

Oscillations in dynamic models of the Wilson-Cowan type system

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Abstract: A review of samples of oscillations in a system of ordinary differential equations that arise in mathematical models of complex networks is provided. Starting from the low-dimensional systems, we go up in the sense of system dimensionality, commenting on various patterns that appear. We overlook examples of relatively large systems (with dimensionality up to 13 equations) that describe leukemia treatment and cellular aging. Visualizations and examples are supplied. The methods used are of geometrical and computational nature, revealing phase space structures and specifics.

Key-Words: Dynamical systems, gene networks, regulatory matrix, attractors, periodic solutions, phase space, cellular ageing

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1 Introduction

Oscillatory behavior is a hallmark of biological systems, manifesting across scales—from circadian rhythms and calcium signaling to gene expression cycles and neural activity. These rhythmic patterns are often emergent properties of underlying dynamical network models, where feedback loops, time delays, and nonlinear interactions give rise to sustained oscillations. Understanding the mechanisms that generate and regulate these oscillations is critical for deciphering cellular decision-making, developmental timing, and pathological states. Mathematical modeling has played a pivotal role in revealing how network topology and parameter regimes influence oscillatory dynamics. Classical models such as the Goodwin oscillator and the repressilator have demonstrated how negative feedback and time delays can induce limit cycles. More recent approaches incorporate bifurcation analysis, stochastic perturbations, and chaos theory to explore transitions between steady states, periodic behavior, and complex attractors. This communication synthesizes current advances in modeling oscillations within biological networks, with emphasis on gene regulatory circuits. We highlight analytical techniques,

including phase plane analysis and numerical continuation, which enables a satisfactory characterization of oscillatory regimes.

2 Wilson - Cowan system

The developers of the Wilson-Cowan model are Hugh R. Wilson, a theoretical chemist turned neuroscientist, and Jack D. Cowan, a mathematical biologist at the University of Chicago. In 1972, the basic mean-field equations for excitatory and inhibitory neural populations were introduced, [1]. In 1973, the model was extended to include spatial dependence and pattern formation, [2]. Mathematically, it became a system of integro-differential equations to reflect how the activity at a point depends on inputs from neighboring regions. Further expansion of this model has led to the symmetric system

$$\begin{cases} x_1' = \frac{1}{1 + e^{-\mu_1 (w_{11}x_1 + \dots + w_{1n}x_n - \theta_1)}} - x_1, \\ x_2' = \frac{1}{1 + e^{-\mu_2 (w_{21}x_1 + \dots + w_{2n}x_n - \theta_2)}} - x_2, \\ \dots \\ x_n' = \frac{1}{1 + e^{-\mu_n (w_{n1}x_1 + \dots + w_{nn}x_n - \theta_n)}} - x_n \end{cases} \quad (1)$$

which was believed to model a gene regulatory network. The unknown variables $x_i(t)$ stand

for the level of expression of proteins by the i -th gene. In some models, there are additional factors such as stress. Multiple parameters (μ_i , θ_i) describe the individual properties of each gene. The matrix

$$W = \begin{pmatrix} w_{11} & w_{12} & \dots & w_{1n} \\ w_{21} & w_{22} & \dots & w_{2n} \\ \dots & \dots & \dots & \dots \\ w_{n1} & w_{n2} & \dots & w_{nn} \end{pmatrix}. \quad (2)$$

is used to describe the interrelations in a modeled network. The typical forms of interactions are activation, inhibition, and a mix of both. The latter produces periodic solutions of attracting type that can be seen in a picture when considering the 2-dimensional (2D in short) and 3D systems.

