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Об алгоритмической сущности биологии

Я. Ухманьски

Университет Кардинала Стефана Вышинского,
Польша, 01-938 Варшава, ул. Войцицкого 1/3

Тюменский государственный университет,
Россия, 625003, г. Тюмень, ул. Семакова, д. 10

E-mail: j.uchmanski@uksw.edu.pl

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Степень математизации физики чрезвычайно высока, и это позволяет понимать законы природы путем анализа математических структур, которые их описывают. Но это верно лишь для физических законов. Напротив, степень математизации биологии весьма невелика, и все попытки ее математизации ограничиваются применением тех математических методов, которые употребляются для описания физических систем. Такой подход, возможно, ошибочен, поскольку биологическим системам придаются атрибуты, которых у них нет. Некоторые думают, что нам нужны новые математические методы, которые соответствуют нуждам биологии и не известны физике. Однако, рассматривая специфику биологических систем, мы должны говорить об их алгоритмичности, а не об их математичности. В качестве примеров алгоритмического подхода к биологическим системам можно указать на так называемые индивидуальные модели (individual-based models), которые в экологии употребляются для описания динамики популяций, или на фрактальные модели, описывающие геометрическую структуру растений.

Ключевые слова: математизация физики, математизация биологии, алгоритмичность биологии, индивидуальные модели, фрактальные модели

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On algorithmic essence of biology

J. Uchmański

Cardinal Stefan Wyszyński University,
Wóycickiego 1/3, 01-938 Warsaw, Poland

Tyumen State University,
10 Semakova st., Tyumen, 625003, Russia

E-mail: j.uchmanski@uksw.edu.pl

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Mathematicity of physics is surprising, but it enables us to understand the laws of nature through the analysis of mathematical structures describing it. This concerns, however, only physics. The degree of the mathematization of biology is low, and attempts to mathematize it are limited to the application of mathematical methods used for the description of physical systems. When doing so, we are likely to commit an error of attributing to biological systems features that they do not have. Some argue that biology does need new mathematical methods conforming to its needs, and not known from physics. However, because of a specific complexity of biological systems, we should speak of their algorithmicity, rather than of their mathematicity. As an example of algorithmic approach one can indicate so called individual-based models used in ecology to describe population dynamics or fractal models applied to describe geometrical complexity of such biological structures as trees.

Keywords: mathematicity of physics, mathematicity of biology, algorithmicity of biology, individual-based modeling, fractal modeling

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1. Introduction

Mathematics is the language of the natural sciences. This statement is certainly true with respect to physics [Wigner, 1960]. All physical theories are formulated in mathematical language. Although no one-to-one relationship exists between the subjects of mathematics and physics, and mathematics covers many more subjects than physics needs, the achievements of mathematics and its astonishing development are largely due to the needs of physics.

If “God was thinking mathematically when creating the universe”, why would He limit the possibility of mathematical description to inanimate nature, allowing only physicists to enjoy this wonderful chance of discovering the world with mathematical tools? When estimating to what extent and how mathematics is used in biology, we draw some very pessimistic conclusions. Biology is insignificantly mathematized. It does not influence mathematics. It is difficult to indicate a mathematical concept developed for the needs of biology. On the other hand, there is not the slightest doubt that biology uses mathematical methods developed for the needs of physics. Thus, many questions arise: why is it that the degree of the mathematization of biology is low [Herrero, 2007], is it correct to apply in biology methods appropriate for application in physics, and finally, what can we do in the future to understand and solve these problems?

