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STRUCTURAL MEMBRANE MODELLING OF GENETIC INFORMATION PROCESSING BY TIMED TRANSDUCERS

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Abstract. *This paper is a study of the structure-functional organization of molecular genetic machinery, which plays a central role in receiving, storing, processing and transmitting information by the living cell. We introduce a concept of one-dimensional structural membrane system of timed transducers with localization to model the functional mechanisms of temporal behavior of active proteins responsible for the main cellular functions, for instance, the transcriptional regulation of gene expression, the protein biosynthesizing system etc. An essential novelty of the DNA (in genes) and RNA modeling is that the DNA and RNA are mapped by means of one-dimensional structural membranes for capture in detail their structure-functional organization.*
Keywords: *proteins, transcription, translation, structural membranes, finite transducers.*

Introduction

Living cells are complex and highly structured and organized systems, consisting of discrete interacting components and, in many aspects, can be considered as information DNA computing devices. Cell structure and function are closely related. The cell structure is determined by membrane structures [1]. 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 and structure-functional organization of DNA (in genes) and of RNA copies of genes [2]. Our aim is to model the input/output information processing by the (one-dimensional) *structural membrane system of timed transducers* (*M systems*) to understand the functioning of the living cell in terms of genetic information processing. Introduced formalism of the M systems is an extension of P systems [1]. The proteins, such as regulatory enzymes, transcription factors, RNA polymerases, ribosomes, etc. are modeled using the concept of the *finite timed transducers with localization* (*TTL*s). The structure-functional organization of single-stranded DNA (in a gene), and RNA segments (copies of genes) are viewed as one-dimensional (1D) structural membranes. The relevant features of 1D membrane structure are reflected by regulatory elements (specific nucleotide sequences) considered as input "signals" translated by *TTL*s into output signals. It is known that a living cell reacts to external factors considered as input signals. The influence of environmental circumstances on the rates of regulatory enzymatic reactions is taken into account.

Timed transducer

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 [3]. 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;

$\Gamma=\{b_1, b_2, ..., b_s\}$ – output symbol alphabet,

δ: $Q\times(\Sigma\cup\{\varepsilon\})\times(\Gamma\cup\{\eta\}) \rightarrow Q\times(\Gamma\cup\{\eta\})$ – 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 $\forall x=a_1a_2....a_n$, $a_i \in \Sigma^*$, takes place the relation:

$\delta(q_i, a_1a_2...a_n)=\delta(\delta(...\delta(\delta(\delta(q_i,a_1),a_2),a_3)...) a_n)$.

The obtained result is $y= b_1, b_2, ..., b_s \in \Gamma^*$.

Thus, *DFT* translates an input string $x \in \Sigma^*$ if and only if there is a *some* path $(q_0; a_1 a_2 ...a_n, \eta) \vdash (q_1; a_1a_2 ...a_{n-1}, b_1). \vdash ... \vdash (q_i; a_ia_{i+1} ...a_i, b_1b_2...b_{n-i...b}) \vdash ... \vdash (q_f; \varepsilon, b_1b_2 ...b_n)$ from the initial start state $q_0 \in Q$ (through $q_1,...,q_i \in Q$ – 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 h the temporal characteristics.

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 $q_i \in Q$ $(i=0,...,n)$, reading the input signal $a_i \in \Sigma^*$ and the instant t_{i+1}, in which the transducer passes into the state $q_k \in Q$ $(k=0,...,n)$ and produces the output signal $b \in \Gamma^*$ in correspondence to the determined transition function δ. $\tau_m=t_{i+1} - t_i$.

In biological processes $F=\varnothing$ because the functional mechanisms of proteins, described below, are cyclic. The deterministic finite timed transducer can be determined in such way:

DEFINITION 1. The *deterministic finite timed transducer* is a following construct:

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

where Q, Σ, Γ, ε, η, q_0, 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 $\delta(q_i, a_i, b_k, \tau_m) = (q_k, b_k)$, (for shortly, $\delta(q_i,a_i,\tau_m) = (q_k, b_k)$) 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 following we show how to describe the input/output signal processing by the cellular biosensor using the timed transducer.