The system (1) is quasi-linear with a nonlinearity represented by the sigmoidal logistic function $f(z) = 1/(1 + \exp(-\mu z))$. The linear part, excluding the nonlinear one, corresponds to a network without interaction between its elements, resulting in an exponential decay of the unknowns $x(t)$. These functions stand for the expression of proteins by each gene. Each gene may influence any other one, and the entry w_{ij} of the matrix (2) has the following meaning: positive w_{ij} means activation of x_i by x_j , negative w_{ij} means inhibition, and a zero value means no relation. The modulus of w_{ij} refers to the intensity of the influence. To a great extent, this is also true for the networks theory. Having this in mind, look at the system of ODE

$$\begin{cases} x'_1 = f_1(x_1, \dots, x_n) - x_1, \\ x'_2 = f_2(x_1, \dots, x_n) - x_2, \\ \dots \dots \dots \\ x'_n = f_n(x_1, \dots, x_n) - x_n. \end{cases} \quad (3)$$

Suppose that f_i are sigmoidal functions that monotonically increase from 0 to 1. Assume that generally nonlinear functions f_i are for the description of the relations between elements of a network. These elements have the characteristic x_i , which is dependent on the argument t , interpreted as time. Solutions of the system (3) are meant as smooth functions $x_i(t)$, satisfying the equations in (3). The specific structure of the system (3) can be explained in the following way. It is assumed that elements of a network interrelate generally in a nonlinear way and the x_i -th element is affected by the total effect of the remaining elements. To be realistic, this total effect is bounded. The second linear term $-x_i$ means the degradation of the i -th gene expression product; w_{ij} —the

connection weight or strength of control of gene j on gene i . Positive values of w_{ij} signify activating influences, whereas negative values denote repressing influences; θ_i —the impact of external stimuli on gene i is reflected in its ability to modulate the gene's responsiveness to activating or suppressing factors.

Definition 1. An invariant region in the phase space is the region that cannot be left by a trajectory of the system (3).

Proposition 1. The cube $Q_n = \{x \in R^n | 0 < x_i < 1, \quad i = 1, \dots, n\}$ is an invariant set.

Consider the system of equations

$$\begin{cases} 0 = f_1(x_1, \dots, x_n) - x_1, \\ 0 = f_2(x_1, \dots, x_n) - x_2, \\ \dots \dots \dots \\ 0 = f_n(x_1, \dots, x_n) - x_n. \end{cases} \quad (4)$$

Proposition 2. The system (4) has a solution in the invariant set Q_n .

Sketch of the proof. On the border of the invariant set Q_n vector field $\Phi = \{f_i(x_1, x_2, \dots, x_n) - x_i, \quad i = 1 \dots, n\}$ is directed inward. Therefore, the continuous map Φ maps the topological ball Q_n into itself. So the map Φ has a fixed point in Q_n .

Definition 2. A set of points defined by the relation $f_i(x_1, x_2, \dots, x_n) - x_i = 0$ is called an i -th nullcline of the system (3).

Definition 3. Cross points of all nullclines are called critical points of the system (3).

Corollary of Proposition 2. System (3) has a critical point in an invariant set Q_n .

Proposition 3. All critical points of system (3) are in the invariant set Q_n .

Proof. Any critical point belongs to all nullclines. Any nullcline lies in the strip $\{0 < x_i < 1, \quad i = 1, \dots, n\}$ for some $i = 1, \dots, n$. These strips intersect by the set Q_n .

Remark. System (3) has at least one critical point but can have multiple critical points.

Critical points are subject to analysis. The standard analysis of a critical point $x^* = (x_1^*, \dots, x_n^*)$ involves the following procedure.

Standard analysis. The goal is to obtain a vector $\lambda = (\lambda_1, \dots, \lambda_n)$, that consists of characteristic numbers. The characteristic numbers, with some degenerate cases, provide information on the type of a critical point.

