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DISCRETE DYNAMICAL MODELING OF SYSTEM CHARACTERISTICS OF A TURTLE'S WALK IN ORDINARY SITUATIONS AND AFTER SLIGHT STRESS

In the paper a class of discrete dynamical models, based on the intra- and between-specific relationships (interactions), which adopted in biology and ecology, is suggested. The relevance of the models in the form of a convergence in probability of sample correlation coefficients is grounded. One of the introduced models, applied to the analysis of a turtle's walk under two states, allowed to reveal deep systemic factors of biomechanics of animal's walking.

DYNAMICAL SYSTEMS, BIOMECHANICS OF WALK, DISCRETE MODELS, SYSTEM IDENTIFICATION, INTERSPECIFIC INTERACTIONS

Introduction

There are concepts that describe an animal's walk as a complex process of system character, which has been known at least since the first half of 20-th century, and are used to analyze the walking characteristics of different animals from human beings to dinosaurs [1, 2, 6, 7, 8]. Beginning with reptiles, the relation between factors guaranteeing stability of an animal's body along with the motion rate in the process of motion is of very importance. Considerable difficulties arise when it is impossible to trace the entire sequence of an animal's motion during each phase. To get over these difficulties, in this paper we used a mathematical apparatus of discrete modeling and dynamic systems with feedback (DMDS), to develop with some of the authors participation [3, 4, 5], a way to obtain the sequence of phases of a cycle of system changes (system trajectory) based on the partial information, when only separate phases are known but not their sequence. The objective of this paper is to investigate the relation between the rate of motion and body stability factors, in a rather simple case, of a turtle's walk using the DMDS method.

1. Theory

In this paper, the authors suggest an approach to determine the relationships between biological objects (say, species) in the framework of some discrete dynamical model. In brief, this approach is presented in illustration [3], which we will discuss in more details.

Let a biological or ecological system be described by N components A_1, A_2, \dots, A_N . These components can have different representations, for example, they can be

express the numbers of animals or the amount of biomass of different species. We assume that components only take discrete values $1, 2, \dots, K$, i. e. K values. The value 1 means a minimum amount of a component, the value K means its maximum value, i. e. a component varies from 1 to K . Indeed, the real range of component's varying may differ from the range $[1, K]$, but for our model the only important thing is that the component varies in some quantitative scale from minimum to maximum.

The value of each of the components is observed and measured at discrete instants of time $t = 0, 1, \dots$. Thus, the values of the component A_i (i. e. i -th component) at the instants of time $t = 0, 1, \dots$ are numbers $A_i(0), A_i(1), \dots$.

The trajectory of the system is described by an infinite-right matrix

$$\begin{pmatrix} A_1(0) & A_1(1) & A_1(2) & \dots \\ A_2(0) & A_2(1) & A_2(2) & \dots \\ \vdots & \vdots & \vdots & \dots \\ A_N(0) & A_N(1) & A_N(2) & \dots \end{pmatrix}. \quad (1)$$

This trajectory, as always, includes all states of the system at the instants of time $t = 0, 1, \dots$. Hence the state of the system at the instant of time t is the vector $(A_1(t), A_2(t), \dots, A_N(t))^T$, where T means the matrix transposition. We suppose that the system is strictly determined, and its state at the instant of time t is fully determined by the state at the moment $t - 1$. According to the theory of mathematical systems [9], such a system is called a free dynamical system with discrete time, but in our paper we shall use own terminology. Since the

system has only finite number of states (namely, K^N), there exists a positive integer T , for which the conditions of periodicity hold

$$A_j(s) = A_j(s + T), \forall s \geq s_0,$$

for some integer $s_0 > 0$.

It is natural to call a number T the period of the system. Let us extract the minor

$$\begin{pmatrix} A_1(s) & A_1(s+1) & \dots & A_1(s+T-1) \\ A_2(s) & A_2(s+1) & \dots & A_2(s+T-1) \\ \vdots & \vdots & \ddots & \vdots \\ A_N(s) & A_N(s+1) & \dots & A_N(s+T-1) \end{pmatrix} \quad (2)$$

from the matrix (1) ($s \geq s_0$), which gives full description of the behavior of the system.

