Simulation of bio-like systems and processes using movable cellular automata

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Abstract. In this work, the method of movable cellular automata is applied to the simulation of different biological systems and processes. A significant advantage of this method is the possibility of transition from a static grid to the concept of neighbours. Four examples are considered, namely the worm-like movement, the amoeba-like locomotion, the self-replication process and the biological engine. An object of simulation in all cases is divided into small parts, which are called cellular automata, that interact with each other by the rules of interactions. The basic principles of these interactions are the same, although the observable examples are diverse. According to the concept of neighbours, rules of cellular automata interactions were found for the constructed models. As a result, a computer models for each example were obtained. The models are qualitative, not quantitative, and allow you to demonstrate the fundamental possibility of movable cellular automata for such simulation.

Keywords: Movable cellular automata, Bio-like systems, Computer simulation, Worm-like movement, Amoeba-like locomotion, Self-replication, Biological engine.

1 Introduction

Nowadays computer modelling is one of the most powerful tools of scientific research and engineering applications. It provides an opportunity not only to reproduce the results of real experiments with a fairly high degree of confidence but also to reduce financial costs and eliminate of dangerous precedents. Moreover, in some cases, an alternative to computer models does not exist at all.

Simulation biological processes and systems is one of the most relevant and most promising areas of research. In contradiction to examples of physical phenomena, the mechanisms of many bioprocesses are unknown at this time. Thus, one of the tasks that are solved through simulation is the search for answers to questions that are still open. These issues, in particular, include: the path of self-organization and the evolution of living matter (Origin of Life); mechanisms of synergistic cooperation in the

colonies of unicellular organisms and their organization in the form of multicellular organisms, accompanied by cell differentiation (acquisition of specific functions by individual cell types within a single organism); self-organization of various signal flow in the neural subsystem of organisms and the formation of the phenomenon of consciousness. The last problem is particularly relevant in the field of artificial intelligence. It is obvious that all the achievements in this direction have nothing to do with the real intelligence of the human brain today, since their implementations are not based on the processes that take place in it. At the same time, the identification of key mechanisms leading to the self-organization and the evolution of consciousness will give impetus to the next scientific, technological and humanitarian revolution. In this case, it will be possible to talk not about artificial intelligence, but about the computer model of real intelligence.

The tools that are used to build models of biological objects and their dynamics are quite diverse – from describing investigating processes in terms of the theory of differential equations and then finding their numerical solution, to building imitational complex models that reflect the individual components of the corresponding processes or systems. Simulation by the method of movable cellular automata (MCA) can be attributed precisely to the simulation approach that has long been used to implement a wide range of artificial biosimilar structures. In general, this direction of simulation is name “Artificial Life” (Artificial Life), its purpose is to develop general approaches for constructing artificial models of living organisms. At the same time, the use of MCA as a simulating tool attracts with the possibility of creating simple models of rather complex systems.

The first researcher on “Artificial Life” was John von Neumann, who studied the possibilities of implementing self-replicating structures. The ability of self-reproduction (or self-replication) is a unique phenomenon that characterizes all living organisms. Neumann showed and described [1] the possibility of constructing a discrete deterministic self-replicating automaton, the certain analogue of the Turing machine. It was capable of copying the contents of a control program and fragments of the automaton structure.

However, within the framework of the Neumann and similar models, no processes of self-organization and self-complication (evolution) are observed. This is due to the fact that in such structures there is no implementation of the mechanisms that occur in real living organisms. It is well known, that biological objects are a combination of a large number of regulatory processes interconnected among them and organized in the form of extensive networks of various transformations of molecular complexes. The overwhelming majority of stimuli, that is, deviations from organic natural dynamics (if they are not destructive for the organism), are perceived by the corresponding receptor complexes that initiate certain chains of transformations and lead to the formation of an appropriate reaction. Thus, all regulatory processes have the nature of feedback. According to such principles, for example, the regeneration of damaged parts of organisms, the normalization of the state of the internal environment (homeostasis), the management of the organism's behaviour, its development, etc., occurs. The network of regulatory processes is determined by the organism’s genotype. Moreover, the genotype is also subject to self-regulation (for example, the process of DNA re-

pair). But, at the same time, the biosystems are characterized by variability that associated with genotype mutations. These mutations are not renewed by regulatory mechanisms, because they harmoniously interact with them. During mutations processes, the genotype may become more complex, that leads to a complication of the phenotype of the organism and expands the network of regulatory processes. And, against the backdrop of Darwinian natural selection, this leads to the evolution of biological objects.