3 Equilibria

What are nullclines and how do they affect the behavior of trajectories? Nullclines of the system (3) are continuous hypersurfaces defined by the relations (4). They can be visualized using appropriate software for 2D and 3D systems. For higher dimensional systems, the projections of nullclines onto the lower order subspaces are possible. To imagine how they look for higher dimensions is problematic. This is beyond the human senses, but quite the usual thing for theoretical mathematics. Look at the system

$$\begin{cases} x_1' = \frac{1}{1 + e^{-\mu_1(w_{11}x_1 + w_{12}x_2 - \theta_1)}} - x_1, \\ x_2' = \frac{1}{1 + e^{-\mu_2(w_{21}x_1 + w_{22}x_2 - \theta_2)}} - x_2. \end{cases} \quad (5)$$

This system uses the sigmoidal function $f(z) = 1/(1 + e^{-\mu(z-\theta)})$ which has the graph in Figure 1.

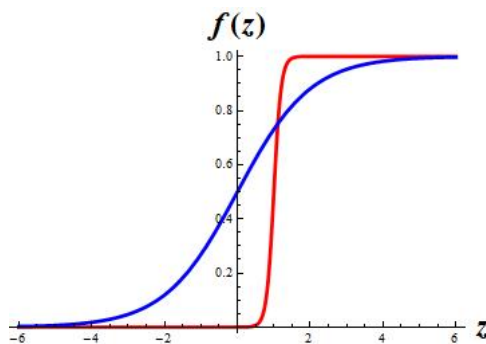


Fig. 1: Sigmoidal functions: $f(z) = 1/(1 + e^{-\mu(z-\theta)})$, $\mu = 1$, $\theta = 0$ for blue; $\mu = 10$, $\theta = 1$ for red.

Source: created by the authors.

What is the impact of parameters in the $f(z)$ function. The graph stretches in the strip between 0 and 1. Increasing the parameter μ results in the steeper middle segment of the graph. This segment becomes almost vertical as μ tends to $+\infty$. Changing the parameter θ results in shifting the graph in the horizontal direction. In a model function f is used depending on multiple variables x_i . Moreover the combination of variables may be transformed in many ways. The system (5) has the nullclines

$$\begin{cases} 0 = \frac{1}{1 + e^{-\mu_1(w_{11}x_1 + w_{12}x_2 - \theta_1)}} - x_1, \\ 0 = \frac{1}{1 + e^{-\mu_2(w_{21}x_1 + w_{22}x_2 - \theta_2)}} - x_2. \end{cases} \quad (6)$$

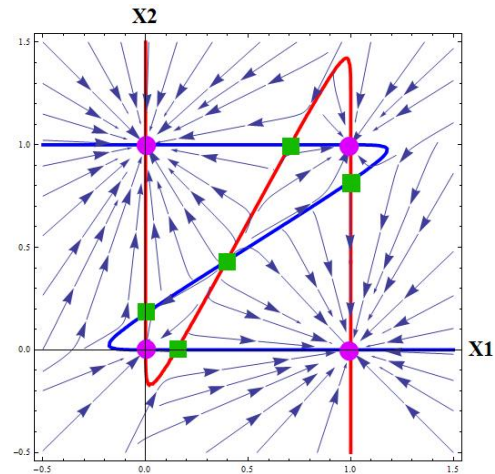


Fig. 2: The nullclines (6): $w_{11} = w_{22} = 8$, $w_{12} = w_{21} = -4$, $\mu_1 = \mu_2 = 6$, $\theta_1 = \theta_2 = 1.5$. Source: created by the authors.

What are critical points, and how many they are. The critical points are points of intersection of nullclines. How many critical points are possible for the 2D system? Figure 2 shows the nullclines for some particular choice of parameters. Since the nullclines are intersected at 9 points, and additional intersections are not possible, we are led to the conclusion that the maximal number of critical points is 9. Of them, four critical points are attractive, and the remaining are saddle points. Generally, the number of critical points depends on the dimensionality of a system, but is finite.

Looking for attractors, it is natural to address critical points first. Critical points are located at the intersection of nullclines. For 2D systems, the maximal number of critical points is nine. The configuration of the nullclines is two intersecting figures Z, one rotated by 90 degrees. The number of stable nodes is four.

