DYNAMICAL SYSTEMS MODELING GENE NETWORKS

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We consider systems of ordinary differential equations that appear in mathematical models of gene networks and neuronal networks. These systems in a general form are

$$\begin{aligned} x_1' &= \frac{1}{1 + e^{-\mu_1(w_{11}x_1 + w_{12}x_2 + \dots + w_{1n}x_n - \theta_1)}} - v_1 x_1, \\ x_2' &= \frac{1}{1 + e^{-\mu_2(w_{21}x_1 + w_{22}x_2 + \dots + w_{2n}x_n - \theta_2)}} - v_2 x_2, \\ \dots \\ x_n' &= \frac{1}{1 + e^{-\mu_n(w_{n1}x_1 + w_{n2}x_2 + \dots + w_{nn}x_n - \theta_n)}} - v_n x_n, \end{aligned}$$
(1)

where $x_i(t)$ (in the case of genetic networks) are interpreted as expressions of protein by the *i*-th gene. Collectively the reaction of the entire network is elaborated, which leads to a reaction of an organism, or a cell, or a tissue, to current conditions. Mathematically, the main object of the study is the evolution of the vector $X(t) = (x_1(t), ..., x_n(t))$, which is heavily dependent on the attractors in the phase space. The combination of analytical and computational tools allow us to get description of possible attractors, which are dependent on the parameters of the system (1). An important role of the matrix $W = \{w_{ij}\}$ is discussed. This matrix describes the relations (like activation, inhibition, etc.) between network elements.

This is a joint work with Valentine Sengileyev from Daugavpils University.

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