The basis of the above-mentioned dynamics of biological structures is also a process of self-organization, which means the absence of a single control centre. In contrast to the centralized management approach, each element of self-organizing systems acts by itself, interacting with only a small number of neighbouring elements. So, it turns out is enough to streamline chaotic structures. Based on the above, the method of mobile cellular automata is chosen as a simulation method. Or rather, the asynchronous stochastic MCA method with the symbol alphabet, which corresponds to the set of states of the MSA. This method is a further development of deterministic synchronous automata [2], which are used to simulate physico-mechanical processes in solid deformable bodies.

The aim of the work is not only to build a model in terms of cellular automata, but also to search for cellular automaton interactions that lead to the dynamics of a system imitating bio-like processes and structures. That, in turn, is an important both theoretical and practical task.

2 Simulation of worm-like movement

It is quite promising to use a multi-agent approach implemented on the basis of the MCA for simulation the processes of locomotion. To do this, the biosystem is decomposed into separate constituent elements and each element is represented by an MCA with a corresponding behaviour depending on the type of element and the state of the environment, that is, on the state of the neighbouring MCA. Similar artificial organism is also called an “animat” (from Artificial Animal). The advantages of using MCA in creating animats are: the possibility of a fairly flexible formation of an arbitrary morphology of an artificial organism and its organs; an imitation of the processes of differentiation, division and death of cells; a wide range of functional properties of cells, what form the corresponding tissues (muscular, nervous, skin, etc.).

These approaches are used by many researchers. For example, in [3], the authors describe the process of morphology formation of elementary animats by using the idea of encoding the forms of artificial organisms as an analogue of the genotype. The change in the content of the genotype is displayed as a corresponding change in the shape of the organisms. It is possible to use the operators of genetic algorithms (mutations, crossing, selection) to looking for various biosimilar forms. In addition, in models of animats, imitation of the spreading of signals along the diffusion nervous system is carried out, and muscle contraction take place. The whole body of the animat is a collection of cells and a kind of excitable medium in which nerve impulses can propagate in the form of waves. Under the influence of these waves, the distance

between cells is reduced or increased in order to imitate the contraction of the muscles of an artificial organism. In fig. 1.a) shows an example of a worm-like organism constructed in such a way.

The examples of other forms of animats (jellyfish, fish, turtles, hydras, etc.) are also given in [3]. Nevertheless, many researchers pay attention precisely on the worms. Nematode Caenorhabditis elegans was chosen as an object for computer modelling in the international project OpenWorm [4]. The aim of the project is to build a dynamic computer model of C.Elegans at the cellular level. It was expected that, knowing the complete information about the structure of the organism, including the structure of the connectome, it would be possible to create an adequate artificial analogue of a real organism with similar behaviour. The Open-Worm project has been actively developed since 2011, but the goals have not been already achieved.

On our opinion, it is not necessary to strive to realize the absolute equivalent of the real analogue, as the participants of the OpenWorm project try to do. Building a complex detailed model requires a lot of time and computational resources and, that most importantly, it can interfere with the search for regulatory mechanisms that maintain the wholeness and durability of an artificial organism, as well as ensure the natural harmony of its components. In addition, the development of a universal method for modelling bio-like systems, which could be applied to different objects, is quite relevant.

Regarding to this theory, the MCA method, what, in fact, was used by the authors of [3], is very promising, in our opinion. In addition, this method provides the possibility of a variety flexible modifications, partially described earlier. In fig. 1.c). an example of a model of the worm-like organism proposed by us is showed. This model is also based on the MCA method.