4 Periodic attractors and closed trajectories

Periodic attractors may exist in n -dimensional systems. For dimension 2, there is the example:

$$\begin{cases} x_1' = \frac{1}{1 + e^{-4(x_1 + 2x_2 - 1.5)}} - x_1, \\ x_2' = \frac{1}{1 + e^{-4(-2x_1 + x_2 + 0.5)}} - x_2. \end{cases} \quad (7)$$

The respective periodic solution is a stable limit cycle.

The three-dimensional systems (8)

$$\begin{cases} x_1' = \frac{1}{1+\exp[-\mu_1(w_{11}x_1+w_{12}x_2+w_{13}x_3-\theta_1)]} - x_1 \\ x_2' = \frac{1}{1+\exp[-\mu_2(w_{21}x_1+w_{22}x_2+w_{23}x_3-\theta_2)]} - x_2 \\ x_3' = \frac{1}{1+\exp[-\mu_3(w_{31}x_1+w_{32}x_2+w_{33}x_3-\theta_3)]} - x_3 \end{cases} \quad (8)$$

can have multiple periodic solutions. Consider the example:

$$\begin{cases} x_1' = \frac{1}{1+\exp[-4(x_1+2x_3-1.5)]} - x_1 \\ x_2' = \frac{1}{1+\exp[-6(x_2-0.5)]} - x_2 \\ x_3' = \frac{1}{1+\exp[-4(-2x_1+x_3+0.5)]} - x_3. \end{cases} \quad (9)$$

A set of nullclines for this system is depicted in Figure 3. The second nullcline is just a union of

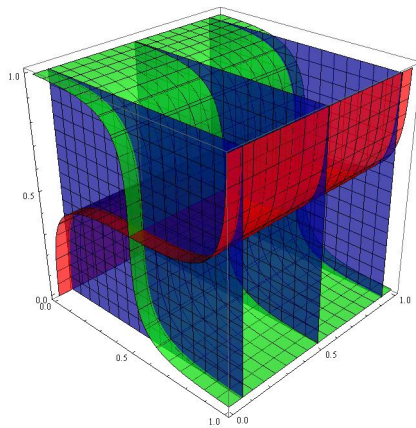


Fig. 3: The nullclines for the system (9).
Source: created by the authors.

three parallel planes.

The limit cycles generated by the first and the third equations in (9), arise in the three planes forming the second nullcline. They are shown in Figure 4. The two side closed trajectories attract trajectories from their neighborhoods, while the middle one attracts only trajectories lying in the middle plane.

5 Remarks on periodic solutions in higher order systems

An interesting case occurs when two 2D systems are concerned, which have limit cycles of different character. Imagine two limit cycles interacting in a four dimensional uncoupled system. The inserted coupling in the form of a single parameter can lead to almost chaotic behavior of the resulting 4D system.

Nullclines of the system (1) are continuous hypersurfaces defined by the relations (4). They can be visualized using appropriate software for

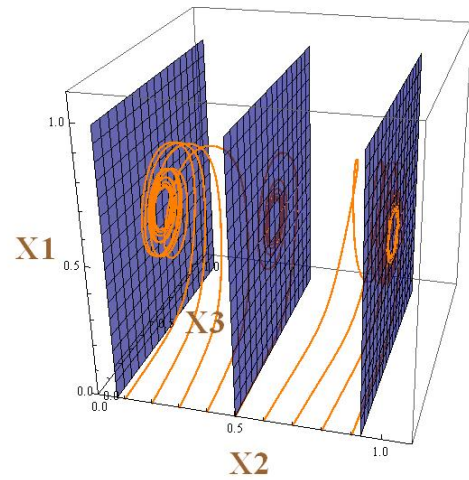


Fig. 4: The trajectories of three periodic solutions in system (9).
Source: created by the authors.