One could observe that mathematical statistics can serve as an example of mathematics developed for the needs of biology, as the methods it uses respond to real needs of biologists or farmers. But this is a bad example. At this point, such application of mathematics has nothing to do with what is discussed here. Statistics is a tool used solely to produce order in the information we obtain from experiments. Physicists using mathematics to describe physical reality, and then analyzing the properties of the resulting mathematical structures, are proceeding in a way as equally valid as that of their colleagues who empirically examine the same objects. Empirical physicists using technology go beyond the boundaries of their senses, while theoretical physicists using mathematical apparatus overcome the limits of their mind or habits and ways of thinking. If “the book of Nature is written in mathematical language”, then the analysis of mathematical structures describing the nature enables us to understand it [Heller, 2014]. As previously stated, this is certainly the case of physics [Tegmark, 2014]. We term this property of physics its “mathematicity” [Heller, Życiński, 2010; Lemańska, 2013]. This will later be the reference point in our considerations of the application of mathematical language in biology.

Let us note also that one of the unexpected advantages arising from the use of mathematics in biology in the same way as in physics is that it allows us to see the order, arrangement, and symmetry in nature, and this is what gives us the feeling of understanding the world, and the feeling of its beauty [Hardy, 1969; Hammond, 1979; Lemańska, 2001].

2. Analytical character of physics

All biological objects are macroscopic: they are of relatively large size. For this reason, when discussing problems of the mathematicity of biology, and comparing its state with the mathematicity of physics, we will refer to classical macroscopic fields of physics, such as classical mechanics.

The way of constructing mathematical models of the physical world is basically always the same. First, we define state variables specifying the state of the system examined, and then we formulate equations describing changes in the state of the system, that is, equations that will determine what influences the dynamics of state variables and in which way. In classical mechanics, where material objects are described, state variables characterize their position and velocity, and Newton’s equations of dynamics tell us how their positions and velocities will change if we ascribe to them some initial values.

With such a mathematical description of the object of interest, we can analyze its mathematical structure. The mathematical description or model of physical reality enable us not only to predict future states of the system, which is very useful from a practical point of view, but also to perceive

“things” the existence of which we would not even suspect without analysis of their mathematical structure. Who could presume that the analysis of the mathematical structure of classical mechanics would lead to the development of the principle of extreme action, that is, to the alternative formulation of Newton’s equations describing the dynamics of systems composed of material objects. Or that the formulation of Newton’s equations of dynamics requires the concept of mass. What a vast field of considerations about what mass is, and why it must be present in equations of system dynamics.

This method of the application of mathematics in physics, and this way of using mathematical structures for this purpose, I would call analytical. One of the properties of this analytical method is the wholeness of physical theories. We do not deal with single models but with a coherent theory expressed in mathematical language describing the whole of the subjects at a high level of abstraction. Mathematical structure can be analyzed by the methods available in mathematics, and the conclusions from this analysis of say, solutions of respective equations, can be obtained by analytical methods without resorting to numerical methods. Sometimes we have to use numerical methods, when the mathematical approach is applied in a concrete case, but we should always remember that each particular application of the general theory expressed in mathematical language must conform to general analytical conclusions emanating from the mathematical structure of the original physical theory. This can be exemplified by the fact known from the classical theoretical mechanics that there is no analytical solution to the three-body problem. This is a consequence of the general properties of the mathematical structure used in the classical mechanics. This is also the statement of a very high order. It is valid everywhere and always when the application of classical mechanics is justified. But because systems of three and more bodies are not rare in nature, we can always go to their numerical solution, remembering what the general theory says.

3. Application of physics to biology

It is more or less known what is living matter, and thus the subject of biology, and what is nonliving matter and thus the subject of physics. This boundary is well defined. But the boundary of the application of mathematical models of physical phenomena and processes to biology is elastic. At many points the mathematical descriptions known from physics enter the area of biology. In such cases we are fully convinced that we are justified in doing so, that we do not err, and the mathematical description we obtain is correct, even though it concerns biological objects.

Traditionally we distinguish levels of organization in the living part of nature. To name a few: the molecular and cellular levels, and, at the other extreme, individuals, populations, ecosystems, and the whole biosphere. I do not believe, as some biologists argue, that these levels are governed by their own specific principles. I rather support the idea of reducing the attributes of higher levels to the attributes of lower levels, using reasonable biological arguments (we will discuss this issue later on). Here I use this level concept only to show the map of the application of physics in biology.