To implement the model, was chosen a scheme of neighbourhood. According the scheme each cell has four neighbours for a two-dimensional model and six in the case of a three-dimensional one. In this work we consider two-dimensional model, and in this case the neighbours are divided into two groups what simulate longitudinal and transverse muscles.

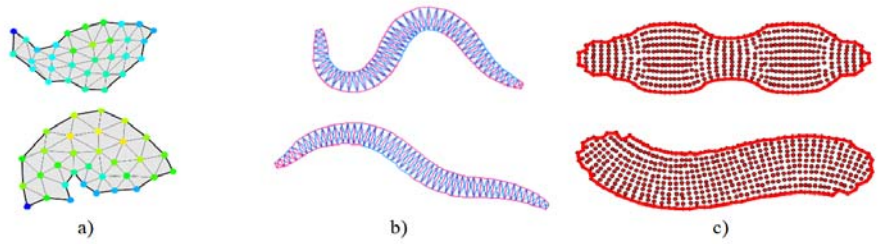

Fig. 1. Examples of models of worm-like organisms: a) the model given in [3]; b) the model from [4]; c) the model proposed by us.

When the transverse muscles are reduced, the corresponding body fragments should be increased in length and compressed, and with the reduction of longitudinal

vice versa - decrease in length and expand. The signal for muscle contraction is the state of the corresponding "nerve ending" of the neural subsystem, which is associated with the corresponding MCA. In fig. 2 shows examples of the mutual arrangement of MCA in interaction. Fig. 2.a) reflects the state of the MCA in cases of whether absence of muscle contraction signals for the selected cell, or attempts to reduce both muscles (longitudinal and transverse). Fig. 2.b) reflects the state of the MCA in the case of a signal of reduction of longitudinal muscle. And Fig. 2.c) reflects the state of the MCA in the case of a signal of reduction a transverse one.

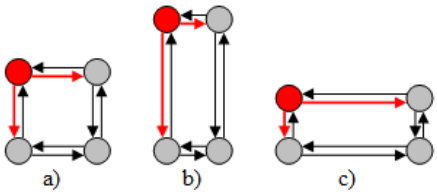

Fig. 2. Examples of the mutual arrangement of MCA

The essence of MCA interactions is to establish the distance between neighbours depending on the state of the corresponding efferent neuron, what also locate in the structure of the automaton. Moreover, according to the properties of incompressibility, the volume of the elements of the worm body is unchanged. The model provides for the possibility of the presence in the MCA structure, in addition to the efferent neuron, also of an afferent (receptor) one what responds to a specific state (form) of the surroundings. Connections between the neural parts of the MCA can be not only within the nearest neighbours, but also between distant ones. (fig. 3). Moreover, these connections can dynamically change, drifting from one cell to another, imitating the growth of dendrites and axons of real nerve cells. The signal flows in the nervous subsystem of an artificial organism lead to a corresponding contraction of the muscles and form a variety dynamic, examples of which are shown in Fig. 1.c).

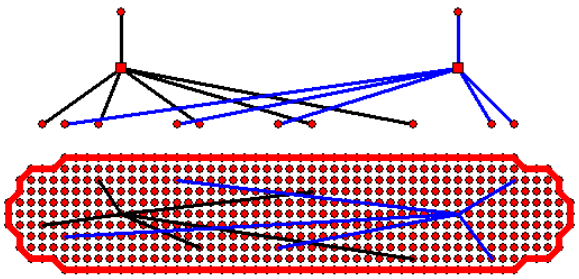

Fig. 3. Simple schematic representation of the neural subsystem

To describe the mathematical model of the neural network, we define the transformation function f: $X \rightarrow Y$, which forms one of three output values (0 is the absence of

a signal, 1 - reduce the longitudinal muscle, 2 - reduce the transverse muscle). It depends from the value of the amount of input signals multiplied by weight coefficients. Each input has its own synaptic weight what gives input the effect needing for the adder function of the processing element:

$$y_j = \begin{cases} 0, 0 \le \sum_{i=1}^{K} x_i w_i < 2K/3, \\ 0, 2K/3 \le \sum_{i=1}^{K} x_i w_i \le 4K/3, \\ 2, 4K/3 < \sum_{i=1}^{K} x_i w_i \le 2K, \end{cases} \quad (1)$$

where n – number of MCA in the modelled object; K – the maximum number of connections for neurons; x_i (x_i = 0, 1, 2) – input signals; $w_i \in [0 \dots 1]$ – weighted coefficients, what are the measure of the force of the input bonds and simulate the various synaptic forces of the biological neurons.