Let us introduce a concept of relationships between components. Let $\Omega = \{-, 0, +\}$, i. e. the set Ω consists of three elements. We determine a relationship between components A_i and A_j as an entry from the set $\Omega \times \Omega$ and denote it as $\Lambda(A_i, A_j) = (\omega_1, \omega_2)$, where $\omega_1 \in \Omega$, $\omega_2 \in \Omega$. If $\Lambda(A_i, A_j) = (\omega_1, \omega_2)$, this means of this relationship following:

1. If $\omega_1 = \{-\}$ then large values of the component A_j implies decreasing the value of the component A_i .
2. If $\omega_1 = \{0\}$ then the value of the component A_j doesn't influence the value of the component A_i .
3. If $\omega_1 = \{+\}$ then the large values of the component A_j implies increasing the value of the component A_i .

The relationship Λ is antisymmetric, i. e. if $\Lambda(A_i, A_j) = (\omega_1, \omega_2)$, then $\Lambda(A_j, A_i) = (\omega_2, \omega_1)$. It is obvious that all combinations (ω_1, ω_2) correspond to relationships (interspecific interactions) of neutralism, competition, amensalism, predation, commensalism and mutualism, widely used in ecology and biology. We assume, that each component A_j can have with itself only following relationships — $(0, 0)$, $(-, -)$ and $(+, +)$, i. e. symmetric relationships.

Assume that all relationships $\Lambda(A_j, A_i)$ between all pairs (A_j, A_i) of components A_1, A_2, \dots, A_N are fixed. Let us define for each A_j the set of components, for which A_j has the relationship (s, u) , $s, u \in \Omega$, i. e. (s, u) is some fixed relationship from the set $\Omega \times \Omega$

$$L_j(s, u) = \{A_i \mid \Omega(A_j, A_i) = (s, u)\}.$$

The sets $L_j(+, +)$, $L_j(-, -)$, $L_j(0, 0)$ can have from 0 to N entries, other sets $(L_j(\omega_1, \omega_2), \omega_1 \neq \omega_2)$ can have from 0 to $N - 1$ entries. It is convenient to express relationships by a relationships matrix. If we have N components A_1, A_2, \dots, A_N , the relationships matrix is called the following table

$$\begin{bmatrix} & A_1 & A_2 & \dots & A_N \\ A_1 & (\omega_1, \omega_1) & & & \\ A_2 & (\omega_2, \omega_1) & (\omega_2, \omega_2) & & \\ \vdots & \vdots & \vdots & \ddots & \\ A_N & (\omega_N, \omega_1) & (\omega_N, \omega_2) & \dots & (\omega_N, \omega_N) \end{bmatrix}. \quad (3)$$

The relationships above the main diagonal are omitted, since they are recovered by the relationships below the diagonal (according to the antisymmetric property).

Let $\varkappa = \{1, 2, \dots, K\}$ and $N_j(s, u)$ is the number of components in the set $L_j(s, u)$, $j = 1, 2, \dots, N$. A transition from the state $(A_1(t), A_2(t), \dots, A_n(t))^T$ to the state $(A_1(t+1), A_2(t+1), \dots, A_n(t+1))^T$ is described by N transition functions F_j . Each function defines the mapping

$$\varkappa^{N_j(+,+) + N_j(+,0) + N_j(+,-) + N_j(0,+) + N_j(0,0) + N_j(0,-)} \rightarrow \varkappa.$$

This mapping in symbolic form may be expressed by the formula

$$\begin{aligned} A_j(t+1) &= F_j(A_k(t) \in L_j(+, +), A_k(t) \in L_j(+, 0), \\ A_j(t) &\in L_k(+, -), A_k(t) \in L_j(-, +), \\ A_k(t) &\in L_j(-, 0), A_k(t) \in L_j(-, -)), j = 1, 2, \dots, N, \end{aligned} \quad (4)$$

where $A_k(t) \in L_j(+, +)$, $A_k(t) \in L_j(+, 0)$, ... are the values $A_k(t)$ of all A_k , belonging to $L_j(+, +)$, $L_j(+, 0)$, ... correspondingly.