2D and 3D systems. For higher-dimensional systems, the projections of nullclines onto the lower order subspaces are possible. Visualizing their (nullclines) structure in higher dimensions is problematic. This is beyond the human senses, but quite the usual thing for theoretical mathematics.

Periodic solutions for any dimension system can be constructed by merging different matrices W in one large matrix, posing small matrices along the main diagonal. The system is then uncoupled, composed of smaller dimension matrices. Often, making a large system coupled by adding elements outside the main diagonal makes the system chaotic.

6 4D system

The easiest way to see an attractor in a 4D system is to take two copies of a 2D system that has an attractor and build a 4D uncoupled system of them. For instance, take the system (7) and construct the 4D system

$$\begin{cases} x_1' = \frac{1}{1 + e^{-4(x_1+2x_2-1.5)}} - x_1, \\ x_2' = \frac{1}{1 + e^{-4(-2x_1+x_2+0.5)}} - x_2, \\ x_3' = \frac{1}{1 + e^{-4(x_3+2x_4-1.5)}} - x_3, \\ x_4' = \frac{1}{1 + e^{-4(-2x_3+x_4+0.5)}} - x_4. \end{cases} \quad (10)$$

This is an uncoupled system. Since both 2D internal systems have their own limit cycles, the

existence of an attractor for the system (10) in the 4D phase space is evident. The attractor is not directly observable, but projections to 2D and/or 3D subspaces are. By construction of this system, the projections onto (x_1, x_2) and (x_3, x_4) planes are identical (the 2D limit cycle for both systems). The projections onto the 3D subspaces (x_1, x_2, x_3) and (x_2, x_3, x_4) subspaces are depicted in Figure 5 and Figure 6.

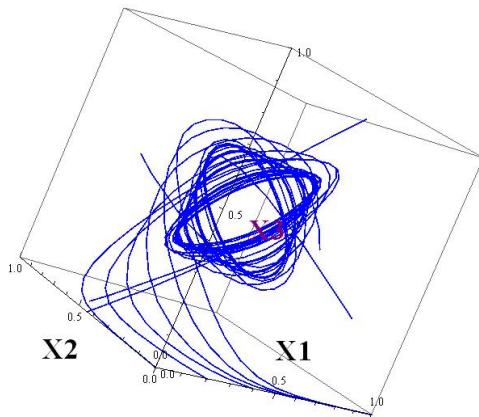


Fig. 5: The projection of the 4D attractor in system (10) onto the (x_1, x_2, x_3) -space.
Source: created by the authors.

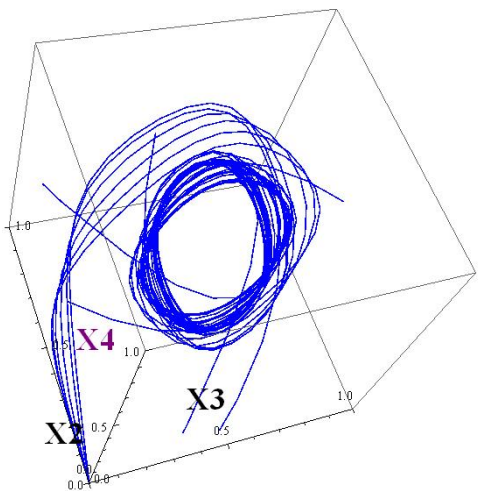


Fig. 6: The projection of the 4D attractor in system (10) onto the (x_2, x_3, x_4) -space.
Source: created by the authors.

7 High-dimensional systems in existing models

High-dimensional systems can be used to see which type oscillations can occur in a system, and how these types change following the changes in the matrix W .

7.1 Realistic model

Consider two systems that appear in the works, [3], [4], [5]. In the first one, leukemia treatment is considered using the model involving a 3D system of GRN type. The main concern was to interpret the phase-space points as the current states of a network. The disease was treated as tending a trajectory in a phase space to a wrong attractor. To improve, the interception of a trajectory was considered by changing adjustable parameters. The system in the article, [3], has 60 dimensions. It is possible to extract a single segment and consider it as a subsystem. The standard software (Wolfram Mathematica) can solve the system of at least 13 equations. The graphs of all components of a solution are available, as are projections of multi-dimensional phase space onto lower-dimensional subspaces. In this way, attracting points in a phase space can be detected.