The weights of the substantial input are increased and, conversely, the weights of the non-essential input are reduced, which determines the intensity of the input signal. It should be noted that the values of the weight coefficients and the order of the conditional operators in formula (1) may change and they define a characteristic of the individual MCA.

3 Simulation of amoeba-like locomotion

Another interesting microorganism for research is the unicellular amoeba protea (Amoeba Proteus). It is moving in space by changing the shape of its body. At the same time certain protrusions, so-called pseudopodia ("false-feet") and posterior uropods, are formed. Amoeba recognizes various microscopic organisms that serve it as food. It goes away from bright light, mechanical irritation, and elevated concentrations of substances dissolved in water. In addition to these unconditioned reflexes, some researchers have documented the formation of conditioned reflexes in amoebas. Conditioned reflexes of a unicellular organism with a missing nervous subsystem! Many scientists, which watch about amoebas, ask themselves: how it is possible? It is also interesting to note that the size of the amoeba genome is almost 200 times the size of the human genome. This paradox indicates that there is not always a direct connection between the size of the genome and the complexity of the organism.

Let us focus on the problem of modelling the movement of the amoeba, which occurs, as already noted, due to the growth of the membrane in the form of so-called pseudopodia. At the same time some other parts of the membrane are reduced. Changes in the membrane are due to reversible transformations "sol" ↔ "gel". These processes are guided by the cytoskeleton, whose structure is constantly changing (Fig. 4. a)). The result of complex membrane-cytoskeletal interactions is the harmonious dynamics of the movement of the microorganism.

All existing models of amoeba do not have taken into account the cytoskeletal subsystem of the body, but nevertheless quite realistically reflect the processes of movement, including in the direction of nutrients, or a leaving from lighting (phototaxis) or

from chemical stimuli (chemotaxis). One of the implementation options described in [5]. In this work, the amoeba body is a set of related spatial elements, where a gradient of a certain continuous parameter is formed. The internal environment of the unicellular organism (cytoplasm) moves along the gradient. This movement, leads to the growth of pseudopodia and contraction of the amoeba body in the opposite direction (Fig. 4.b)).

To build a model of the described microorganism, it is also possible to present it in the form of some multicellular analogue, and therefore use the MCA approach. This, in particular, will provide an opportunity to simulate membrane-cytoskeletal interactions. The MCA are able to change their state by defining interaction functions with neighbours as weakly or rigidly interconnected, when modelling the internal and membrane environment of a microorganism. That means forming the corresponding properties of the cellular environment, which form as "sol" or "gel". Also, the model includes self-assembly and self-destruction of cytoskeleton fragments. Self-assembly usually occurs in centrioles. Different types of filaments (filaments or microtubules) of the cytoskeleton can be distinguished, which have different effects on the transformation in the membrane (actin and myosin filaments). In cases of interacting with the appropriate types of the end of filament thread, a transition from the gel state to the sol state occurs and the membrane reduced, in the other positions the reverse process occurs and the membrane grows in the form of a pseudopodia (Fig. 4.c)).

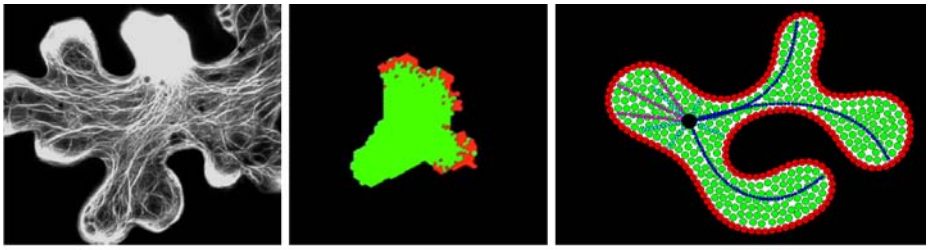

Fig. 4. Examples of models: a) an image of a real amoeba with a cytoskeleton; b) the model of amoeba-like organism described in [5]; c) the model proposed by us.