The transition function, introduced by the above formula, is quite natural in its structure. The given component A_j is influenced only by those components, which indeed influence A_j , i. e. the components from the sets $L_j(+, \omega)$ and $L_j(-, \omega)$ for any $\omega \in W$.

Now, let us describe types of relationships, inherent to real biological and ecological systems.

The formula (4) expresses a general form of transition of the system from the state at the moment t to the moment $t + 1$. For a more detailed description of the behavior of biological or ecological system, we have to specify an explicit form of transitional functions, which express dynamical properties of the system.

We suggest two approaches to such a dynamics, which are based on concepts of biological interactions.

Let us introduce the following functions defined on the set \varkappa

$$\begin{aligned} Inc(A) &= \min\{K, A + 1\}, \\ Dec(A) &= \max\{1, A - 1\}. \end{aligned}$$

First we define a type of relationships, which takes into account the weighted sum of all $A_j(t)$ (inclusive $A_i(t)$) for calculating the value of component A_i at the instant of time $t + 1$. We call this type of relationships a weight functions' approach. Now, this is the exact definition.

For each j ($j = 1, 2, \dots, N$) we introduce a set of functions $\varphi_{j,1}^{(s,u)}(\cdot)$, $\varphi_{j,2}^{(s,u)}(\cdot)$, ..., $\varphi_{j,N_j}^{(s,u)}(\cdot)$. These are the functions of interactions of those components, where A_j has relationships (s, u) , $s \in \{+, -\}$, $u \in W$. The properties of these functions are the following:

1. The functions are defined on the discrete set \varkappa .
2. $\varphi_{j,k}^{(+,+)}(\cdot)$, $\varphi_{j,k}^{(+,0)}(\cdot)$, $\varphi_{j,k}^{(+,-)}(\cdot)$ are increasing functions.
3. $\varphi_{j,k}^{(-,+)}(\cdot)$, $\varphi_{j,k}^{(-,0)}(\cdot)$, $\varphi_{j,k}^{(-,-)}(\cdot)$ are decreasing functions.

$$4. \varphi_{j,k}^{(+,+)}(1) = \varphi_{j,k}^{(+,0)}(1) = \varphi_{j,k}^{(+,-)}(1) = \\ = \varphi_{j,k}^{(-,+)}(1) = \varphi_{j,k}^{(-,0)}(1) = \varphi_{j,k}^{(-,-)}(1) = 0.$$

Now define a set of numbers $\delta_j > 0$ ($j = 1, 2, \dots, N$) and call them thresholds of sensivity. For the system's state at the instant of time t the following value is calculated

$$d_j = \\ = \sum_{A_k \in L_j(+,+)} \varphi_{j,k}^{(+,+)}(A_k(t)) + \sum_{A_k \in L_j(+,0)} \varphi_{j,k}^{(+,0)}(A_k(t)) + \\ \sum_{A_k \in L_j(+,-)} \varphi_{j,k}^{(+,-)}(A_k(t)) + \sum_{A_k \in L_j(-,+)} \varphi_{j,k}^{(-,+)}(A_k(t)) + (5) \\ \sum_{A_k \in L_j(-,0)} \varphi_{j,k}^{(-,0)}(A_k(t)) + \sum_{A_k \in L_j(-,-)} \varphi_{j,k}^{(-,-)}(A_k(t)),$$

(it is clear that d_j depends on t , but t is omitted for short in the left side).

The value of the component A_j changes according to the value d_j by the following rules

1. if $d_j \geq \delta_j$, then $A_j(t+1) = Inc(A_j(t))$;
2. if $d_j \leq -\delta_j$, then $A_j(t+1) = Dec(A_j(t))$;
3. if $-\delta_j < d_j < \delta_j$, then $A_j(t+1) = A_j(t)$.