Input/output signal processing by the cellular biosensor as the timed transducer

The input/output signal processing by the 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 protein;

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_0^4 indicates the penetration time of endogenous factor in cytoplasm;

τ_1^4 – influence time of endogenous factor to the citoplasme components;

τ_2^4 – producing time of fluorescent protein G;

τ_3^4 – citoplasme escape time;

q_0^C 0 Q^C – initial state of TT_c.

Figure 1 illustrates the functional mechanism of regulatory enzyme modeling by TT_c

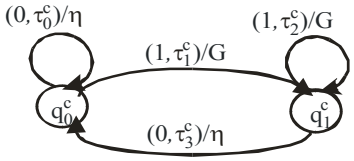

Figure 1. Input/output signal processing by the cellular biosensor modeled by TT_c.

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 and structure-functional organization of DNA (in genes) and of RNA copies of genes. The structure-functional organization of the living cell in terms of genetic information processing and its functionality can be modeled using the concept of M systems. To define a M System, first of all, we determine the *deterministic finite timed transducer with localization* as active elements (objects) of the M systems.

DEFINITION 2. The deterministic finite timed transducer with localization is a following construct:

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

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 $\delta(q_i, a_i, b_k, \tau_m l_j) = (q_k, b_k, l_k)$, (for shortly, $\delta(q_i, a_i, \tau_m l_j) = (q_k, b_k, l_k)$) means that the *TTL* being into the state $q_i \in Q$ reads $a_i \in \Sigma^*$ in the location $l_j \in L$. After that *TTL* passes into the state $q_k \in Q$ and writes $b_k \in \Gamma^*$ in the location $l_k \in L$.

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

M system of timed transducers with localization

DEFINITION 3: The M system of the timed transducers with localization can be defined in the next way:

$$M = (\mu, w_1, \ldots, w_k, O, \Sigma, \Gamma, Q, \delta, b),$$

where:

μ – structural membrane system of degree k ≥1 (k - number of membranes);

$w_1, \ldots, w_k$ – the initial state of the M system;

O – sets of objects (sets of timed transducers with localization TTL_i, i=1,…, |O|);

Σ – input signals alphabet, $\Sigma = \bigcup_{i=1}^{|O|} \Sigma^i$, where Σ^i is the input signals alphabet of TTL_i;

Γ – output signals alphabet, $\Gamma = \bigcup_{i=1}^{|O|} \Gamma^i$, where Γ^i is the output signals alphabet of TTL_i ;

δ: $Q\times(\Sigma\cup\{\varepsilon\})\times(\Gamma\cup\{\eta\}) \rightarrow 2^{(Q\times\Gamma\cup\{\eta\})}$ – the transition function of *STTL* that describes the order in translation;

Q – states of *TTLs*, $Q = \bigcup_{i=1}^{|O|} Q^i$;

b – environment (i.e., input signals that influence the system and output signals, produced by the living cell as response to the input signals).

Gene transcription

Transcription is the mechanism by which a template strand of DNA is utilized by specific RNA polymerases to generate RNA copies of the gene [4]. All RNA polymerases are dependent upon a DNA template strand in order to synthesize RNA. 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 living cells, the ability to express biologically active proteins comes under regulation at several points:
The physical structure of the DNA, as it exists compacted into chromatin, can effect 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 mode for control of gene expression. Specific factors that exert control include the strength of promoter elements within the DNA sequences of a given gene, and the interaction between multiple activator proteins and inhibitor proteins.
Synthesis of RNA exhibits several features that are synonymous with DNA replication. 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.
Signals are present within the DNA template that act in *cis* to stimulate the initiation of transcription. These sequence elements are termed *promoters*. The promoter region contains important sequences that are required for RNA polymerase to bind. These sequences are similar in both prokaryotic and eukaryotic genes, but the locations are different.
Promoter sequences promote the ability of RNA polymerases to recognize the nucleotide at which initiation begins. Transcriptional promoters are important sequences used in the control of gene expression. 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 start 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* 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).
In the next section the functional mechanism of the RNA polymerases are modeled using the concept of deterministic finite timed transducers with localization.

