

Jugowice, 11th-15th September 2017

ANALYSIS OF A POSSIBLE MECHANISM OF NOISE REDUCTION IN BIOLOGICAL SYSTEMS

Marzena Dołbniak¹, Jarosław Śmieja²

¹ Silesian University of Technology
Akademicka 2A, 44-100 Gliwice

¹marzena.dolbniak@polsl.pl, ²jaroslaw.smieja@polsl.pl

ABSTRACT

This work is concerned with model based analysis of microRNA-mediated regulation of gene and protein expression. Three simple, generic models, are introduced. These models differ in the way the system is activated, representing hypothetical versions of the regulatory system. Their responses to pulse inputs are analyzed numerically. These pulses are of varying periods and strengths, which determine if the input is a random disturbance that should be filtered out by the system, or an actual change in the environment, to which a cell should built a response. Transient system responses have been analyzed in each case. The settling time, the mean and maximum change of each variable have been chosen as response characteristics. They were subsequently used to identify the model the one which exhibits noise reduction property.

ACKNOWLEDGEMENTS

The authors were supported by grant nr BKM/506/RAU1/2016/t.6 (MD) and by NCN (National Science Centre, Poland) DEC-2013/11/B/ST7/01713 (JS). Calculations were partially performed on the Ziemowit computational cluster (http://www.ziemowit.hpc.polsl.pl) created in the POIG.02.01.00-00-166/08 project (BIO-FARMA) and expanded in the POIG.02.03.01-00-040/13 project (Syscancer).

REFERENCES

- [1] N. Bushati and S. M. Cohen, microRNA functions. Annu Rev Cell Dev Biol, vol 23, pp 175-205, 2007.
- [2] J. S. Dickey and F. J. Zemp and O. A. Martin and O. Kovalchuk, *The role of miRNA in the direct and indirect effects of ionizing radiation*, Radiat Environ Biophys, vol 50(4), pp 491-499, 2011.
- [3] Dong, H. and Lei, J. and Ding, L. and Wen, Y. and Ju, H. and Zhang, X., MicroRNA: function, detection, and bioanalysis, Chem Rev, 113(8), 6207-33,2013
- [4] Liu, J. and Zhang, C. and Zhao, Y. and Feng, Z., MicroRNA Control of p53, J Cell Biochem, vol118(1),pp 7-14, 2017,
- [5] Ma, X. and Becker Buscaglia, L. E. and Barker, J. R. and Li, Y., *MicroRNAs in NF-kappaB signaling*, J Mol Cell Biol, vol 3(3),pp 159-66,2011
- [6] Xie, W. and Li, Z. and Li, M. and Xu, N. and Zhang, Y., miR-181a and inflammation: miRNA homeostasis response to inflammatory stimuli in vivo, Biochem Biophys Res Commun, vol 430(2), pp 647-52,2013
- [7] Xue, X. and Xia, W. and Wenzhong, H., A modeled dynamic regulatory network of NF-kappaB and IL-6 mediated by miRNA, Biosystems, vol114(3), pp 214-8,2013
- [8] Yan, F. and Liu, H. and Liu, Z., Dynamic analysis of the combinatorial regulation involving transcription factors and microRNAs in cell fate decisions, Biochim Biophys Acta, vol1844(1 Pt B), pp 248-57, 2014
- [9] Schmiedel, J. M. and Klemm, S. L. and Zheng, Y. and Sahay, A. and Blüthgen, N. and Marks, D. S. and van Oudenaarden, A., MicroRNA control of protein expression noise, Science vol 348(6230),pp 128–132,2015