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The CA-model of populations' dynamics of organisms living in lake Baikal

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Abstract. The cellular automata model of populations' dynamics of eight types of organisms is proposed and investigated. The results of two computational experiments of simulation of population density distribution over space are presented. The first experiment was carried out is for the case of the emergence fishes at outfall shoal of Selenga. The second one was for the case of food declining in the North.

1. Introduction

Self-organization is the process of time and spatial elements ordering in the system due to its elements interaction. This definition was given by Haken in 1980 [1]. Self-organization processes are known in Biology, Chemistry, Physics, Sociology and Economy. Examples are phase transition, laser, proteins compression, homeostasis, animals staining, etc.

The investigation of self-organization processes requires computer simulation techniques. As usual, models are based on nonlinear partial differential equations, which are difficult or even impossible to be solved and efficiently parallelized. An alternative approach is Cellular-Automata (CA) models, which allow simulation of complex nonlinear processes, including self-organization processes using comparatively simple rules. The CA-models for self-organization processes were studied by Wolfram [2], Chua [3], Vanag [4]. The CA-models for some kinds of Belousov–Zhabotinsky reactions are given in [5]. The CA-model for the "phase-separation" process has been investigated in [6, 7].

A cellular automaton is a structured set of finite (elementary) automata named cells. For each cell, a set of adjacent cells is defined. Functioning of a CA is given by a transition function. A transition function is defined for each cell and depends on the states of adjacent cells. As usual, the modeling space structure for a two-dimensional case is presented by a square, a triangular or a hexagonal mesh. Complex phenomena are simulated using CA-composition techniques proposed in [6]. The CA under investigation uses a parallel CA composition. The main idea of the parallel composition is that several CA are functioning simultaneously and their transition functions depending not only on the cell states of a given CA, but, also, on the states of cells of other CA in the composition.

A parallel composite CA-model of an abstract prey-predator system consisting of two groups of organisms is proposed and investigated in [8].

Up till now population dynamics has been investigated with help of differential equations systems given in [9, 10]. The following restrictions being admitted:

1. Population parameters are proposed to be uniformly distributed through the area of modeling (mean-field hypothesis).
2. The number of interacting organisms groups is less or equal to 3.

A model of eight populations in Baikal has been proposed and investigated in [11] using ODE. Thus, the second restriction was overcome using the numerical simulation.

Here a CA-model is proposed that allows the simulation of a spatial distribution of organisms when some perturbations occur. This model takes into account eight organisms groups. The data about the organisms population used in the model are given in paper [11].

The first part of the paper is about the task definition, demographic and food chain interactions. The CA-model is considered in the second part. In the third part, the results of computational experiments for the following two cases are given: emergency shoal of fishes in the outfall of Selenga and initial decline of food in the North.

2. The task definition

Taking into account all Baikal's organisms is an extremely complicated task. Comephorus takes leadership according to biomass criteria (about 60% of the all lake biomass). Its basic food is macrohectopus and its own youngest. Similar to [11] the three species are taken into account: macrohectopus, comephorus dybowski, and comephorus baicalensis. Macrohectopus is a sandhopper. Comephorus dybowski and baicalensis are predatory fishes. Each of the species is divided into groups by the age criteria:

Species	One-year-old individuals	Immature individuals	Puberal individuals
Macrohectopus		m_1	m_2
Comephorus dybowski	d_1	d_2	d_3
Comephorus baicalensis	b_1	b_2	b_3

In the explanations to follow, let us assume that the upper parameters' index presents species $\alpha \in \{m, d, b\}$ and the lower parameters' index presents the age $i \in \{1, 2, 3\}$. Demographic and prey-predator relationships are displayed in Figure 1.

