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Self-similarities of periodic structures for a discrete model of a two-gene system

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ABSTRACT

We report self-similar properties of periodic structures remarkably organized in the two-parameter space for a two-gene system, described by two-dimensional symmetric map. The map consists of difference equations derived from the chemical reactions for gene expression and regulation. We characterize the system by using Lyapunov exponents and isoperiodic diagrams identifying periodic windows, denominated Arnold tongues and shrimp-shaped structures. Period-adding sequences are observed for both periodic windows. We also identify Fibonacci-type series and Golden ratio for Arnold tongues, and period multiple-of-three windows for shrimps.

1. Introduction

In the last 20 years, a considerable amount of work has been done on nonlinear systems analyzing bifurcations in two-dimensional parameter spaces [1–6]. As a result, the existence of regular orbits can be properly visualized on continuous sets of parameter spaces, generating periodic islands (windows) embedded into quasi-periodic or chaotic regions. Thus, noticeable periodic windows, such as Arnold tongues and shrimps, have been identified both for discrete-time and continuous-time systems [7–12].

In general, the periodic window distributions appear highly organized in parameter space. Recently, a striking spiral organization of shrimps has received significant attention [13–17]. The global organization of these periodic regions is composed of an infinite hierarchy of shrimps with different periods continuously connected in a spiral sequence. As another example of interesting result for periodic windows, Medeiros and co-workers have shown that weak periodic perturbations used to control chaos provoke replications of shrimps [18,19].

As is well known, nonlinear dynamics approaches have been used extensively to study different types of systems, including plasma physics [20], impact oscillators [21], dripping faucets [22], circadian rhythms [23], heart rhythms [24], and peroxidase–oxidase reactions [25], just to mention a few. In the biochemistry context, nonlinear mathematical models are generally derived from the chemical reactions, like the two-gene model proposed by Andrecut and Kauffman [26]. In this case, the chemical reactions correspond to gene expression and regulation. The dynamics are obtained from a two-dimensional map, whose discrete dynamical variables describe the evolution of the concentration levels of transcription factor proteins.

In this Letter, we provide numerical analysis in the parameter space for the two-gene system. Numerical studies for this system have shown a rich dynamical behavior with several nonlinear phenomena, such as quasi-periodic attractors, chaotic regimes, crises, and coexistence of attractors. As examples of periodic windows in two-dimensional parameter space, we identify Arnold tongues and shrimps. To characterize the possible solutions (attractors) we evaluate the Lyapunov exponents. In addition, we use isoperiodic diagrams to investigate the self-similarities commonly observed in these periodic structures. Our main purpose in this study is to shed further light on the topic of periodic windows characterization.

This Letter is organized as follows. In Section 2 we present the mathematical model used to study dynamics of the two-gene system. In Section 3, we examine self-similarities associated with periodic windows identified in the two-parameter space. The last section contains our main remarks.

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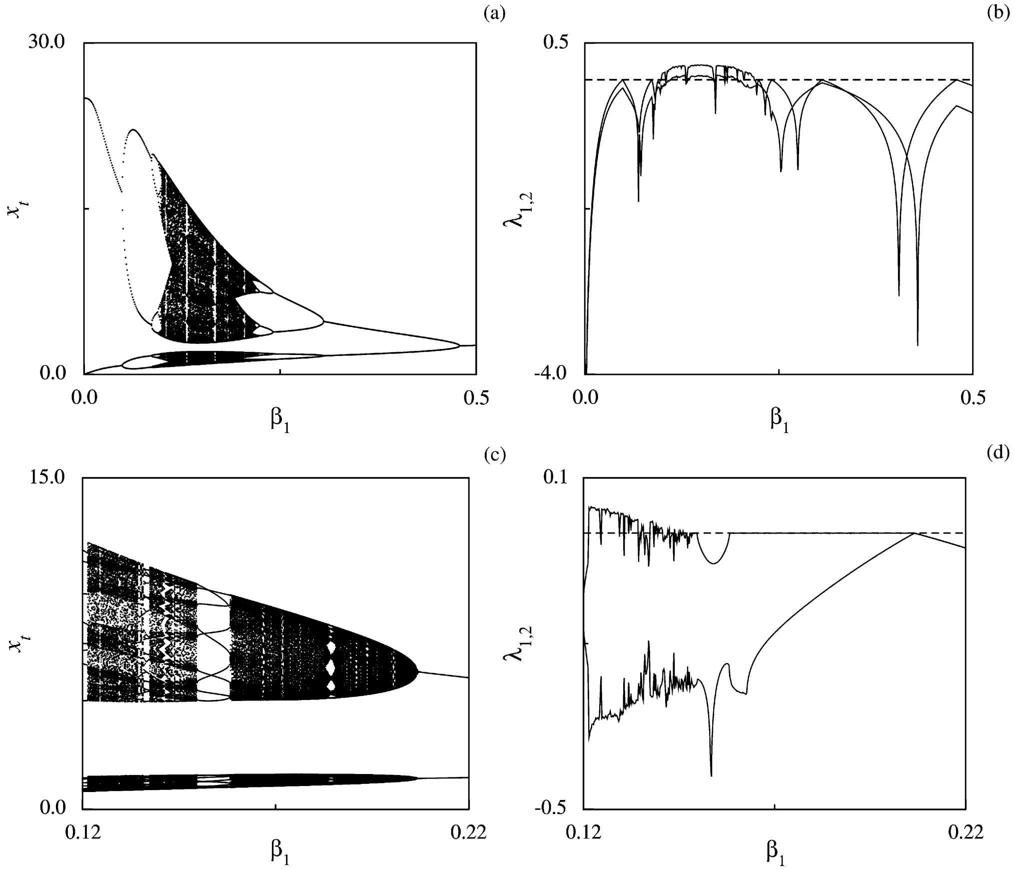

