

A Fixed-Point from MAPK Cascade and a Measure for Cellular Signaling

Jian-Qin Liu (National Institute of Information and Communications Technology)

In cellular signal transduction networks, one of the well-known functions of MAPK (Mitogen-Activated Protein Kinase) cascade is to act as an amplifier for intracellular signaling processes. But, an unexpected phenomenon – a fixed-point that occurs at a four-layered MAPK cascade where a feedback is embedded – is observed by simulation [1], which shows that in theory the second messengers' signals can be kept in a constant value during their relay processes within cells. Based on Michaelis-Menten kinetics, a scheme for encoding intracellular signals – phosphoproteins and GTPases – is proposed [2, 3]. For an individual phosphorylation pathway regulated by a kinase, the measure of mutual information is estimated by encoding the concentration of phosphoproteins, and the maximum value of mutual information (i.e., channel capacity) – 1 bit/per pathway – is obtained [4]. Consequently, Michaelis-Menten kinetics can be the dynamics basis of information-theoretical study on the cell communications although the simulation of signal transduction network reported here is still empirical. However, Katori-Masuda-Aihara's method [5] has been proven to be successful for neural codes and the network dynamics with gap junctions. The next step of the computational study on cellular signal transduction networks will be to formulate a model to quantify the dynamics of cellular signal transduction networks based on mutual information measures [5].

References:

- [1] J.-Q. Liu, On Quantitative Aspect of an Information Processing Model Inspired by Signaling Pathways in Cells: An Empirical Study, IPSJ MPS Technical Report, 2007 (43) May 2007, 21-24.
- [2] J.-Q. Liu, Self-Configuration of Dynamical Networks Based on an Information Theoretic Criterion, IPSJ MPS Technical Report, 2008 (41) May 2008, 15-18.
- [3] J.-Q. Liu, K. Shimohara, Biomolecular Computation for Bionanotechnology, Boston&London: Artech House, 2007.
- [4] J.-Q. Liu, K. Leibnitz, Modeling the Dynamics of Cellular Signaling for Communication Networks, a chapter in: Bio-inspired Computing and Communication Networks, Y. Xiao, F. Hu (Eds.), Auerbach Publications, CRC Press, in press, 2008.
- [5] Y. Katori, N. Masuda, K.Aihara, Dynamic Switching of Neural Codes in Networks with Gap Functions, Neural Networks, 19 (2006), 1463-1466.