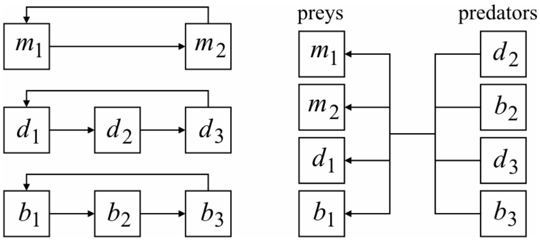

Figure 1. Demographic (left) and prey-predator (right) relationships

3. A composite CA-model

The following assumptions are used in the CA-model:

1. The influence of organisms not listed above is assumed to be constant. For example, macrohectopus are always satiated, and phoca always eat a strictly constant amount of comephorus (on a percentage basis).
2. Environmental influence is assumed to be constant.
3. All individuals parameters (speed, size, diet, gender ratio) are averaged over groups.
4. Only the last age groups individual propagate.
5. Predators' saturation is not taken into account.

Let us define a CA-model of the populations dynamics of Baikal organisms as

$$\aleph = \langle \Sigma, M, f, \rho \rangle,$$

where Σ is an alphabet of states, M is a set of cells names, f is a global transition operator, and ρ is a functional mode.

The model is a parallel composition of eight CA, each being designed to simulate a concrete group population dynamics. A set of cells names can be split to eight pairwise disjoint subsets, each one for a concrete group of organisms. Each of subsets can be presented by a square mesh with a set of cells Q:

$$M = M_1^m \cup M_2^m \cup M_1^d \cup M_2^d \cup M_3^d \cup M_1^b \cup M_2^b \cup M_3^b,$$

$$M_i^\alpha \cap M_j^\beta \neq \varnothing \iff i = j \wedge \alpha = \beta,$$

Assume that the bijective mapping $\psi_i^\alpha : Q \to M_i^\alpha$ exists.

Let us define the *cell* as an element of the set $M \times \Sigma$. The subset Ω of the set $M \times \Sigma$ is called a *cells array* if and only if $|\Sigma| = |M|$ and there are no cells with equal names. The cells states are integers $n \in \Sigma$, meaning the number of organisms in this cell. Let us call twins the cells $\psi_i^\alpha(q)$ and $\psi_j^\beta(q)$

for each $q \in Q$. *The closest neighbors pair* is the pair of cells such that these cells are neighbors in terms of a square mesh.

A finite collection $S(m) = \{(\phi_1(m), n_1), \ldots, (\phi_k(m), n_k)\}$ is a *local configuration*, where $n_i \in \Sigma$ and $\phi_i : M \to M$. The cells with the names $\phi_1(m)$, $\ldots$, $\phi_k(m)$ are *neighbors.*

In the general case, a *local transition operator* f_{loc} is

$$f_{\text{loc}} : \{S(m)\} \to \{S(m)\}.$$

The result of applying the operator f_{loc} to the cell (m, n) is the replacement of the local configuration $S(m)$ by the local configuration $f_{\text{loc}}(S(m))$. *Iteration* or *global operator application* consists of local operators applied to all cells. *Evolution* is a consecutive process of the global operator application.

In this paper, two global transition operators are used:

1. The operator f_1 for modeling organisms' movement.
2. The operator f_2 of the organisms' quantity changing due to the prey-predator mechanism.

The two basic functional modes are known: *synchronous* and *asynchronous.* In synchronous mode the arguments of the local transition operator are the cell states on the current iteration t. The new cells states are calculated, and all the cells change their states simultaneously. In asynchronous mode is that the new cell state is calculated based on the current states of the neighbors, and the cell state is changed immediately. The cell, whose state is to be updated, is randomly chosen [12].

The CA-model under investigation uses a slightly more complex composite functional mode, which combines synchronous and asynchronous modes. First, the operator f_1 of organisms movement is applied asynchronously several times for each subset M_i^α independently. Second, the operator f_2 is applied with a functional mode specified in Section 3.2.

3.1. The movement operator

Let f_{loc}^d and f_d be local and global transition operators of the integer diffusion according to [13]. The operator f_{loc}^d is defined for each set M_i^α:

$$f_{\text{loc}}^d : \{S_1(m)\} \to \{S_1(m)\},$$

where $S_1(m)$ is a set of neighbors of a cell with the name m.