Now we can explain the mean of introduced transition functions. For example, the functions $\varphi_{j,k}^{(-,+)}(\cdot)$ ($k = 1, 2, \dots, N_j(-,+)$) reflects the influence upon component A_j of those components, which related with A_j by relationship $(-, +)$, i. e. the components from the set $L_j(-, +)$. The greater this influence (i. e. the greater values of $A_i(t)$ from the set $L_j(-, +)$), the less values of d_j . An influence of other components, where A_j has other relations, are "weighted" in similar way. If cumulative influence of the components, interacting with A_j and expressed by (5), exceeds the threshold value δ_j , then the value of A_j changes by unit.

From the rules for definition of transitional function one can observe, that an increment of the value of A_j is less or equal to 1 ($|A_j(t+1) - A_j(t)| \leq 1$). This means, that the rate of changes of A_j is invariable. It is possible to avoid such an unnatural restriction, for example, by introducing a dependence of the increment on $|d_j|/\delta_j$. However, in this paper we do not consider such extensions.

It is clear that the threshold δ_j influences the dynamics of the system in following way: the greater δ_j , the greater absolute value of the weighted sum d_j required for overcoming δ_j in changing the value of A_j . So, if δ_j is very large, the system becomes very inert. When

$$\delta_j > \max \left\{ \sum_{A_k \in L_j(+,+)} \varphi_{j,k}^{(+,+)}(K) + \sum_{A_k \in L_j(+,0)} \varphi_{j,k}^{(+,0)}(K) + \right. \\ \left. + \sum_{A_k \in L_j(+,-)} \varphi_{j,k}^{(+,-)}(K), - \left(\sum_{A_k \in L_j(-,+)} \varphi_{j,k}^{(-,+)}(K) + \right. \right. \\ \left. \left. + \sum_{A_k \in L_j(-,0)} \varphi_{j,k}^{(-,0)}(K) + \sum_{A_k \in L_j(-,-)} \varphi_{j,k}^{(-,-)}(K) \right) \right\},$$

the value of A_j never changes ($A_j(t) = const, t = 0, 1, \dots$). If we wish to avoid this trivial case, the value of δ_j should be not very large.

A second approach, proposed here, is based on the famous Justus von Liebig's law of limiting factors. This concept was originally applied to plant or crop growth. This approach is described in brief [3] and now we give detailed description of this approach. Our following results are based on it.

Assume, that the system of relationships between A_1, A_2, \dots, A_N is given. Let us introduce two constant matrices C and C^* of size $N \times N$. The transition functions are based on the following algorithm.

Let the system in the instant of time t has the state $(A_1(t), A_2(t), \dots, A_N(t))^T$ and A_j is an arbitrary fixed component. Let i runs from 1 to N , by u we denote any entry from the set W .

1. If for the current i the equality $\Lambda(A_j, A_i) = (-, u)$ holds, we assume

$$f_i = \begin{cases} -1, & \text{if } A_i(t) \geq c_{ji}^*, \\ 0, & \text{if } c_{ji} + 1 \leq A_j(t) \leq c_{ji}^* - 1, \\ 1, & \text{if } A_j(t) \leq c_{ji}. \end{cases}$$

Note, that no matter the specific value of u , only the influence on A_j from the side of A_i plays the role.

2. If for the current i the equality $\Lambda(A_j, A_i) = (+, u)$ holds, we assume

$$f_i = \begin{cases} -1, & \text{if } A_j(t) \leq c_{ji}, \\ 0, & \text{if } c_{ji} + 1 \leq A_j(t) \leq c_{ji}^* - 1, \\ 1, & \text{if } A_j(t) \geq c_{ji}^*. \end{cases}$$

3. If for the current i the equality $\Lambda(A_j, A_i) = (0, u)$ holds, we assume $f_i = 1$.

After the cycle termination, we obtain the sequence f_1, f_2, \dots, f_N . Then we can calculate the value $A_j(t+1)$ according to the following rule:

$$A_j(t+1) = \begin{cases} Dec(A_j(t)), & \text{if } \min_{1 \leq i \leq N} \{f_i\} = -1, \\ A_j(t), & \text{if } \min_{1 \leq i \leq N} \{f_i\} = 0, \\ Inc(A_j(t)), & \text{if } \min_{1 \leq i \leq N} \{f_i\} = 1. \end{cases} \quad (6)$$

Applying this algorithm for each $j = 1, 2, \dots, N$, we shall obtain the system's state at the instant of time $t+1$.