We used a dynamic index array, allowing not only to identify any MCA in the system, but also containing the indices of its nearest neighbours. As parameters, we choose: the type of MCA, which determines its properties; coordinates (for simplicity and clarity let us dwell on a two-dimensional model); indices of the nearest neighbours. The simulation used a hexagonal neighbourhood pattern (M = 6), providing for weak and rigid connectivity of pairs. In addition, to reduce the number of neighbours, we add zero values to the index of neighbours. The method of finding for the nearest neighbours under the conditions of their fixed value is described in [5]. In this paper, the criterion for finding neighbouring cells is the minimum distance between them, and the search is carried out by introducing an additional index array. Neglect of the inertial properties of the amoeba body allows one to abandon the content of the MCA velocity vector components in the index array (Fig. 5).

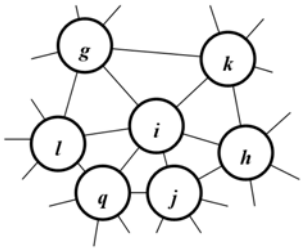

Fig. 5. The fragment of the MCA set.

The main essence of the algorithm is iterative modification of the contents of the index array. For this, an asynchronous approach is implemented, in which one of the N MCAs and one of the M of its nearest neighbours are selected in an equiprobable way. The choice of the asynchronous approach when developing the MCA algorithm is due to the fact that it allows to avoid collisions, that is, to satisfy the criterion of correctness (there will not be a single attempt to change the state of the same cell more than once at the same time t).

The cellular automaton model admits six possible states of movable cellular automata, which have a different purpose and functionality and are described using the alphabet $A = \{a_1; a_2; \ldots; a_6\}$. For the difference are used circles of radii r_i, $i = 1, 2, 3$ ($r_1 < r_2 < r_3$). After selecting two adjacent MCAs, the interaction function is implemented. This function depends on the types of interacting MCA, and is convenient to present in a matrix form (Fig. 6). Naturally, the matrix should be symmetric. Wherein, in some cases described below, interactions are carried out with the participation of more than two MCA.

	a_1	a_2	a_3	a_4	a_5	a_6
a_1	F_2	F_2	F_0	F_0	F_0	F_0
a_2	F_2	F_3	F_1	F_4	F_5	F_1
a_3	F_0	F_1	F_1	F_7	F_7	F_7
a_4	F_0	F_4	F_7	F_6	F_0	F_0
a_5	F_0	F_5	F_7	F_0	F_6	F_0
a_6	F_0	F_1	F_7	F_0	F_0	F_6

Fig. 6. Matrix representation of the MCA interaction function

Each of the functions F is a composition of separate elementary operations carried out during interactions of the corresponding types. The functions' appointments are as follows:

— F_0 imitation of thermal fluctuations;
— F_1 repulsion of two MCA at their interpenetration;

- F_2 repulsion at move in and attraction at move away (imitation of the condensed state of the environment);
- F_3 MCA alignment (for modelling elastic properties of cytoskeleton threads and membrane surface);
- F_4 catalysis of the sol-gel transformation, in which the MCA of the internal environment a_1 is converted into the MCA of the membrane a_2;
- F_5 catalysis of the gel-sol inverse transformation.
- F_6 is an analogue of F_3, but if the MCA is the end of the cytoskeleton thread (terminal), then it behaves as F_1 when interacting with the same type of MCA;
- F_7 imitation of the growth of thread from centrosome.