Application of f_{loc}^d to a cell named m is performed according to the following algorithm:

1. Let $m_1, \ldots, m_k$ be the names of the neighbors of a cell named m. The square mesh structure reveals that $k \leq 4$.

2. A cell with the name m_i is randomly chosen with equal probability.
3. Let n and n_i be the cells states named m and m_i, respectively.
4. The new states n' and n'_i are given by the formulas:

$$n' = n - [\sigma \cdot n] + [\sigma \cdot n_i], \quad n'_i = n_i + [\sigma \cdot n] - [\sigma \cdot n_i],$$

where σ is an integer diffusion ratio.

The global transition operator f_d assumes the asynchronous functional mode.

Let us define the movement operator f_1. Let S be the area of Baikal. Let N be a number of cells equal to $|M_i^\alpha|$. The edge size for a cell is given by the formula $a = \sqrt{S/N}$. Let v_{cr} be the cruising speed of an individual organism of species α from age group i. Let δt be a physical time step equivalent to a model iteration. A maximum number of cells visited by the individual can be calculated as

$$K_i^\alpha = \frac{v_{\mathrm{cr}}\delta t}{a}. \tag{1}$$

Let us define $f_1|_{M_i^\alpha}$ as a K-wise sequential application of f_d:

$$f_1|_{M_i^\alpha} = (f_d)^{K_i^\alpha}.$$

Let us define the movement operator f_1 as

$$f_1(S(m)) = \begin{cases} f_1|_{M_1^m}(S(m)) & \text{if } m \in M_1^m, \\ f_1|_{M_2^m}(S(m)) & \text{if } m \in M_2^m, \\ \quad \dots & \\ f_1|_{M_3^b}(S(m)) & \text{if } m \in M_3^b. \end{cases}$$

3.2. The quantity changing operator

The local quantity changing operator is

$$f^2_{\mathrm{loc}} : \{S_2(m)\} \to \{S_2(m)\},$$

where $S_2(m)$ is a collection of twin cells. The schematic view of $S_2(m)$ is given in Figure 2.

The mode of the global transition operator f_2 is slightly more complex than conventional synchronous or asynchronous modes. The choice of a twins set is random and f^2_{loc} is used synchronously for each set of twins. The new cell state after applying the operator f^2_{loc} is

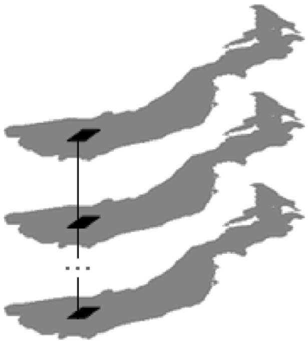

Figure 2

$$n' = \begin{cases} n + \lfloor \Delta n \rfloor & \text{if } \xi < \operatorname{frac}(\Delta n), \\ n + \lceil \Delta n \rceil & \text{otherwise}, \end{cases},$$

where $\xi \in (0,1)$ is a random number, Δn is the population growth, and $\operatorname{frac}(\Delta n)$ is the fractional part of the population growth.

The population growth of the ith age-group is given by the formula:

$$\Delta n_i = (\rho_i n_j - \lambda_i n_i - \theta_i n_i)\Delta\tau,$$

where j is the age-group number whose individuals produce individuals from the ith age-group, $\Delta\tau$ is the physical time corresponding to one CA iteration, $\rho_i n_j$ is the ith age-group quantity growth due to propagation (case $i = 1$) or aging (case $i > 1$), $\lambda_i n_i$ is the number of dead individuals, and $\theta_i n_i$ is the number of grown up individuals.

The propagation ratios ρ_1^m, ρ_1^d, ρ_1^b, the aging ratios ρ_2^m, ρ_2^d, ρ_3^d, ρ_2^b, ρ_3^b, and the death ratios λ_1^m, λ_2^m, λ_1^d, λ_1^b are taken from [11].

