MODELING OF GENETIC INFORMATION PROCESSING BY FINITE TRANSDUCERS

Aurelia Profir [1], Elena Boian [2]

[1] Institute of Applied Physics, Academy of Sciences, Republic of Moldova
e-mail: aurelia@cc.acad.md
[2] Institute of Mathematics and Computer Sciences, Academy of Sciences,
Republic of Moldova,
e-mail: lena@math.md

Abstract. Our aim is to model the work of cellular information processing. We model gene transcription and translation processes as well as how genes and the factors acting on them are organized. This concept, 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. The functioning of active elements (proteins) is modeled using the concept of finite deterministic transducers.

Keywords: finite transducers, DNA, RNA, transcription, translation.

INTRODUCTION

Cell structure and function are closely related. The cell structure is determined by membrane, 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 functional organization of DNA (in genes) and RNA copies of genes. The functioning of active elements (proteins), such as regulatory enzymes, transcription factors, RNA polymerase, ribosome, etc. are modeled using the concept of finite deterministic transducers.

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.

TRANSCRIPTION

Transcription is the mechanism by which a template strand of DNA (gene) is utilized by specific RNA polymerases to generate RNA copies of genes. The resultant RNA is, therefore, complimentary to the template strand of the DNA duplex and identical to the non-template (coding) strand. However, in RNA, U is substituted for T.

Transcriptional initiation is the most important mode for control of eukaryotic 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. Mechanism of RNA polymerases synthesis of RNA exhibits several features. 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.

Let us describe by the transducer T_1 the functional mechanism of the RNA polymerase. $T_1 = (Q^1, \Sigma^1, \Gamma^1, \delta^1, q_0^1)$, where $Q^1 = \{q_0^1, q_1^1, q_2^1, q_3^1, q_4^1\}$ is the finite set of states: q_0^1 – RNA polymerase as holoenzyme, denoted by p^σ ; q_1^1 – RNA polymerase, without σ –factor, denoted by p; q_2^1 – RNA polymerase moves along gene regulatory region; q_3^1 – RNA polymerase transcribing a gene; q_4^1 – RNA polymerase that leaved gene–coding region; $\Sigma^1 = \{\gamma, \beta, \rho, s, \alpha, t, \sigma\}$ – the finite vocabulary of the input objects: γ – promoter; β – operator is repressed; ρ – nucleotides of the gene regulatory region; s – transcriptional start point of gene; α – nucleotides, $\alpha \in \{A, T, C, G\}$; t – transcriptional termination site of gene; σ – σ-factor; $\Gamma^1 = \{\rho', s', \theta, t'\}$ – finite vocabulary of the output objects, where ρ' – nucleotides of the cap mRNA, s' – beginning of mRNA, θ – represents the nucleotides of mRNA, $\theta \in \{C, A, T, U\}$, t' – end of mRNA. $\delta^1 : Q^1 \times (\Sigma^1 \cup \{\varepsilon\}) \to Q^1 \times (\Gamma^1 \cup \{\lambda\})$ – transition function of T_1.

$$\delta^1(q_0^1, \gamma) = (q_1^1, \lambda) \qquad \delta^1(q_1^1, \beta) = (q_1^1, \lambda) \qquad \delta^1(q_1^1, \rho) = (q_2^1, \rho') \qquad \delta^1(q_2^1, \rho) = (q_2^1, \rho')$$

$$\delta^1(q_2^1, s) = (q_3^1, s') \qquad \delta^1(q_3^1, \alpha) = (q_3^1, \theta) \qquad \delta^1(q_3^1, t) = (q_4^1, t') \qquad \delta^1(q_4^1, \sigma) = (q_0^1, \lambda)$$

$q_0^1 \in Q^1$ – the initial state.

TRANSLATION

Translation is the RNA directed synthesis of polypeptides. This process requires all three classes of RNA. The ribosomes "read" the mRNA in the 5' to 3' direction; active translation occurs on polyribosomes (also termed polysomes). 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. The initiation of translation requires recognition of an AUG codon.

The transducer T_2 describes the biosynthesis of *mRNA* copies of *recA* and of y genes and can be represented in the following way: $T_2 = (Q^2, \Sigma^2, \Gamma^2, \delta^2, q_0^2)$, where $Q^2 = \{q_0^2, q_1^2, q_2^2\}$ is the finite set of states; q_0^2 – the polymerase is free p^σ ; q_1^2 – the polymerase p^σ is binding to the promoter; q_2^2 – the polymerase begin to work in the absence of repressor; $\Sigma^2 = \{\zeta, \tau, t'.\varphi\}$ -- the finite input vocabulary: ζ – is combination of *ρ'* and *s';*; τ – represents the codons; φ – φ-factor; $\Gamma^1 = \{\omega\}$ -- the finite vocabulary of output objects, ω – represents the amino acids; *t'* – the end mark of gene, $\delta^2 : Q^2 \times (\Sigma^2 \cup \{\varepsilon\}) \to Q^2 \times (\Gamma^2 \cup \{\lambda\})$ – the transition function of T_2 ;

$\delta^2(q_0^2, \xi) = (q_1^2, \lambda)$ $\delta^2(q_1^2, \tau) = (q_1^2, \omega))$ $\delta^2(q_1^2, t') = (q_2^2, \lambda)$ $\delta^2(q_2^2, \varphi) = (q_1^1$

$q_0^2 \in Q^2$– the initial state.

CONCLUSION

Living cells are very complex and highly structured and organized systems, consisting of discrete interacting components and, in many respects, can be considered DNA computing devices. Using the concept of finite transducers we model the molecular machinery responsible for receiving, processing and transmitting information by living cells. We model gene transcription and translation processes as well as how genes and the factors acting on them are organized.

REFERENCES

1. Aho, A. V., Ullman, J. D. The Theory of Parsing, Translation and Compiling. Prentice - Hall, Inc. Englewood Cliffs, N. J., 1992