The second system, [5], aims to investigate the mechanism of cellular aging in a theoretical model using the framework of Waddington's epigenetic landscape, [6]. The authors in [5], construct an aging gene regulatory network (GRN) consisting of the core cell cycle regulatory genes (including p53). A model parameter (activation rate) is used as a measure of the accumulation of DNA damage. A conceptual model was obtained to capture three distinct stable steady states (or attractors) corresponding to homeostasis, cell cycle arrest, and senescence or apoptosis. A computational method was applied to quantify the potential landscape, which displays: I) one homeostasis attractor for low accumulation of DNA damage; II) two attractors for cell cycle arrest and senescence (or apoptosis) in response to high accumulation of DNA damage. The authors in [5], consider the aging process as the state transitions from landscape I to landscape II. Using a system of ordinary differential equations, the authors claim the discovery of four basins of attraction: homeostasis, cell cycle arrest, senescence (or apoptosis), and cancer. Their analysis also showed that for the same perturbed network with low DNA damage, the landscape displays only the homeostasis

attractor. The authors express the opinion that “the mechanistic model offers theoretical insights that can facilitate discovery of potential strategies for network medicine of age-related diseases such as cancer.”

In search of periodic solutions, let us look at the second system, which consists of 13 equations. We reproduce this system in the form (1). The respective regulatory matrix W that is defined below

$$(11) \quad \begin{pmatrix} x_1 & x_2 & x_3 & x_4 & x_5 & x_6 & x_7 & x_8 & x_9 & x_{10} & x_{11} & x_{12} & x_{13} \\ x_1 & a & b & a & 0 & 0 & 0 & 0 & 0 & 0 & a & 0 & a \\ x_2 & a & 0 & a & b & 0 & 0 & a & 0 & 0 & 0 & 0 & b \\ x_3 & a & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ x_4 & 0 & 0 & b & a & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ x_5 & a & 0 & 0 & 0 & 0 & 0 & b & 0 & 0 & 0 & 0 & 0 \\ x_6 & a & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ x_7 & 0 & 0 & 0 & 0 & 0 & b & 0 & 0 & 0 & 0 & 0 & 0 \\ x_8 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ x_9 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & a & a & b & 0 & 0 \\ x_{10} & 0 & 0 & 0 & 0 & a & 0 & 0 & 0 & 0 & b & b & 0 \\ x_{11} & 0 & 0 & 0 & 0 & b & 0 & 0 & 0 & a & 0 & 0 & 0 \\ x_{12} & 0 & 0 & 0 & 0 & b & 0 & 0 & a & 0 & 0 & 0 & 0 \\ x_{13} & 0 & 0 & 0 & 0 & 0 & 0 & a & 0 & 0 & 0 & 0 & 0 \end{pmatrix},$$

is constructed following the scheme of relations between genes proposed in [5]. The different modes of behavior of GRN can be examined by modifying the elements in the matrix (11) and performing a computational analysis of the system of 13 equations presented in the form (1). In the system (1), the logistic sigmoidal function was used. In the above-mentioned examples, [3], [5], the Hill's sigmoidal function was used, where the activation is represented by the function $f(z) = \frac{z^\mu}{\theta^\mu + z^\mu}$. The inhibition is represented by a similar but different behavior function $\phi(z) = \frac{\theta^\mu}{\theta^\mu + z^\mu}$. The elements $a = 10$ and $b = -0.05$ mean activation and inhibition correspondingly. The values are taken from [5]. Other parameters are $\mu = 4$, $\theta = 0.5$. A solution of the system (1) with the initial data $(0.10 + i 0.4)$, $i = 0, \dots, 12$, was calculated and visualized in Figure 7, Figure 8, Figure 9 and Figure 10. This solution evidently tends to an attracting critical point in a 13-dimensional phase space.

