

Uniqueness and stability of a cycle in the Elowitz–Leibler type dynamical system

Golubyatnikov V.^{1,2*}, Minushkina L.¹

¹ Sobolev Institute of Mathematics, SB RAS, Novosibirsk, Russia

² Novosibirsk State University, Novosibirsk, Russia

* Vladimir.golubyatnikov1@fulbrightmail.org

Key words: circular gene network, positive feedbacks, negative feedbacks, stable cycle

We consider 6D block-linear dynamical system of Elowitz–Leibler type:

$$\begin{aligned} dx_1/dt &= k_1(L_1(y_3) - x_1); \quad dy_1/dt = d_1(\Gamma_1(x_1) - y_1); \quad dx_2/dt = k_2(L_2(y_1) - x_2); \\ dy_2/dt &= d_2(\Gamma_2(x_2) - y_2); \quad dx_3/dt = k_3(L_3(y_2) - x_3); \quad dy_3/dt = d_3(\Gamma_3(x_3) - y_3). \end{aligned} \quad (1)$$

This dynamical system simulates functioning of circular gene network described in [1]. The decreasing step-functions L_i describe negative feedbacks, increasing step-functions Γ_j correspond to positive feedbacks in the gene network; $j = 1, 2, 3$. We have constructed in [2] an invariant toric domain W_1 in the phase portrait of the system (1) and we have shown there that this domain contains at least one cycle of this system. Now, our main result is:

Theorem. If $L_j(0) = \max L_j > 1$, and $\max \Gamma_j > 1$, then the system (1) has exactly one cycle in the domain W_1 ; this cycle is stable.

Acknowledgements: Supported by grant FWNF-2022-009 of SB RAS.

References

1. Elowitz M.B., Leibler S. A synthetic oscillatory network of transcriptional regulators. *Nature*. 2000;403:335-338.
2. Golubyatnikov V.P., Minushkina L.S. Combinatorics and geometry of circular gene networks models. *Lett Vavilov J Genet Breed*. 2020;6(4):188-192.