At many points we can observe purely physical processes in biology: the flow of blood through blood vessels, diffusion of molecules through cell membranes, or transmission of electrical impulses in neural networks. In all these cases we can use mathematical procedures known from physics, and get correct results. Problems of this kind are often assigned to the field of physics rather than biology, and considered as biophysics. Note that all these issues belong to the field of physiology. In this area we can really use mathematical models and methods known from physics. In addition, if we consider chemistry as a branch of the application of physics, then the area of the application of mathematical language used in physics will also involve biochemical reactions. At this point we move to the level of cellular processes. It can thus be seen that in many cases at lower levels of biological organization we can safely use mathematical apparatus known from physics. As in pure physics, we can expect correct, reliable results and possibly also new results derived from the analysis of the mathematical structures used there.

There is one further area of the application of physics, although not directly related to the application of physics in biology: at the junction where these two sciences are closely connected. Life goes on in the environment. It is often modified by living organisms, but in the first instance this is a physi-

cal environment that can be described by the mathematical apparatus known from physics. Oceanic currents, movements of water in lakes and rivers, distribution of temperatures in water bodies, movements and temperatures of air masses — all these processes are governed by the laws of hydrodynamics. Oxygen diffusion and flow of water through soil are also physical processes for which we can find respective mathematical models in physics. All of them specify the framework in which life has to find its place, and the mathematical tools known from physics enable us to analyse almost all aspects of the influence of the physical environment on living organisms.

I believe that this provides evidence that biology can be mathematized, and this implies [Lemańska, 2013] that it is possible to develop single models of concrete biological phenomena and processes (unfortunately, with the dominance of physics). But this is not a proof of the mathematicity of biology in the same sense as it is applied with reference to the mathematicity of physics.

4. Theoretical biology

In some areas of biology, I think in most of them, and certainly in very essential and very “biological” areas, the direct application of physics is no longer possible. This area begins with the level of individuals and extends up through the level of populations and communities to the level of ecosystems. Why is the individual a boundary point? It is so because, to put it bluntly, life exists in the form of individuals. If evolution through natural selection is the basic mechanism of biological processes, and we will call the product of natural selection “living”, then the individual appears to us as the product of natural selection — the most important and perhaps the only one. Its traits, including its behavior, and its goals in life are outcomes of natural selection. They must guarantee it the greatest possible reproductive success under concrete environmental conditions. Physical objects are not products of natural selection, thus they are not subjected to biological evolution. That is what constitutes the difference between the Newtonian material points and living organisms.

Material points have their dynamics described by equations of theoretical mechanics. What kind of mechanics is appropriate for living biological organisms? The answer is very simple. Starting with the level of individuals we ask how many there are. This is a question about the dynamics of populations and communities. How has theoretical biology approached this problem as yet? I mean the question about the mathematical structures used to get a mathematical description of the dynamics of populations and their communities.

Physics has made enormous achievements. Thus, it is no wonder that theoretical biology precisely follows the methods used in physics [Kingsland, 1995]. Firstly, state variables describing the system are specified, and then differential or difference equations characterizing the dynamics of these variables are derived. State variables used in theoretical biology for mathematical description of populations and their communities are their so-called densities (numbers of individuals per unit area or volume of the environment). The equations describing the dynamics are so-called Volterra models [Volterra, 1931]. To approach the mathematical structure of these models, I will quote their simplest version describing the dynamics of a single population (so-called logistic equation very often used in biology):

$$dN/dt = r(1 - N/K)N, \quad (1)$$

where N is density of the population, r and K are parameters of the model. The density of such population will asymptotically increase to a value which is defined by these parameters.

