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On a stochastic gene expression with pre-mRNA, mRNA and protein contribution

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, A. Tomski, *On a stochastic gene expression with pre-mRNA, mRNA and protein contribution*, Journal of Theoretical Biology 387 (2015), pages=54–67.
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- [3] J. Hu, W. Wu, 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.