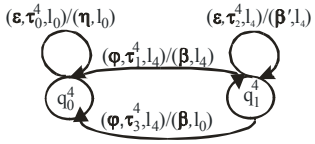

Figure 5. The functional mechanism of the repressor molecules by *TMT4.*

$L^4 = \{l_0, l_4\}$ - locations for repressor molecules: l_0 and l_4 mapping the cytoplasm and the operator site, respectively; $q_0^4 \in Q^4$ – initial state of *TMT 4*..

8. CONCLUSION

The cell structure is determined by membrane structures. The main cellular functions connected to the genetic information processing such as the regulation of gene expression, protein biosynthesis, etc. are determined by the proteins present that perform different cellular tasks. In this paper we introduced two formalisms: *deterministic finite timed transducer* and *timed membrane transducer.* It is shown that the functional mechanism of proteins can be modeled by timed membrane transducers (with localization), and the action of environmental factors on cellular biosensors can be described by deterministic finite timed transducer.

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Recommended for publication: 27.04.2011.