As opposed to [11], the CA-model takes into account the dependence on the death ratios λ_2^d, λ_3^d, λ_2^b, λ_3^b on lack of food. Let χ_i^α be a relative overpopulation of the group α_i:

$$\chi_i^\alpha = \frac{n_i^\alpha}{\bar{n}_i^\alpha},$$

where $\bar{n}_i^\alpha$ is the average individuals quantity of α_i group [11].

Let $\xi_{ji}^{\beta\alpha}$ be a ratio of a relative lack of food:

$$\xi_{ji}^{\beta\alpha} = 1 - \frac{\chi_j^\beta}{\chi_i^\alpha}.$$

If $\xi_{ji}^{\beta\alpha}$ is greater than zero, it is multiplied by a constant c depending on the predator diet and is added to the constant predators' death ratio $\bar{\lambda}_i^\alpha$. Let $\gamma(\xi) = \max\{\xi, 0\}$. Then, the death ratios are calculated as follows:

$$\lambda_i^\alpha = \bar{\lambda}_i^\alpha + (1 - \bar{\lambda}_i^\alpha)\left(c_\alpha \frac{\gamma(\xi_{1i}^{m\alpha}) + \gamma(\xi_{2i}^{m\alpha})}{2} + (1 - c_\alpha)\frac{\gamma(\xi_{1i}^{b\alpha}) + \gamma(\xi_{1i}^{d\alpha})}{2}\right),$$
$$i = 2, 3, \quad \alpha \in \{b, d\},$$

where $c_b = 0.37$, $c_d = 0.07$ are ratios depending on the predators' diet. The terms meanings are as follows:

$(1 - \bar{\lambda}_i^\alpha)$ is an alive individuals part after subtracting the death ratio $\bar{\lambda}_i^\alpha$,

$\dfrac{\gamma(\xi_{1i}^{m\alpha}) + \gamma(\xi_{2i}^{m\alpha})}{2}$ is a relative lack of macrohectopus,

$\dfrac{\gamma(\xi_{1i}^{b\alpha}) + \gamma(\xi_{1i}^{d\alpha})}{2}$ is a relative lack of one-year-old comephorus.

4. Computational experiments and program implementation

In the computational experiments, the model area size is $|M_i^\alpha| = 234296$ cells. Baikal area S is 31722 km^2. Therefore, the cell size is 368×368 meters. The physical time $\Delta\tau$ corresponding to an iteration is taken two days. An individual organism trajectory length in meters per two days with allowance for vertical and random migrations is given in Table 1. The numbers K_i^α are defined according to (1) in Table 2.

Table 1. Individual trajectory lengths

Age group	Macro-hectopus	Comephorus dybowski	Comephorus baicalensis
1	200	1000	2000
2	400	2000	3000
3		4000	5000

Table 2. Values of K_i^α

Age group	Macro-hectopus	Comephorus dybowski	Comephorus baicalensis
1	1	2	5
2	1	5	8
3		10	13

The program has been developed in C++ language using Qt and OpenGL libraries. Calculations parallelization is done with OpenMP technology. Sets of cells for each group of organisms are integer arrays. Application profiling was done before parallelization. The results of profiling are given in Table 3. Intel Core i7-2600, 4 cores × 3.4 GHz, 8 Gb RAM was used for timing.

From Table 3 it follows that parallelization should be done only for the step of movement modeling. Since the movement operators for each set can be applied independently, the following 4-thread parallelization method was chosen:

Table 3. Single-threaded application profiling results in seconds

Cell count	Painting	Quantity changing (1 call)	Movement (1 call)
1464 K	1.0	0.44	18.14
2109 K	1.5	0.63	34.03
3749 K	2.6	1.13	87.96

Thread 1: movement of m_1 (immature macrohectopus) and d_3 (puberal comephorus dybowski);

Thread 2: movement of m_2 (puberal macrohectopus), b_1 (one-year-old comephorus baicalensis), and d_2 (immature comephorus dybowski);

Thread 3: movement of b_2 (immature comephorus baicalensis) and d_1 (one-year-old comephorus dybowski); and

Thread 4: movement of b_3 (puberal comephorus baicalensis).