Now we can explain the mean of an introduced transition from t to $t+1$. E. g., stating that the given component A_j has the relationship $(+, -)$, which is the current component A_i (see algorithm). According to the mean of relation $(+, -)$, large values of A_i lead to decreasing A_j . Indeed, according to the item 1 of the algorithm, if $A_i(t) \geq c_{ji}^*$ (i. e. $A_i(t)$ is "large enough"), $f_i = -1$ and, according to (6), A_j will decrease if $A_j(t) > 1$. Other cases of this transition works analogically.

When we investigate real data, we do not observe the dynamics, described by relationships (3), by the matrix of the trajectory (1) or by its minor (2).

The result of this observation is the following table of cases

$$\tilde{M} = \begin{pmatrix} C_{11} & C_{12} & \dots & C_{1B} \\ C_{21} & C_{22} & \dots & C_{2B} \\ \vdots & \vdots & \ddots & \vdots \\ C_{N1} & C_{N2} & \dots & C_{NB} \end{pmatrix},$$

where columns correspond to cases and rows correspond to components (N components and B cases).

We propose an algorithm that reveals the system relationships of above mentioned type, on the base of transition functions F_j , $j = 1, 2, \dots, N$ and the observation table \tilde{M} .

This algorithm allows us to determine between- and intra-components relationships, which are as close as possible relationships that form matrix (2) in a certain mean. Assume, that a number K and transition functions are given. In this case, for initial will be $(A_1(0), A_2(0), \dots, A_N(0))^T \in \mathcal{X}^N$ and the given sets $L_1(u, s)$, $L_2(u, s)$, \dots , $L_N(u, s)$, $u \in \{-, 0, +\}$, $s \in \{-, 0, +\}$, which makes it possible to calculate the matrix (1) or the minor (2). Let

$$P = \begin{pmatrix} 1 & r_{12} & \dots & r_{1N} \\ r_{21} & 1 & \dots & r_{2N} \\ \vdots & \vdots & \ddots & \vdots \\ r_{N1} & r_{N2} & \dots & 1 \end{pmatrix}$$

be a Pearson correlation matrix between rows of minor (2). Now for the matrix \tilde{M} let us calculate Pearson correlation matrix of its rows

$$\tilde{P} = \begin{pmatrix} 1 & \rho_{12} & \dots & \rho_{1N} \\ \rho_{21} & 1 & \dots & \rho_{2N} \\ \vdots & \vdots & \ddots & \vdots \\ \rho_{N1} & \rho_{N2} & \dots & 1 \end{pmatrix}.$$

Let us introduce the measure of distance between correlation matrices P and \tilde{P}

$$D(P, \tilde{P}) = \sum_{j=1}^{N-1} \sum_{i=j+1}^N (r_{ij} - \rho_{ij})^2. \quad (7)$$

Consider the task of minimization $D(P, \tilde{P})$ by all possible vectors of initial states $(A_1(0), A_2(0), \dots, A_N(0))^T \in \mathcal{X}^N$ and all allowable sets $L_j(s, u)$, $s, u \in W$ for all j

$$D(P, \tilde{P}) \mapsto \min$$

by all initial states and by all allowable $L_j(s, u)$.

Now, we can explain the mean of the stated task. Suppose, that a process in some real system is described by cyclical trajectory (2). One cannot the possibility to observe the dynamic of this trajectory, i. e. a full length cycle. The observation are taken from the system at random instants of time t from s to $s + \mathcal{T} - 1$ with equal probability. When an observation is fixed, the column $(A_1(t), A_2(t), \dots, A_N(t))^T$ from (2) is attached to table of observations. In other words, the columns of table of observations \tilde{M} are obtained from (2) by an equiprobable choice of columns. The stated task means a search of

such relationships between components, that the minor (2) is to be as close as possible to the table of observations in the mean of the measure (7).

The following theorem shows, that this task is well-grounded in some mean.