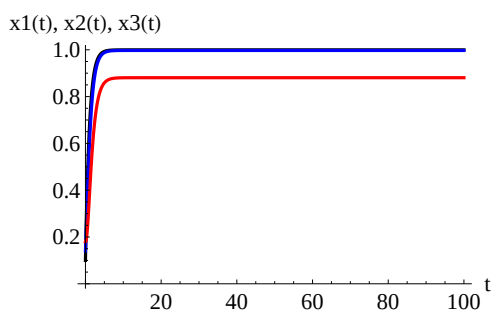


Fig. 7: $x_1(t), x_2(t), x_3(t)$
Source: created by the authors

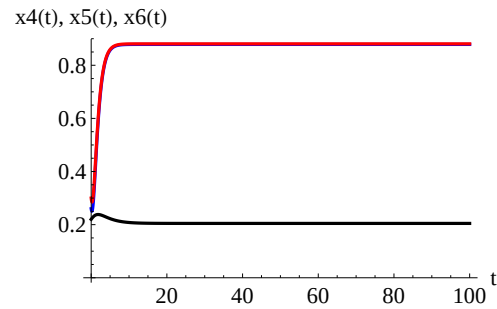


Fig. 8: $x_4(t), x_5(t), x_6(t)$
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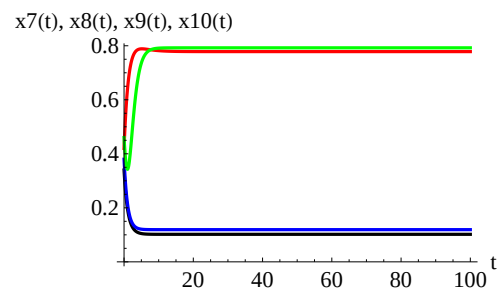


Fig. 9: $x_7(t), x_8(t), x_9(t), x_{10}(t)$
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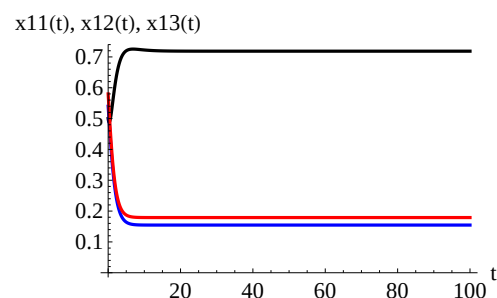


Fig. 10: $x_{11}(t), x_{12}(t), x_{13}(t)$
Source: created by the authors

In search of periodic solutions, change the interrelation matrix (11) by adding five units in the right lower corner. The resulting matrix is

$$\begin{pmatrix} & x_1 & x_2 & x_3 & x_4 & x_5 & x_6 & x_7 & x_8 & x_9 & x_{10} & x_{11} & x_{12} & x_{13} \\ x_1 & a & b & a & 0 & 0 & 0 & 0 & 0 & 0 & 0 & a & 0 & a \\ x_2 & a & 0 & a & b & 0 & 0 & a & 0 & 0 & 0 & 0 & 0 & b \\ x_3 & a & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ x_4 & 0 & 0 & b & a & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ x_5 & a & 0 & 0 & 0 & 0 & 0 & b & 0 & 0 & 0 & 0 & 0 & 0 \\ x_6 & a & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ x_7 & 0 & 0 & 0 & 0 & 0 & b & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ x_8 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\ x_9 & 0 & 0 & 0 & 0 & 0 & 0 & 0 & a & a & b & 0 & 0 & 0 \\ x_{10} & 0 & 0 & 0 & 0 & a & 0 & 0 & 0 & 0 & b & 0 & b & -1 \\ x_{11} & 0 & 0 & 0 & 0 & b & 0 & 0 & 0 & a & 0 & 1 & 1 & 0 \\ x_{12} & 0 & 0 & 0 & 0 & b & 0 & 0 & a & 0 & 0 & 0 & 0 & -1 \\ x_{13} & 0 & 0 & 0 & 0 & 0 & 0 & a & 0 & 0 & 0 & 1 & 0 & 0 \end{pmatrix} \quad (12)$$

