

Jacek Miekisz

UNIVERSITY OF WARSAW

e-mail: miekisz@mimuw.edu.pl

Simple stochastic models of gene regulation

We will discuss simple models of gene regulation. We assume that the number of mRNA and protein molecules is small and therefore to describe biochemical processes of transcription, translation, and degradation, we use birth and death processes. We linearize Hill functions which describe regulation, use the generating function approach to the Masters equations, and show that translational repression contributes greater noise to gene expression than transcriptional repression [1].

Our main goal now is to derive analytical expressions for the variance (noise) of the number of protein molecules in models where changes of the DNA state between an active and inactive one are governed by birth and death processes whose intensities depend on the number of protein molecules [2]. We will discuss different approaches to the problem of closure of an infinite chain of equations for moments of the protein probability distribution and apply it to systems with two gene copies [3].

REFERENCES

- [1] M. Komorowski, J. Miekisz, and A. M. Kierzek, Translational repression contributes greater noise to gene expression than transcriptional repression, *Biophysical Journal* 96: 372384 (2009).
- [2] J. E. M. Hornos, D. Schultz, G. C. P. Innocentini, J. Wang, A. M. Walczak, J. N. Onuchic, and P. G. Wolynes, Self-regulating gene: an exact solution. *Phys. Rev. E* 72: 51907 (2005).
- [3] J. Miekisz and P. Szymanska, work in progress.