According to Table 1, a theoretical speedup peak is 3.5 (restricted by the movement of b_3 on the 4th thread). The results of profiling after parallelization are given in Table 4.

The parallelization efficiency is about 80.8 %, or 92.3 % of the theoretical peak. The main advantage of such a parallelization method is its realization

Table 4. Parallelization timing results

Cell count	Movement 1 thread (s)	Movement 4 threads (s)	Speedup	Speedup peak
1464 K	18.14	5.77	3.14	3.5
2109 K	34.03	10.52	3.23	3.5
3749 K	87.96	27.51	3.20	3.5

simplicity. On the other hand, the solution is not scalable for the number of threads greater than 4.

In population maps shown below, the lighter color means the larger density and the darker color means the smaller density. The following drawing procedure was used: a cell with the largest value has the lightest color 255. The color of other cells linearly depends on their values from 0 to 255. Thus, the pictures show only a relative difference between colors. As one can see further, such a case contains sufficient information for making analysis.

4.1. Experiment 1: Shoal of fishes at the outfall of Selenga

The experiment is aimed at investigation of the CA-model evolution for the case of enormous concentration of predators in some local area.

The comephorus quantity in the initial state is increased at the outfall of Selenga up to three times as compared to values at a steady state, and inversely depends on the distance from the outfall of Selenga. The macrohectopus quantity over the whole model area is equal to the steady state (Figure 3).

The evolution result is a steady state. In this experiment, the population dynamics is a local process at the outfall. There is no population change outside the outfall (Figure 4). Therefore, for this experiment it is needed to analyze local processes at the outfall. A few snapshots of evolution are given in Figure 5.

It is possible to notice the population spatial wave (see Figure 5) for $t = 100$ and 200. Population values for each group in cells inside and outside

