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ON A STOCHASTIC GENE EXPRESSION WITH PRE-MRNA, MRNA AND PROTEIN CONTRIBUTION

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ABSTRACT

During my speech I will present a model of gene expression, where stochastic effects originate from random fluctuations in gene activity status, but we precede mRNA production by the formation of pre-mRNA, which enriches classical transcription phase [1]. We obtain a stochastically regulated system of ordinary differential equations describing evolution of pre-mRNA, mRNA and protein levels. We describe mathematical analysis of a long-time behavior of this stochastic process, identified as a piece-wise deterministic Markov process. We observe that in the deterministic (adiabatic) limit state of the process, it can exhibit two specific types of behavior: bistability and the existence of the limit cycle [2]. We will also shortly mention more complex hybrid stochastic models which are under investigation [3].

REFERENCES

[1] R. Rudnicki and A. Tomski: *On a stochastic gene expression with pre-mRNA, mRNA and protein contribution*, Journal of Theoretical Biology 387 (2015), 54–67.

[2] J. Jaruszewicz, P. Żuk, and T. Lipniacki: *Type of noise defines global attractors in bistable molecular regulatory systems*, Journal of Theoretical Biology 317 (2013), 140–151.

[3] J. Hu, W. Wu, and S. Sastry: *Modeling subtilin production in Bacillus subtilis using stochastic hybrid systems*, Lecture Notes in Computer Science: 7-th International Workshop, Hybrid Systems: Computation and Control (2004), 417–431.