Fig. 1. Bifurcation diagram showing x_t in terms of β_1 for $\beta_2 = \beta_1$ (a) and for $\beta_2 = 0.42$ (c). The two corresponding Lyapunov exponents, (b) and (d). The remaining control parameters are fixed at $\alpha = 25.0$, $\varepsilon = 0.1$, and $n = 3$.

2. Andrecut–Kauffman map

For our numerical analysis, we consider a two-dimensional map proposed by Andrecut and Kauffman [26]. The map was used to investigate the dynamics of two-gene model for chemical reactions corresponding to gene expression and regulation. The discrete dynamical variables, denoted by x_t and y_t, describe the evolutions of the concentration levels of transcription factor proteins. The map is given by the following difference equations:

$$x_{t+1} = \frac{\alpha}{1 + (1-\varepsilon)x_t^n + \varepsilon y_t^n} + \beta_1 x_t, \tag{1}$$

$$y_{t+1} = \frac{\alpha}{1 + (1-\varepsilon)y_t^n + \varepsilon x_t^n} + \beta_2 y_t. \tag{2}$$

As can be noted, the difference equations are obtained by coupling, with parameter ε, two single (one-dimensional) maps. For the values of the control parameters, the following ranges can be used $\alpha \in [0, 100]$, $\beta_1 \in [0, 1)$, $\beta_2 \in [0, 1)$, $n = 1, 2, 3, 4$, and $\varepsilon \in [0, 1]$.

In order to calculate the Lyapunov exponents [27], we evaluate $\lambda_i = \lim_{t\to\infty}(1/t)\ln|\Lambda_i(t)|$ $(i = 1, 2)$, where $\Lambda_i(t)$ are the eigenvalues of the matrix $A = J_1 \cdot J_2, \ldots, J_t$, with the Jacobian matrix, J_t, computed at time t.

3. Arnold tongues and shrimp-shaped structures

The dynamics was investigated using bifurcation diagrams, Lyapunov exponents, parameter plane diagrams, and isoperiodic diagrams. We consider the control parameters β_1 and β_2 for our simulations. The remaining parameters are fixed at $\alpha = 25.0$, $\varepsilon = 0.1$, and $n = 3$. Furthermore, the simulations are performed with the initial conditions fixed at $(x_0, y_0) = (0.5, 0.5)$.

First of all, to obtain a representative example of the kind of dynamics could be generated by the two-gene model, we use bifurcation diagrams identifying the possible solutions (attractors) in terms of one-dimensional parameter with fixed initial conditions. This diagram is constructed varying one control parameter. For each value of the parameter, we neglect a sufficiently large number of iterations to eliminate the transient behavior, then we plot the subsequent points of the dynamical variable x_t. To characterize the nature of the attractors obtained, we evaluate the Lyapunov exponents. The positive largest Lyapunov exponent (LLE) for maps indicates a chaotic attractor, the negative a periodic, and the zero a quasi-periodic (or a bifurcation point).

In Fig. 1(a) for $\beta_1 = \beta_2$, we plot a bifurcation diagram showing the asymptotic values of x_t as a function of β_1. The corresponding Lyapunov exponents are shown in Fig. 1(b). In this case, as can be seen, the bifurcation diagram is composed of a period-bubbling scenario with chaotic region (positive LLE) interrupted by periodic windows (negative LLE). One of the Lyapunov exponents is zero at the bifurcation points. In addition, there are solutions with two positive Lyapunov exponents for a small range of the parameter. (This kind of solution is commonly observed for systems composed of one-dimensional coupled maps.) For the parameter value $\beta_2 = 0.42$, we also identify in terms of β_1, as shown in Figs. 1(c)–(d), chaotic and quasi-periodic (zero LLE) attractors also interrupted by periodic windows (negative LLE).

As a result of the preliminary numerical analysis, we verify here that the two-gene model presents a plethora of complex dynamical phenomena. In order to obtain a better understanding of the rich dynamics involved and associated with periodic windows,