

Hypothesis of biological networks as a system of linked oscillators.

Very briefly

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Many years ago systems dynamics went to quite understandable results that was about every network containing negative feedback loop have *possibility* of oscillatory behavior existence (Cheong and Levchenko, 2010). It means that when negative feedback loop is strong enough it creates conditions for oscillatory regime occurrence in this isolated loop in a network. If several loops are close to each other it can be supposed that conditions for linked oscillations are created. Of course positive feedback also leads to oscillator behavior if input is discrete. So it is obvious that such networks can be represented as a system of linked oscillators.

Experimental data about gene expression and signaling cascades dynamics partially confirm this model. Signaling cascades show periodic dynamics of its members activity (Paszek et al., 2010, Lee and Covert, 2010). Dynamics of gene expression induced by such cascades is also periodic. Recent data show periodic expression of thousands of genes. In response to TGF- α induced MAPK cascade over 5000 genes are expressed periodically (Sun et al., 2008). These are located in different parts of network. The robust periodic pattern of more than 3000 genes in yeast was also demonstrated (Slavov N et al, 2011).

So we can conclude that oscillations are uniform in network. Taking into account large number of genes it is quite possible that almost all of these genes are connected between each other. Involving the uniform presence of negative (and positive) feedbacks we obtain negative (and positive) feedback loops connected between each other. That is the way we can consider such gene, metabolic and signaling networks as a system of linked oscillators.

If described model is true then every negative feedback loop (cycle) could be a kind of local clock. Periods of oscillations are separately discussed. All cycles connected with each other create some global clock in cell. Possible consequence of this model is that some diseases can be caused by local clock disruption because of mutations and therefore make mistakes in global clock work. The sufficient difference between not-oscillator and oscillator models is that "lateral" signal transduction between different cascades, gene and metabolite networks motifs in such systems must be faster.

Few years ago I thought about some confirmation of very hypothetical point of view presented here. Now it seems to be real to confirm it at least partially.

References:

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* Alexander Belostotsky (2011) Conception of biological networks at the molecular level as orchestrated systems of oscillators representing interconnected modular molecular clocks, Journal of Metabolomics and Systems Biology, 2(2):15-19

*This is a very brief paper about hypothesis in which the hypothesis is described a little bit more deeply.