If the table of observations \tilde{M} is obtained from the minor (2) by equiprobable choice of columns, then the correlation matrix of the observations table \tilde{P} converges to the correlation matrix of minor P (in probability)

$$\lim_{B \rightarrow \infty} \rho_{ij} = r_{ij}, \quad i = 1, 2, \dots, N, \quad j = 1, 2, \dots, N.$$

Proof. Since the Pearson coefficient is a pairwise characteristics (between two variables), it is enough to prove the theorem for the case $N = 2$. Let

$$\begin{pmatrix} x_{1,1} & x_{1,2} & \dots & x_{1,\mathcal{T}} \\ x_{2,1} & x_{2,2} & \dots & x_{2,\mathcal{T}} \end{pmatrix}$$

be the minor (2), where we use the notation $x_{i,j}$ instead

$A_i(j + s - 1)$ for convenience. Let $\bar{x}_i = \frac{1}{\mathcal{T}} \sum_{j=1}^{\mathcal{T}} x_{i,j}$, $i = 1, 2$, are to be the means of rows. If a sample variance of both rows is not 0, the Pearson correlation coefficient (between rows) is equal to

$$R_0 = \frac{\sum_{j=1}^{\mathcal{T}} (x_{1,j} - \bar{x}_1)(x_{2,j} - \bar{x}_2)}{\sqrt{\sum_{j=1}^{\mathcal{T}} (x_{1,j} - \bar{x}_1)^2} \sqrt{\sum_{j=1}^{\mathcal{T}} (x_{2,j} - \bar{x}_2)^2}}.$$

Now we can present the observation matrix \tilde{M} as a frequency table

$$\begin{bmatrix} x_{1,1} & x_{1,2} & \dots & x_{1,\mathcal{T}} \\ x_{2,1} & x_{2,2} & \dots & x_{2,\mathcal{T}} \\ m_1 & m_2 & \dots & m_{\mathcal{T}} \end{bmatrix},$$

where m_j is a frequency of the column $(x_{1,j}, x_{2,j})^T$, which is taken from the minor (2) and placed into the observation matrix \tilde{M} .

The means of the rows of the observation matrix \tilde{M} are

$$\bar{C}_i = \frac{1}{B} \sum_{k=1}^B C_{i,k} = \frac{1}{B} \sum_{j=1}^{\mathcal{T}} m_j x_{i,j} = \sum_{j=1}^{\mathcal{T}} \frac{m_j}{B} x_{i,j}, \quad i = 1, 2.$$

According to the Bernoulli theorem [10], $\frac{m_j}{B} \rightarrow \frac{1}{\mathcal{T}}$ (in probability, when $B \rightarrow \infty$) for all $j = 1, 2, \dots, \mathcal{T}$. From this it follows $\bar{C}_i \rightarrow \bar{x}_i$ (in probability, $B \rightarrow \infty$), $i = 1, 2$.

The Pearson correlation coefficient (between rows) of the observation matrix \tilde{M} equals

$$R_B = \frac{\sum_{k=1}^{\mathcal{T}} \frac{m_k}{B} (x_{1,k} - \bar{x}_1)(x_{2,k} - \bar{x}_2)}{\sqrt{\sum_{k=1}^{\mathcal{T}} \frac{m_k}{B} (x_{1,k} - \bar{x}_1)^2} \sqrt{\sum_{k=1}^{\mathcal{T}} \frac{m_k}{B} (x_{2,k} - \bar{x}_2)^2}}.$$

Then,

$$\lim_{B \rightarrow \infty} R_B = \frac{\lim_{B \rightarrow \infty} \frac{\sum_{k=1}^T \frac{m_k}{B} (x_{1,k} - \bar{C}_1)(x_{2,k} - \bar{C}_2)}{\sqrt{\sum_{k=1}^T \frac{m_k}{B} (x_{1,k} - \bar{C}_1)^2} \sqrt{\sum_{k=1}^T \frac{m_k}{B} (x_{2,k} - \bar{C}_2)^2}}{\lim_{B \rightarrow \infty} \frac{\sum_{k=1}^T \frac{m_k}{B} (x_{1,k} - \bar{x}_1)(x_{2,k} - \bar{x}_2)}{\sqrt{\sum_{k=1}^T \frac{m_k}{B} (x_{1,k} - \bar{x}_1)^2} \sqrt{\sum_{k=1}^T \frac{m_k}{B} (x_{2,k} - \bar{x}_2)^2}} = \frac{\sum_{k=1}^T \frac{1}{T} (x_{1,k} - \bar{x}_1)(x_{2,k} - \bar{x}_2)}{\sqrt{\sum_{k=1}^T \frac{1}{T} (x_{1,k} - \bar{x}_1)^2} \sqrt{\sum_{k=1}^T \frac{1}{T} (x_{2,k} - \bar{x}_2)^2}} = R_0$$

