

Translation of protein mRNA using coupled equation

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ABSTRACT We analyze translation models of RNA messenger concentration (m) to proteins (p). Using a dynamic translation system of mRNA to proteins, the stationary or experimental solution was obtained. For a set of parameters and ODE45 tool of the MATLAB the concentrations of mRNA and proteins were obtained. It has been shown computationally that it has no periodic solutions because it has no closed orbits according to the Poincare-Bendixson Theorem. It has been shown computationally that the solution is asymptotic to stationary solution. Computational methods predict the production of proteins and that controls can be added to this production.

KEYWORDS translation, genes, mRNA, proteins

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I. INTRODUCTION

This paper gives a solution for the protein-mRNA coupled equation. Generally we study the dynamics of the DNA [1-3]. There are problems related to the functions of the gene and the mechanisms of gene expression (1). The development patterns are explained with the theoretical and experimental models of coupled oscillators (2).

The present study aims to describe in a computational simulation the dynamics of couplers coupled to the messenger system of RNA and proteins. The stationary case is analyzed, which is equivalent to the experimental case, usually in the cell medium. In general, the solutions for a set of parameters are determined and they are observed as they behave as a station after a certain time. The metacognitive part is to implement cancer control programs to prevent the proliferation of unwanted protein.

II. PROTEINS-MRNA

A system of differential equations was used to analyze the dynamics of mRNA concentration (m), and protein concentration (p).

$$\dot{p} = Lm - Up \quad (1)$$

$$\dot{m} = f(p) - Vm$$

The constant L is the translation coefficient and U is the protein degradation coefficient.

U is the degradation coefficient of mRNA. The function $f(p)$ is the transcription function. The classical method of solving systems of differential equations is with Runge-Kutta fourth order method and is computationally processed with the ODE tool 45 of the MATLAB program.

To determine the stationary solution, we have considered the set of parameters: $L = U = V = 1$ and the function $f(p)$ given by:

- $f(p) = 10 / (1 + p^2 / 25)$

The stationary solution was found by solving the system:

$$0 = Lm - Up \quad (2)$$

$$0 = f(p) - Vm$$

III. POINCARÉ-BENDIXSON THEOREM

There are no periodic solutions as indicated in Figure 1. A circuit that is not closed is shown. The Poincaré-Bendixson theorem guarantees the same result. Because the divergent of the associated field is different from zero.

A concentration of $m = p = 5$ will be horizontal asymptote for dynamic solutions.

The system of coupled equations generates two solutions as indicated in figure 2. Figure 2 shows its final vibration equal to 5.

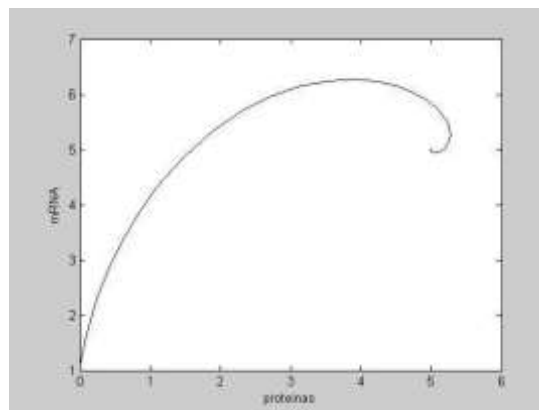


Fig.1. mRNA-proteins

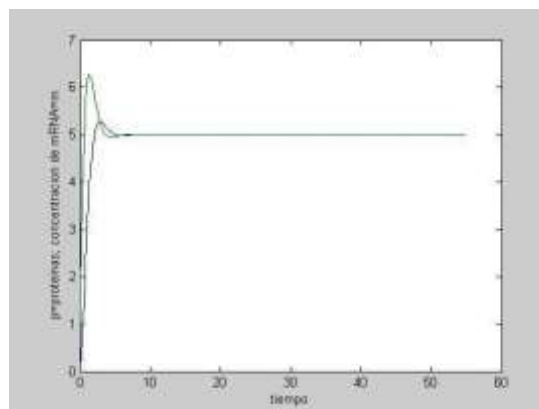


Fig.2. coupled solutions

The system (1) can be controlled in a computational manner depending on the set of parameters. These results can be optimized by manipulating the constants L , U , V and the function $f(p)$. The results of the vibrations are also discussed in reference (1). Similar results with numerical methods with MATLAB are found in Di Stefano's reference (3).

It can be analyzed with an optimal control theory and better control of proteins. Biologically it is based on microRNAs controllers.

IV. CONCLUSION

There are no periodic solutions for the protein – mRNA coupled equation.

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