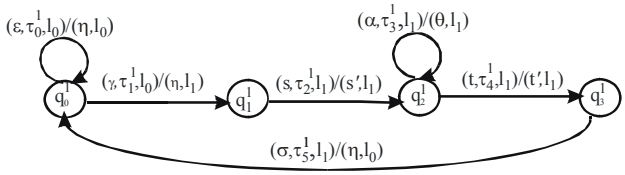

Figure 2. The functional mechanism of RNA polymerase modeling by *TTL1*.

Functional mechanism of RNA polymerase modeling by timed transducer with localization

Let us describe the functional mechanism of RNA polymerase by means the transducer *TTL1*:

$$TTL_1 = (Q^1,\ \Sigma^1,\ \Gamma^1,\ \delta^1,\ q_0^1,\ \Gamma^1,\ L^1),$$

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 TTL_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 0{*A, T , C, G*); *t* –stop signal, i.e., transcriptional termination site of the gene;

$\Gamma^1 = \{s', \theta, t'\}$ 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 0 {*U, A, G, C*);

$\delta^1: Q^1 H(\Sigma^1 \chi \{\varepsilon\}) H(\Gamma^1 \chi \{\eta\}) H T^1 H L^1 \rightarrow Q^1 H(\Gamma^1 \chi \{\eta\} H L^1)$ – transition function of TTL_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; $(\tau_1^1)^{-1}$– 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 structural membrane l_1 maps the gene with its regulatory region.

The functional mechanism of the RNA polymerase modeling by TTL_1 is pictured in Fig.2.

Translation process

The translation is the RNA directed synthesis of polypeptides. 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.

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 transducer TTL_2 describes the functional mechanism of ribosome:

$$TTL_2 = (Q^2, \Sigma^2, \Gamma^2, \delta^2, q_0^2, \mathrm{T}^2, L^2),$$

where:

$Q^2 = \{q_0^2,\ q_1^2,\ q_2^2\}$ is the finite set of the ribosomes states, which indicare: 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 TTL_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;

$\delta^2 : Q^2\ H(\Sigma^2 \chi \{\varepsilon\})\ H(\Gamma^2 \chi \{\eta\})\ H T^2\ H L^2 \rightarrow$ Q^2 H (Γ^2 χ {η} H L^2) – the transition function of TTL_2 that describes the order in translation:

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

$\mathrm{T}^2 = \{\tau_0^2, \tau_1^2, \tau_2^2, \tau_3^2, \tau_4^2\}$ 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;

$L^2 = \{l_0, l_2\}$ is locations of the ribosomes: l_0 and l_2 mapping the cell cytoplasm and the RNA strand, respectively;

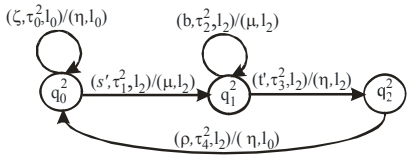

Figure 3. The functional mechanism of ribosomes modeling by TTL_2.

In Figure 3 is represented the functional mechanism of ribosomes by transducer TTL_2.