(The convergence holds in probability).

The theorem is proven.

This result means that if the real dynamical periodic process is described by the minor (2), we can expect that the correlation matrix of the observations table will be close to correlation matrix of real process, i. e. to the correlation matrix of the minor.

So, as mentioned above, we can consider the task (7) as the task of system identification. Initial states $(A_1(0), A_2(0), \dots, A_N(0))^T$ and sets $L_j(s, u)$ in (7) are parameters, which should be identified.

2. Results

By using digital photography, we captured separate walking phases (which by no means form a complete cycle) of a two year-old male *Emys orbicularis* along the bottom of an enameled pool located in a terrarium. In the case of using a stressor, a turtle was kept lying on its back for two minutes. Then another turtle was immediately put into the pool in a back up position (without using a stressor). Using the images, we calculated the ratio of the following distances to the length of the turtle's shell: from the tail head to the ankle of each of the four legs — the right foreleg (**rf**), the right hand leg (**rb**), the left foreleg (**lf**), the left hand leg (**lb**). We considered such a distance to reflect the degree of a leg straightening.

Using DMDS, the structures of relationships and sets of states of the four-component system were obtained for all four parameters **rf**, **rb**, **lf**, **lb** (the components of the system are the turtle's legs). The results correspond to the observations both for the stressed and non-stressed cases in the outmost degree (in the conventional sense for DMDS).

For modeling with DMDS, we used the approach based of the principles of the von Liebig law and proposed that $K = 3$ (three levels of components' values). For these two cases, the system trajectories which showed the sequence of walking phases (the cycle including different combinations of contracting and straightening of each of four legs) were constructed. On these trajectories, the system factors analyzed the body's stability for the stressed and the non-stressed turtles walk.

A marked difference between the system trajectories for each case with and without the stressor was recovered. In the case of the turtle without the stressor, the DMDS obtained the following data in the system trajectory. This is represented in the table 1.

Table 1. System trajectory for the case without stressor.

rf	3	3	3	3	2	1	1	1	2	3	3
rb	1	1	2	3	3	3	2	1	1	1	1
lf	1	1	1	1	2	2	1	1	1	1	1
lb	2	1	1	1	1	1	1	2	3	3	2
Conditional time, steps	1	2	3	4	5	6	7	8	9	10	11

The bold font highlights the sequences of monotone increase of **rf**, **rb**, **lf** and **lb** values which corresponds to apparent motion of extremities (in this paper we neglect differences in the directions of motion). This system trajectory shows that the extremities start their motion in patterns so that only one leg keeps moving, and only at the end of each phase they start to move the other one. Thus, most of the time the turtle's body has three supporting points which guarantees stability of its motion.

In the case of the turtle with the stressor, the DMDS data obtained the following data in the system trajectory. This is represented in the table 2.

Table 2: System trajectory for the case with stressor.

rf	1	2	2	1	1	1	1	2	3	3	3	2	1	1	1
rb	1	1	1	2	3	3	3	2	1	1	1	1	1	1	1
lf	1	2	3	3	3	2	1	1	1	2	2	1	1	1	1
lb	1	1	1	1	1	1	1	1	1	2	3	3	3	3	2
Conditional time, steps	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15

This system trajectory shows that in contrast to the case of a non-stressed turtle the motion of a stressed turtle has phases where two legs are simultaneously moving so there is no guarantee that the body has three supporting points to maintain stability of its motion.