In this case, the following restrictions apply, which are taken into account during interactions:

1. MCA membranes a_2 cannot have more than two neighbours of the same type a_2. This ensures the integrity of the membrane and prevents its adhesion. In the future, when modelling the processes of nutrition as well as the division of amoebas, this restriction will be modified;
2. The MCA of the a_4, a_5 and a_6 cytoskeleton threads, if they are not terminal, cannot have more than two neighbours, which is ensured by entering four zero values in the neighbour indices field of the MCA array;
3. MCA adjacent to a_3 (centrosome cell) are considered related to it. Thus, the MCA of the centrosome can have an arbitrary number of cytoskeleton threads associated with it. In the future, when modelling the amoeba division process, it will be possible to divide the MCA of the centrosome, which, in turn, will initiate the process of amoeba body division into two separate unicellular organisms.

Research and modelling of biosimilar structures also obtain applied goals, besides the fundamental ones. In particular, the study of the features of locomotion of worm-like and amoeba-like organisms, discussed above, allows the use of appropriate approaches in the implementation of so-called soft-bodied robots. These works are quite promising when used for movement in hard-to-reach places, for example: pipelines of various configurations, sewage systems, wells, mines, caves, etc.

4 Simulation of self-replication processes

A separate area of research on the self-generation and evolution of bio-like structures is computer simulation of chemical processes that can lead to similar dynamics (Artificial Chemistry) [7, 8]. In particular, the authors of the work [7] managed to build a model of self-replication of cell-like structures (the so-called "Los Alamos Bugs"), which possess not only elementary metabolism, but also hereditary genetic information. The enzymes are kept inside the cell by a loop of membrane, thus ensuring that only the cell that produced them gets their benefit. A set of reaction rules, each simple and local, allows the cells to copy their genetic information and physically divide. The evolutionary possibilities of the cells are explored, and it is suggested that the system

provides a useful framework for testing hypotheses about self-driven evolution. In this case, researchers argue that the model lays the foundation for the first integrated spatially distributed computer modelling of the entire protocellular life cycle. The method for dynamics' modelling of three-dimensional dissipative particles was used, as a tool for constructing a fairly simple models of the jointed processes of diffusion, self-assembly and chemical reactions.

Analysing the mentioned above approaches to modelling self-replicating structures, we can propose an MCA method. The central problem of constructing a cellular automaton model of self-replication processes, as well as any arbitrary phenomenon or system, is the determination of the rules of automaton interactions. In the case of modelling of self-replicating structures, we propose to form a very wide range of different types of RCAs and establish equilibrium neighbourhood rules among them. These rules presuppose the existence of specific desirable sets of MCA types surrounding specific types of MCA. In such cases, the potential of MCA is minimal, and the structure, which they constitute, is robust. If the MCA is not in positions with its' equilibrium environment, then the structure is unstable, and therefore it can be arranged to move to equilibrium. At the same time, there are two possible options: either the MCA drift toward the potential decrease, and thus self-assembly process is implemented, or the MCA initiate the formation (synthesis) of the equilibrium environment and thus the self-regeneration process is realized. It can be possible to consider the combination of these two options.

As an example, we can consider the equilibrium interaction of two types of MCAs, one of which (S1) must be surrounded by six other RKAs (S2) in an equilibrium state. And for another the S2 type of MCA there must be three equilibrium neighbours – one S1 and two S2. These equilibrium neighbourhood rules can be expressed in tabular form (Tab. 1):

Table 1. Equilibrium Neighbourhood Rules for MCA

Number of neighbours	Type of sells	S1	S2
6	**S1**	-	6
3	**S2**	1	2

Demonstration of the structure's stability formed on the principles of equilibrium neighbourhood by the MCA method is shown in Fig.7. The deviations lead to a non-equilibrium state. At the next moments of time there is an arbitrarily comeback to the state of equilibrium and the initial structure is restored. That is, there is a process of self-regeneration.

Rules of the MCA interactions can be supplemented by the possibility of activation of different subsets that described transitions from one type to another, depending on some continuous parameters (analogue of nutrients supplying). In this way, an arbitrary periodic dynamic will be realized, the partial case of which the self-replicating is. In addition, the algorithm of the method can be supplemented by the mechanism of random addition of new types of MCA to a modelled cell-like structure (analogue of mutations), which can lead to increased stability of its dynamics, or vice versa - coun-

teract replication. Finally, by creating the conditions for natural selection, it is possible to organize the evolution of the studied self-replicating cell-like objects.