Functional mechanism of the regulatory enzyme

It is known that a living cell reacts to internal and external factors (concentrations of DNA breaks that correlates to the concentrations of DNA damage factors (mutagens, UV, temperature, etc.)) considered as input signals, 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^+ (the activated state) and E^- (the 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 TTL_3 :

$$TTL_3 = (Q^3, \Sigma^3, \Gamma^3, \delta^3, q_0^3, T^3, L^3),$$

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 0 Q^3 – initial state of TTL_3;
$\Sigma^3 = \{0,1\}$ – the finite input vocabulary;
$\Gamma^3 = \{\nu\}$ – the finite output vocabulary: ν represents the low concentration of repressor molecule;
$\delta^3 : Q^3 H(\Sigma^3 \chi \{\varepsilon\}) H(\Gamma^3 \chi \{\eta\}) HT^3 HL^3 \rightarrow Q^3 H(\Gamma^3 \chi \{\eta\} HL^3)$ – the transition function of TTL_3 : $\delta^3(q_0^3, 0, \tau_0^3, l_0) = (q_0^3, \eta, l_0)$,

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

$T^3 = \{\tau_0^3, \tau_1^3, \tau_2^3, \tau_3^3\}$ 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 the repressor molecule R, τ_3^3 – DNA escape time;
$L^3 = \{l_0, l_3\}$ is action locations of the regulatory enzymes: l_0 and l_3 mapping the cell cytoplasm and the DNA break, respectively;
Figure 4 illustrates the functional mechanism of regulatory enzyme modeling by TTL_3

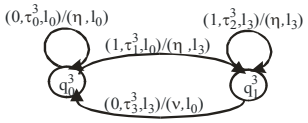

Figure 4. The functional mechanism of regulatiry enzyme modeling by *TTL3*.

Functional mechanism of the repressor molecules

The functional mechanism of repressor molecule can be described by TTL_4:

$$TTL_4 = (Q^4, \Sigma^4, \Gamma^4, \delta^4, q_0^4, T^4, L^4),$$

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;
$L^4 = \{l_0, l_4\}$ is locations for repressor molecules: l_0 and l_4 mapping the cytoplasm and the operator site, respectively;

q_0^4 0 Q^4 – initial state of *TTL 4*.

Figure 5 represents the functional mechanism of the repressor molecules by *TTL4*.

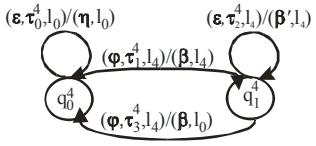

Figure 5. The functional mechanism of the repressor molecules by *TTL4*.

Cellular biosensor modeling by means of the M system

Input/output processing by a cellular biosensor can be represented by means of M system:

$$M = (\mu, w_1, \ldots, w_5, O, \Sigma, \Gamma, Q, \delta, b),$$

where:

μ – structural membrane system of degree 5;

$w_1, \ldots, w_5$ – the initial state of the M system;

O – sets of objects (sets of timed transducers with localization TTL_i, i=1,…, 4);

Σ – input signals alphabet, $\Sigma = \bigcup_{i=1}^{4} \Sigma^i$, where Σ^i is the input signals alphabet of TTL_i;

Γ – output signals alphabet, $\Gamma = \bigcup_{i=1}^{4} \Gamma^i$, where Γ^i is the output signals alphabet of TTL_i ;

δ: $Q \times (\Sigma \cup \{\varepsilon\}) \times (\Gamma \cup \{\eta\}) \rightarrow 2^{(Q \times \Gamma \cup \{\eta\})}$ – the transition function of *STTL* that describes the order in translation;

Q – states of *TTLs*, $Q = \bigcup_{i=1}^{4} Q^i$;

b – environment (i.e., input/output signals, processed by the living cell).

The processes connected with the receiving, storing, processing and transmitting information in the living cell are performed by proteins in a non-deterministic maximally parallel manner.

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. The functional mechanism of proteins are modeled by deterministic finite timed transducers with localization.

Structure-functional organization of DNA sequences (in genes) and of RNA copies of genes is mapped by 1D structural membranes.

Attempting to understand how DNA is transcribed and translated in terms of automata theory is very useful because it provides us with yet another means of representing the nucleic acid chain, and it also enables us to derive mRNA and protein structure from sequence. This approach based on the principles of System biology is going to be essential for biologically as realistic as possible representation of different aspects of biological systems of high architectural complexity.

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