5. Advantages, pitfalls and doubts

What advantages can we get from the models of population dynamics presented in above form? When analyzing the mathematical structure of this model, examining its properties, and surveying what is already known in mathematics on similar structures, we can learn a lot about the functioning of ecological systems. For example, this type of inter-species competition reliably describes the well-

known principle of competitive exclusion, when a superior competitor drives to extinction the population of an inferior competitor. An unexpected result of the analysis based solely on the mathematical structure of this type of the model (though more complex than presented above) is the possible appearance of deterministic chaos.

Does this prove that biology is not only mathematizable — that is, that some mathematical models can be applied not only to simulate certain biological processes and phenomena — but that it also possesses this extremely important property that physics has, namely, that it is possible to speak of its mathematicity, which means that by analyzing solely the mathematical structure of the model we can obtain insights into the biological reality.

To answer this question, let us consider the pitfalls in the application of the approach appropriate for physics in biology to describe population dynamics. If — as in physics — the mathematical structure used for this purpose was incorrect, then all conclusions based on it would be false.

The belief in the enormous possibilities of the Volterra approach in describing the dynamics of ecological systems reached its peak in the 1970s and 1980s. Papers and books by Robert May (for example, [May, 1976] and later [May, McLean, 2007]) speak of a great synthesis being developed that yields a concise, closed theory of the dynamics of ecological systems expressed in mathematical language. May's famous statement, that the complexity of ecological systems indicates their stability, was to be the most general and the most important conclusion derived from this theory [May, 1973]. However, confronting a complex ecological reality, this theory seemed with time to lose its power. Biologists stopped believing in its possibilities because, on the one hand, based on empirical studies, it was very difficult to support the truth of conclusions derived from mathematical models and, on the other hand, almost all the results of mathematical models were known earlier from empirical studies. Mathematicians have continued this approach, but already nobody “shouts” about total success. The matter subsided. Both sides are silent. Neither biologists nor mathematicians discuss basic issues, but when there is a need to apply a model of the dynamics of an ecological system, the Volterra model is still used, though very often this is not the most important element of the problem.

In the 1990s, some comments started to appear criticizing the Volterra approach. It was noticed that individuals are not the same as material points in theoretical mechanics, and that searching for state variables and then equations fitting their dynamics is an incorrect approach [Grimm, Uchmański, 1994]. Individuals are born, they grow, some go through different developmental stages, they reproduce, and finally they die. Material points or other physical bodies have only mass or electric charge, are eternal, and have constant properties. It was emphasized that organisms show a clear individual variability, especially in species reproducing by means of zygotes, and also in those whose individuals grow for a long time and are exposed to strong ecological interactions. At the same time (partly arising from this criticism, and partly contributing to it), the so-called individual-based approach to the modeling of the dynamics of ecological systems appeared (IBM — individual-based modeling). In accordance with this approach, ecological systems are no longer considered as dynamical systems from the mathematical point of view that can be characterized by certain state variables. We start to describe the fates of individuals, their growth, development, and interactions among them that give rise to their individual variability. When we apply the individual-based approach, the population dynamics of an ecological system becomes a by-product of what happens to individuals and between them. When developing such models, we can use only computer simulations to solve the set of equations contributing to the system. As a result, we totally lose the elegance of the Volterra models. However, the results of a single computer simulation when performed with sufficiently deep understanding of modelled system can have the same value as the results of a single experiment that can be conducted by a biologist observing actual nature. As a matter of fact, physicists sometimes use computer simulations. However, they have always a solid analytical theory available, whereas simulation is a solution when analytical solutions of the model equations are too difficult or impossible. For those who are accustomed to analytical advantages from the application of mathematics in physics, it is almost improper to rely on computer simulations as the only quasi-mathematical description without a good underlying analytical model — the means which those who apply individual-based approach in ecology have to use.