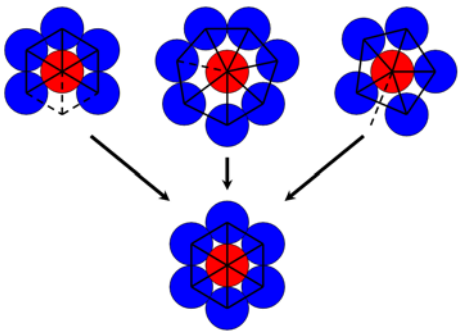

Fig. 7. A schematic demonstration of the stability of structures formed on the principles of equilibrium neighbourhood.

Consider an example of the elementary self-replicative dynamics of some cellular automaton structure. The rules of equilibrium neighbourhood of elements have the form (Tab. 2):

Table 2. The rules of equilibrium neighbourhood of self-replication structure

Number of neighbours	Type of sells	S1	S2	S3	S4	S5	S6
6	**S1**	-	6				
3	**S2**	1	2	1	1	1	1
4	**S3**		2		2		
6	**S4**		3	2	1		
5	**S5**		2			1	2
6	**S6**		4			2	

Here for a type S2 it is possible to see the peculiar ambiguity in sets of equilibrium neighbourhood. This suggests that any combination of three neighbours, which corresponds to the possible variations from Table 2, is equilibrium. For example, there may be different neighbours for S2: or one S1 and two S2, either one S3 and two S2, or one S1 and one S3 and one S4, etc.

In fig. 8 are depicted the stages of the process of self-replication of the cellular automaton structure. This process is accompanied by the transitions of the MCA from one type to another, in particular: S1 → S4 → S6 → S1. Such transitions simulate the growth phases and the division of cell-like objects. Immediately after changing the type of the corresponding MCA structure, it is in a nonequilibrium state, what initiates the process of going to equilibrium, during which the spatial organization of the neighbourhood is rebuilt and new MCAs appear (self-generated).

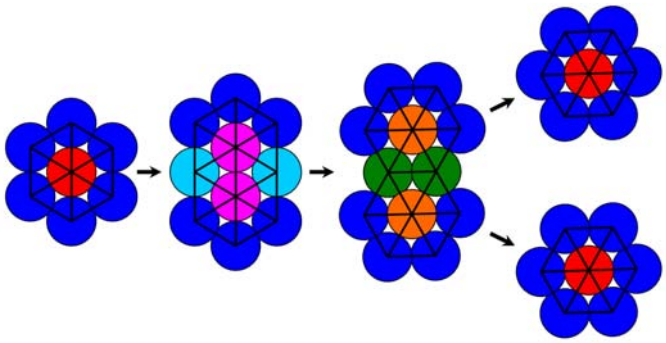

Fig. 8. Demonstration of the process of self-replication.

By changing the rules of equilibrium neighbourhood, it is possible to form various stable structures with arbitrary morphology, examples of which are shown in Fig. 9. Moreover, it should be noted that the rules of the neighbourhood may be asymmetric, that is, some MCA can establish a connection of the neighbourhood with the *k*-th, whereas *k*-th may not perceive it as its neighbour. Nevertheless, the structures will be stable, because the balance is not disturbed.

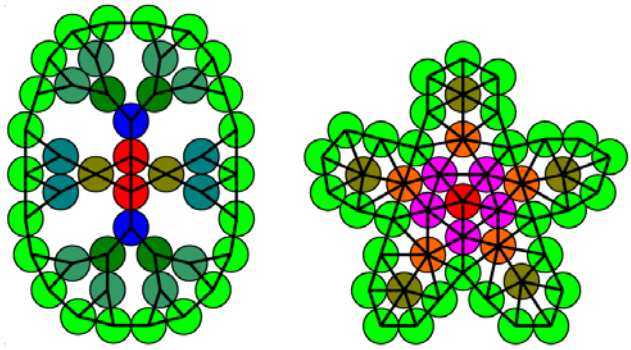

Fig. 9. Examples of structures with arbitrary morphology, formed on the principles of equilibrium neighbourhood of MCA.

