Gene regulatory networks

Jakub Zarzycki*

* University of Warsaw, NCBR IDEAS, Poland
E-mail: jk.zarzycki@student.uw.edu.pl

Recent developments in human biology allowed us to recreate organs from stem cells, as in [1]. Stem cells themselves can be obtained from fully developed cells, which lead to Nobel prize in medicine in 2012, for the method described in the paper [3]. It is even possible to create humans cells from fully developed people, as recently seen in Nature [2]. Those developments would not be possible without a good mathematical model of the human genome. Our model extends the one proposed initially by Waddington in [4]. As it turns out the problem of predicting phenotype from the genome is an NP-complete one, and steering it in the desirable direction is even harder. The purpose of this talk is to describe the model, show exact method for finding attractors following [6], and introduce a framework for RL methods for control of boolean networks, extending the ideas of Papagiannis and Moschoyiannis in [5].

References

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