Set θ_i to the half of the sum of elements in the i -th row of the matrix, and do not change the parameters a, b, μ and the initial values for x_i . Calculate the new solution of the system (1) where the regulatory matrix is given in (12). The components of the resulting 13-dimensional periodic solution are shown in Figure 11, Figure 12, Figure 13 and Figure 14.

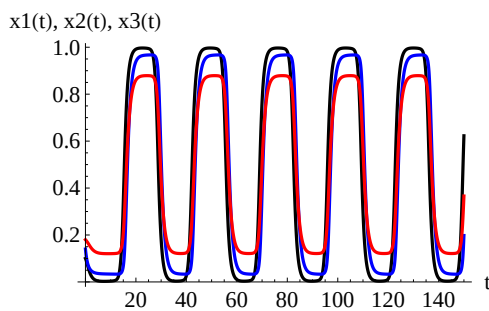


Fig. 11: $x_1(t), x_2(t), x_3(t)$
Source: created by the authors

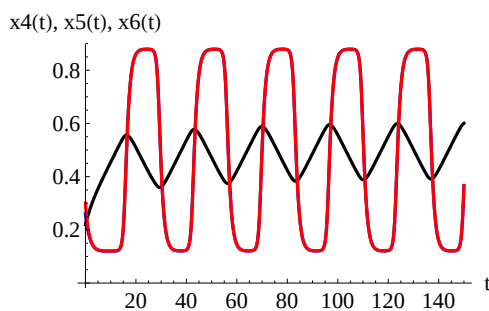


Fig. 12: $x_4(t), x_5(t), x_6(t)$
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The results of computational experiments indicate possibility of rhythmic processes in a gene networks modeled by systems of the form (1).

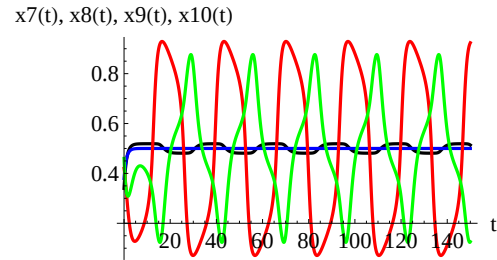


Fig. 13: $x_7(t), x_8(t), x_9(t), x_{10}(t)$
Source: created by the authors

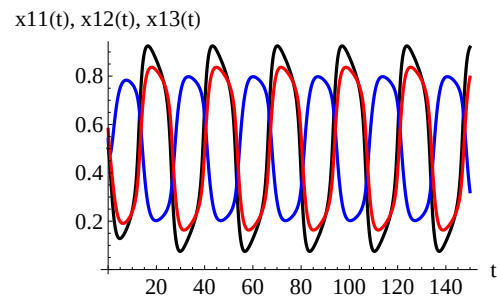


Fig. 14: $x_{11}(t), x_{12}(t), x_{13}(t)$
Source: created by the authors

8 Conclusion

The system (1) is interesting both as a sufficiently complex mathematical object and as a testing ground for the effective application of computational algorithms. Research in the direction of high-dimensional systems of differential equations is very promising. Understanding the structure of multidimensional phase spaces promises progress in other areas as well, not necessarily related to biology. Additional literature on related issues can be found in the following references, [3], [4], [5], [7], [8], [9], [10], [11]. The dynamics and behavior of biological objects associated with the model under consideration remain at the core of biomathematics. Further progress in solving complex problems of genetic and neural theory using mathematical methods remains a priority task for the theory of dynamical systems.

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