ON CYCLES IN NONLINEAR GENE NETWORK MODEL

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We consider a six-dimensional dynamical system

$$\frac{dx_j}{dt} = L_j(y_{j-1}) - \Gamma_j(x_j); \quad \frac{dy_j}{dt} = G_j(x_j) - \gamma_j(y_j), \quad j = 1, 2, 3, \ j - 1 := 3 \text{ if } j = 1, \tag{1}$$

simulating circular gene network called a repressilator, see [1]. In this model concentrations of mRNAs and proteins are denoted by x_j, y_j, negative feedback and positive feedback are described by smooth monotone decreasing functions L_j and by smooth monotone increasing functions G_j respectively. The process of degradation is characterized by smooth nonlinear functions Γ_j, γ_j.

In this paper we assume that the values $\Gamma_j^{-1}(L_j(0))$ and $\gamma_j^{-1}(\sup G_j)$ are defined for all j. All trajectories of this dynamical system are contained in six-dimensional parallelepiped $\mathcal{Q}^6 = \prod\limits_{j=1}^{3} [0, \Gamma_j^{-1}(L_j(0))] \times [0, \gamma_j^{-1}(\sup G_j)]$ and do not leave it as time increases. The system (1) has a unique equilibrium point $\mathcal{S}_0$ in the interior of the invariant domain $\mathcal{Q}^6$. We study trajectories of the system (1) containing in subdomain W_1 stated in [2].

The main result of this paper is Theorem 1.

Theorem 1. *If the linearization matrix of the system (1) has at least two complex conjugate eigenvalues with positive real part and does not have any pure imaginary eigenvalues in the neighbourhood of $\mathcal{S}_0$, then the system (1) have a cycle $\mathcal{C}$ in the invariant subdomain W_1.*

The cycle $\mathcal{C}$ bounds a two-dimensional invariant surface consisting of trajectories of the system (1) as it was noted in [3].

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