

Hidden attractors in models of molecular repressilator

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Motivation and Aim: Detection and description of hidden attractors in phase portraits of dynamical systems is an important problem in applications of nonlinear dynamics, see [1, 2]. This allows to predict behavior of trajectories of these systems, as it was done in [3, 4]. We study here one such system as a model of a simple molecular repressilator. Analogous systems appear in description of various biological processes, such as circadian rhythms and cell cycles in living organisms. The questions of existence and (non)uniqueness of the cycles and description of hidden attractors in these systems are quite necessary, since results of such analysis allow to predict unexpected and potentially dangerous responses of the system to fluctuations.

In this work, a phase portrait of system (1) is constructed. The conditions of compatibility of a hidden attractor and a cycle in this portrait are established.

Methods and Algorithms: We consider a non-linear dynamical system

$$\frac{dx_1}{dt} = L(x_3) - x_1, \quad \frac{dx_2}{dt} = L(x_1) - x_2, \quad \frac{dx_3}{dt} = L(x_2) - x_3, \quad (1)$$

as a model of three-components gene network. The variables $x_j(t)$, denote the concentrations of these components, here and below $j=1,2,3$. As in [3,4], monotonically decreasing function L describes negative feedbacks in the gene network. Following [5] where multistep feedbacks in gene networks were studied, we define L by

$$L(w) = 2c \text{ for } 0 \leq w < c - \varepsilon; \quad L(w) = c \text{ for } c - \varepsilon \leq w < c + \varepsilon;$$

$$L(w) = 0 \text{ for } c + \varepsilon \leq w; \quad c > \varepsilon > 0.$$

Trajectories of all points of $Q := \{0 \leq x_1 \leq 2a; 0 \leq x_2 \leq 2a; 0 \leq x_3 \leq 2a\}$ do not leave this cube as $t \rightarrow \infty$. The planes $x_j = a - \varepsilon$, $x_j = a + \varepsilon$ decompose this cube Q to 27 blocks. We describe these blocks by 3-symbols multi-indices $\{s_1 s_2 s_3\}$ as follows

$s_j = 0$ if $0 \leq x_j < c - \varepsilon$ in this block; $s_j = 1$ if $c - \varepsilon \leq x_j < c + \varepsilon$ in this block; $s_j = 2$ if $c + \varepsilon \leq x_j \leq 2c$ in this block. Analogous combinatorial description of these blocks in different cases of one-step functions L was used in [3,4,6]. It was shown in [3] that all the systems of the type (1) decompose to three independent linear differential equations in each block of similar decompositions. For example, in the block $\{111\}$ the system (1) has the form

$$\frac{dx_1}{dt} = c - x_1, \quad \frac{dx_2}{dt} = c - x_2, \quad \frac{dx_3}{dt} = c - x_3.$$

Results: The point S_0 with coordinates $x_1 = x_2 = x_3 = c$ in the block $\{111\}$ is a stable equilibrium point of the system (1). This system does not have other equilibrium points. The system (1) is symmetric with respect to cyclic permutation of the variables

$$\sigma: x_1 \rightarrow x_2 \rightarrow x_3 \rightarrow x_1.$$

Let $W \subset Q$ be the union of 12 blocks listed in the circular diagram

$$\begin{aligned} &\dots \rightarrow \{220\} \rightarrow \{210\} \rightarrow \{200\} \rightarrow \{201\} \rightarrow \{202\} \rightarrow \{102\} \rightarrow \{002\} \rightarrow \\ &\rightarrow \{012\} \rightarrow \{022\} \rightarrow \{021\} \rightarrow \{020\} \rightarrow \{120\} \rightarrow \{220\} \rightarrow \dots \end{aligned} \quad (2)$$

In contrast with Q , this union W is not an invariant domain of the system (1).

Trajectories of the point of the face $F_0 = \{120\} \cap \{220\}$ which are sufficiently far from its edge $x_3 = c - \varepsilon$ arrive eventually to the face $F_1 = \{220\} \cap \{210\}$. In the same way, trajectories of F_1 arrive to $F_2 = \{210\} \cap \{200\}$, then to $F_3 = \{200\} \cap \{201\}$, and later, step by step, to all faces F_m which separate incident blocks in the diagram (3), $m = 0, 1, \dots, 11$; $F_{12} = F_0$. The analytic representation of these trajectories implies the following

Theorem. If $c > 3\varepsilon$ then the domain W contains at least one cycle C of the system (1). This cycle travels through the blocks of the diagram (2) according to its arrows, and is symmetric with respect to the permutation σ . The system (1) does not have cycles which are not symmetric with respect to σ .

Numerical experiments carried out in the Python programming language, illustrate this theorem. The Fig. 1a and 1b show results of some numerical experiments with the system (1). On Fig. 1a, the parameters of this system satisfy the condition $c > 3\varepsilon$ of the Theorem, and here we see the cycle C , this is an example of nonlocal oscillations in the phase portrait of the system (1) since its equilibrium point S_0 is stable, see [6]. Actually, this point is a Hidden Attractor of the system (1).

On Fig. 1b this condition is not satisfied; here, the trajectories of this system are attracted eventually by the stable equilibrium point S_0 which is depicted in the centers of both Fig. 1.

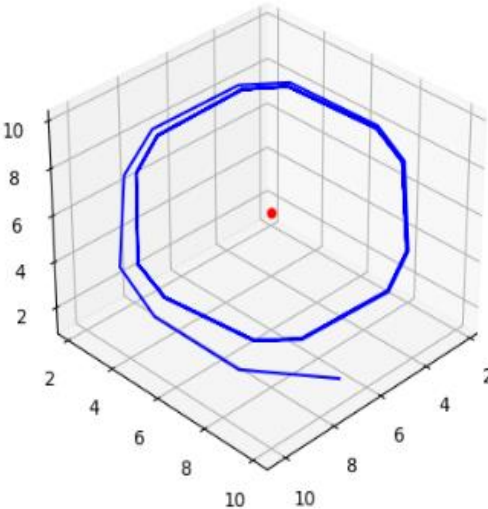


Fig 1a. Limit cycle, $c = 6$; $\varepsilon = 1.2$

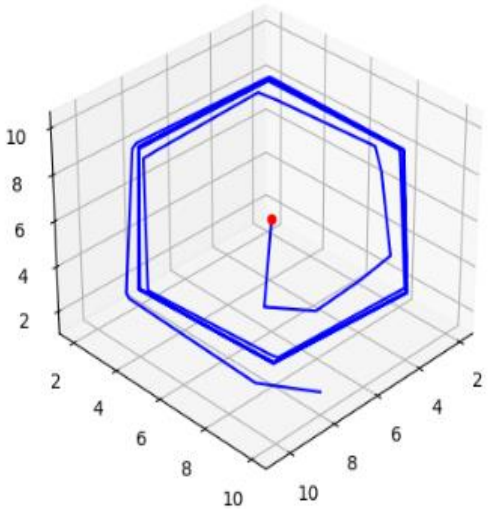


Fig 1b. No cycles, $c = 6$; $\varepsilon = 2.0001$

Conclusion: The cycle C is a typical example of nonlocal oscillations in gene network models, see [7]. In the phase portrait of the system (1) its unique equilibrium point S_0 is a hidden attractor, see [1], and the cycle C does not appear as a result of bifurcation and parameters variations.

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