The results of the DMDS allows us to put forward a working hypothesis: that even under very slight stress in the motion of a turtle there occurs a deviation from the optimal relation between factors providing motion rate, and stability to the deterioration of conditions for stable motion. This deviation can be registered by systems of remote sensing (say, by digital photography) and further analyzed by DMDS with the use of an animal's motion trajectory based on the images representing the separate phases of motion. Information about the time sequence of these phases is not required, so images representing any incomplete fragments of a motion cycle can be used. In the case with the turtle, the requirements to refine the images are not so high. The images can be obtained by digital photography from any altitude, which allows us to alter the resolution degree and recognize the position of the animal's legs at a position with respect to its body silhouette.

Discussion

One should keep in mind that DMDS is mainly the method that we used to form the working hypotheses. The working hypothesis in this paper as well as system trajectories illustrating it, might present some theoretical interest to study rather simple cases of an animals' motion and some practical interest, for example, for the development of systems of ecological monitoring based on the remote (aerospace) methods of photographing animals in nature with further computer image processing of their silhouettes. Deliberately, the important feature is possibly to use the DMDS process and analyze the arrays of incomplete information with data of fragmentary observations for separate phases of an animals' motion, in conditions when it is impossible to observe the time sequence of all motion phases (say, presence of animals' shelters, limited time of photographing etc.), but on the base of which the whole cycle of their motion can be restored.

There are well known papers on mathematical modeling in the biomechanics of animal, reptiles, dinosaurs in particular, and other fossil of animals that have incomplete information [11, 2, 6, 7, 12, 13]. In all of these cases the working hypothesis about the structure of relations between components of a modeled multi-component system is needed (in the case of dinosaurs components are parts of legs taking different but inter-related positions in the process of motion). This working hypothesis should be constructed independently from the results of numerical experiments on the given mathematical model, say, based on the data about the structure and position of the tail of a two-legged dinosaur and analogies with biomechanics of the recent animals. We speak about a structure which contains a certain set of relations from the following list of possible pairs of influences on each other component in a multi-component system of any kind: $(+, +)$, $(-, -)$, $(-, +)$, $(-, 0)$, $(+, 0)$ and $(0, 0)$. (The procedures of DMDS explains that if the previous value of an component, which is a subject to influence, is high then "minus" the influence leads to decreasing and a "plus" influence leads to the increasing of the current value of an component, which is an object of influence; "zero" influence stabilizes the current values of an component, which is an object of influence, on the level of previous ones). In the case of DMDS, the working hypothesis mentioned above appears as a result of modeling, and this provided successful results.

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Дискретне динамічне моделювання системних характеристик ходи черепахи у звичайних обставинах та після легкого стресу / Ю.Г. Беспалов, І.Д. Городнянський, Г.М. Жолткевич, І.Т. Зарецька, К.В. Носов, Т.П. Бондаренко, К.М. Калиновська, Я. Карреро // *Біоніка інтелекту: наук.-техн. журнал.* — 2011. — № 3 (77). — С. 54-59.

У статті пропонується дискретна динамічна модель, що дозволяє виразити структуру внутрішньо- та зовнішньоконпонентних відносин динамічної системи у термінах міжвидової взаємодії, прийнятої у біології та екології. Запропонована модель застосовується до вивчення системних аспектів біомеханіки ходи черепахи у спокійному стані та після легкого стресу.

Табл. 2. Бібліогр.: 13 найм.

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Дискретное динамическое моделирование системных характеристик ходьбы черепахи в обычных условиях и после легкого стресса / Ю.Г. Беспалов, И.Д. Городнянский, Г.М. Жолткевич, И.Т. Зарецкая, К.В. Носов, Т.П. Бондаренко, Е.М. Калиновская, Я. Карреро // *Бионика интеллекта: наук.-техн. журнал.* — 2011. — № 3 (77). — С. 54-59.

В статье предлагается дискретная динамическая модель, которая позволяет выразить структуру внутри- та внешнеконпонентных отношений динамической системы в терминах межвидовых взаимодействий, принятых в биологии та екології. Предложенная модель применяется для изучения системных аспектов биомеханики ходьбы черепахи в спокойном состоянии и после легкого стресса.

Табл. 2. Библіогр.: 13 назв.