Figure 3. Initial state

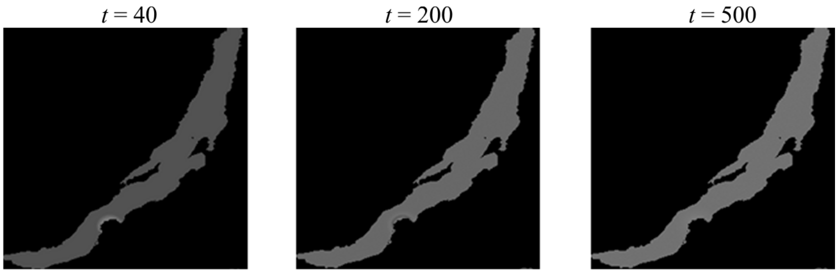

Figure 4. Certain global states of d_2 population

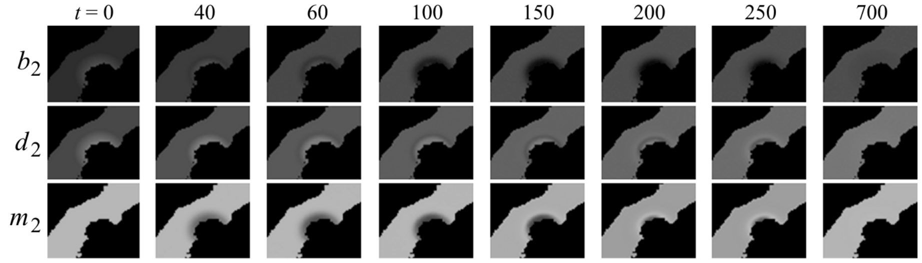

Figure 5. Certain states at the outfall

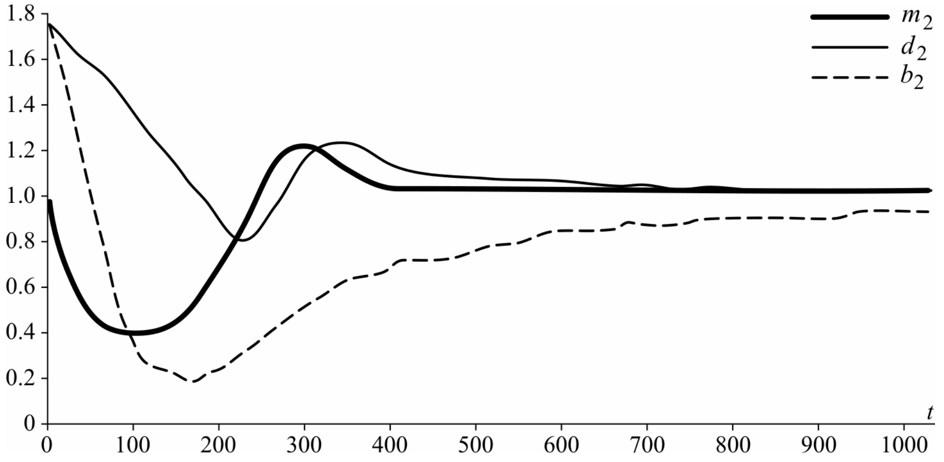

Figure 6. The ratio of the current population to the steady state in a cell at the outfall

of the outfall in steady states are equal within the deviation of about 5 %.

The population dynamics of puberal macrohectopus, immature comephorus dybowsky and immature comephorus baicalensis in a cell at the outfall are given in Figure 6. In the start iteration, the quantity of immature comephorus dybowsky and immature comephorus baicalensis individuals is about 1.8 times greater than the corresponding quantity in the steady state. The puberal macrohectopus quantity on the start iteration is equal to the value in the steady state. In the first iterations, the number of all individuals decreases due to an excessive quantity of predators. Further, the number of preys is growing due to a significant extinction of predators. Finally, the quantity of individuals after the oscillating process becomes closer to a steady state.

Thus, starting with a locally irregular state, the model works for the steady uniform state. No fluctuations are observed for the steady state.

4.2. Experiment 2: Lack of food in the North

The objective of the experiment is to investigate the CA-model behavior in the case of an extreme reduction of food in the local area.

The initial state is shown in Figure 7. The macrohectopus quantity is ten times decreased in the North as compared to the the steady state, while the comephorus quantity is equal to the steady state. As a result of evolution, the system works for the steady state.

Similar to Experiment 1, population dynamics is a local process. There are no population changes outside of the area with unstable initial state (Figure 8). Therefore, in this case, only the area in the North should be taken into account. A number of snapshots of the evolution are presented in Figure 9.

The population dynamics of puberal macrohectopus, puberal comephorus dybowski and immature comephorus baicalensis in a cell in the North