5 Biological engine simulation

In addition to chemical reactions, where the process of imitation of molecular transformations takes place, MCA are also used to simulate the formation of various molecular complexes, as well as the dynamics of molecular and nanoscale structures [9]. It is also appropriate to use the MCA toolkit as an analogue of the molecular dynamics' method. As an example, we present a simple model of a molecular engine (Fig. 10 a)), where rotation is carried out due to the thermal energy of atomic vibrations. Therefore, the structure can be called a perpetual motion machine of the second kind. By the condition that the number of fibres of the external structure of the engine

and the teeth of the inner one is not the same, there is a probability of transition of one of the fibres tangents to the top of the tooth from one segment to another clockwise. This is shown in Fig. 10.b) and 10.c) The probability of the reverse transition is less.

The rules for MCA interactions in this case are as follows. All automata as elementary models of atoms carry out thermal oscillations. In this case, the angle and offset distance are randomly generated. MCA of the external structure, in parallel with thermal fluctuations, tend to align along one line and it pushing away the automata of the internal structure during this process. MCA external structure with three neighbours, tend to align the position of one of the neighbours relatively to the other two. MCA internal structure, in parallel with the heat fluctuations, tend to push away the automata of the external structure.

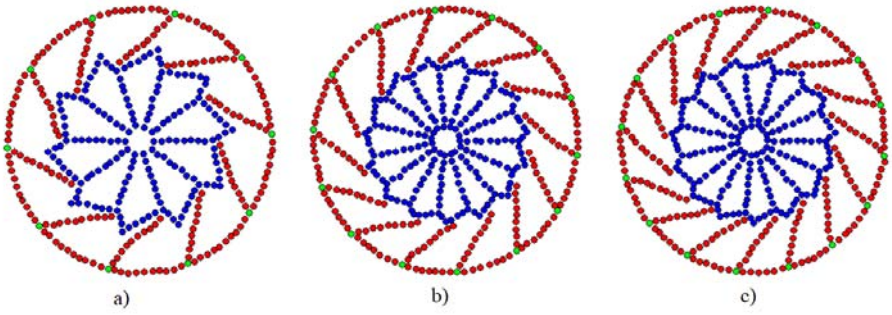

Fig. 10. Examples of molecular engine configurations: a) the number of external fibres and internal teeth coincides - there is no rotation; b) the fibres are one less than the number of teeth – there is rotation; c) one more teeth in the fibres – there is a rotation.

6 Conclusions

As we can see all of examples, mentioned above, leads to the same tasks, which can be solved by the MCA method. This paper describes some of the applications of the movable cellular automata method to the modelling of bio-like processes and systems. A significant advantage of this method is the possibility of transition from a static grid to the concept of neighbours.

For each model, the rules of cellular automaton interactions are found according to the concept of neighbourhood. As a result, computer models mimicking certain natural phenomena were obtained. It should be noted that the models are qualitative, not quantitative, and allow you to demonstrate the fundamental possibility of MCA method for such modelling. The novelty of the research lies in the use of a substantially new approach to modelling.

Bioinspired technologies are also actively used for optimization problems, in particular, for optimization of traffic flows. At the same time, in addition to the well-known ant algorithms, recently imitating models of the Physarum Polycephalum,

including using the MCA, have gained popularity. In the search for nutrients, the moulds first grow up with an almost continuous canopy, and then narrows, forming transport channels between the places where the nutrient medium is located. The structure of these transport channels is distinguished by its rationality and efficiently. It is very interesting example for our future research.

In future, it is planned to model both simple and more complex multicellular organisms, collect data and study their behaviour, embryogenesis, self-organization, self-replication, their nervous system, muscular system, etc. Of course, this will be possible only with more detailed biological analysis of the subject area and with the development of software engineering.

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