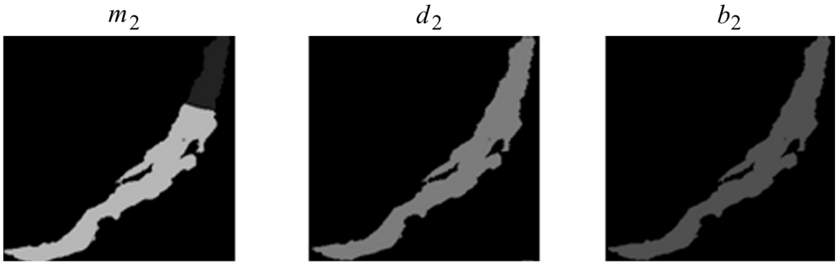

Figure 7. Initial state

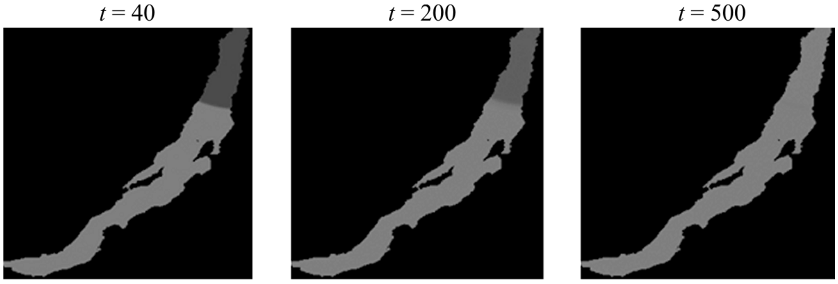

Figure 8. Certain global states of b_2 population

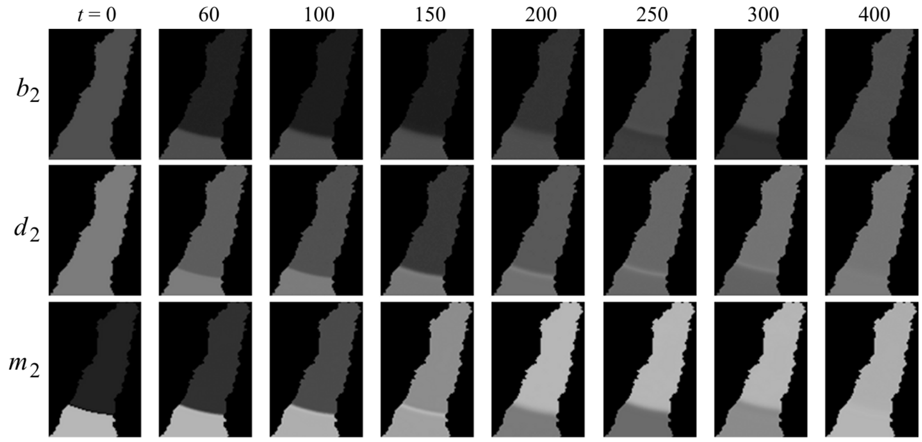

Figure 9. Certain states in the North area

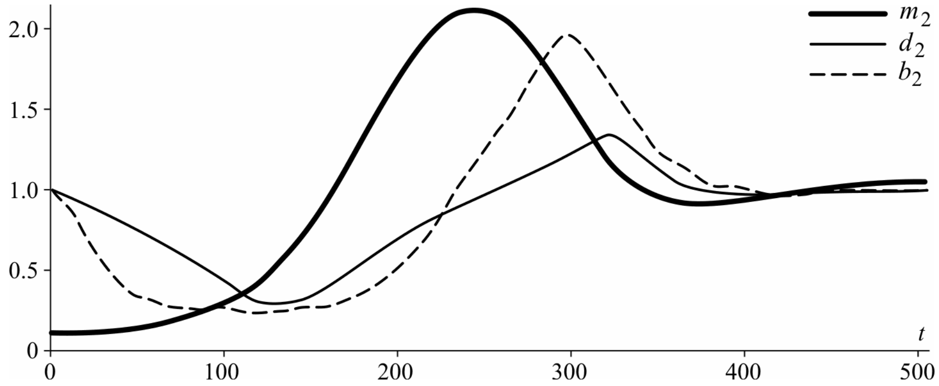

Figure 10. The ratio of the current population to the steady state in a cell in the North

is given in Figure 10. In the initial state, the quantity of puberal macrohectopus is 10 times less than that in steady state. The quantity of predators is equal to the steady state. In the first iterations, the number of predators decreases due to the lack of food. After that, the number of preys and predators starts growing, and the system tends to the steady state as a result of the oscillating process. Thus, the initial state irregular model evolves to the steady uniform state. No fluctuations are observed.

5. Conclusion

The new CA-model of the populations' dynamics of some Baikal organisms is proposed. This model allows one to investigate the spatial distribution of organisms in lake Baikal.

The CA-model proposed does not take into account a seasonal dependence of death and borne rates. In a real situation, this occurs, and the seasonal population fluctuations are observed.

In the future, we are going to introduce time and spatial dependence of borne and death rates in order to take into account seasonal features and possible pollution of the area.

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