6. Algorithmicity of biology

Is there a way out of this situation? Certainly, it may be postulated that we should wait for a new mathematics, conforming to the needs and specific character of biology, and I am — among others — the author of such proposal [Uchmański, 1980, 2015]. Unfortunately, no signs of the emergence of “biological” mathematics can be seen. It is even difficult imagining what kind of mathematics it could be. There are occasional announcements that mathematics of this kind already exists in the form of structured population models, or stochastic models. But I think that the former represents common classical Volterra models, only slightly modified, that can be subject to the same objections as the original version, and the latter has in fact many assumptions from the Volterra model. Also, not all biological processes can be described by stochastic models.

I suppose that the solution to this problem is a total change in our expectations concerning the role of the application of a mathematical approach to the description of living nature, and the recognition of the distinction, in this respect, between living and nonliving nature, as I believe that biology has an algorithmic character [Uchmański, 2016]. In my opinion this is the basic difference between biological and physical objects. For [Dennett, 1995], biological evolution by natural selection is an algorithmic process. His arguments show that he sees this problem from a qualitative and also very general point of view. I would like rather to argue that we should remember about the algorithmicity of living nature when we try to describe it using mathematical language. This statement, I think, is especially important in the case of modeling of ecological systems.

An algorithm, in the general meaning of this term, is a prescription that defines firstly the objects and secondly the procedures that will be performed on these objects. For an informatician or mathematician this will be the computational procedure, usually comprising many steps, that transforms a set of input data into the results of calculations [Corman et al., 1994]. In my opinion, only when using the algorithmic approach it is undoubtedly possible to apply mathematical language to the description of ecological phenomena and processes in which the presence of individuals is directly considered. As it was stated earlier, life exists in the form of individuals. This is the most important reason why mathematical language cannot be used in biology in the same analytical way as it is used in physics, and why we have to use the algorithmic approach in biology.

As previously stated, natural selection does not operate in physics; instead we have here, for example, gravitational interactions between points that have mass. All truly biological objects are the products of natural selection or they are composed of them. Natural selection is not the same as gravitation, and I do not mean here a real difference between these two concepts but the difference in their relations to the basic components of physical systems, on the one hand, and biological systems, on the other hand (the relation material point — gravitational force versus the relation natural selection — individual). In classical mechanics, a material point has a constant property (mass), and the force of gravitation determines the interactions between material points. Natural selection does not directly determine interactions between individuals. Natural selection determines attributes of individuals or, more precisely, it causes these attributes to enhance the reproductive success of an individual under specified conditions that also involve the presence of other individuals. Traits of an individual are a result of the action of natural selection on ancestors of the individual, as genetic information is transmitted from parents to offspring (but there is also epigenetic and cultural transmission of information [Jablonka, Lamb, 2005]). Only then, an individual formed in this way has to interact with the environment and other individuals to reach its goals, and, in fact, to become subject to natural selection. The behavior of a material point in the most simple situation is totally determined by the distribution of masses between material points and gravitational force. In biology individual traits are determined by natural selection, but later on, over the history of its life, the individual has a lot of “freedom” to complete its goals. It is not equally well fitted by natural selection to all the circumstances it will encounter in its future life. Not all individuals will be able to fulfill all their goals. Moreover, traits of individuals are not formed only once, but they develop over a large part of their life. Then, although their limits are set by natural selection, their specific expression

depends on the environment and interactions with other individuals that have their own goals (often contradictory).

For the reasons presented above, in physics we can develop a theory of the movement of material points, formulate it in mathematical language, and fully explore its analytical character. By analyzing this mathematical structure we can acquire information about nature, because between nature and its mathematical model there is a complete one-to-one correspondence (this also concerns as yet unknown attributes of nature that can emerge only from the analysis of the mathematical model). And what can we do in the case of living nature?

Let us rewrite equation (1) in the form that does not imply any mathematical approach to the description of this population-dynamics biological subject. We will slightly simplify its structure, and will consider only one population. We will also neglect the continuity in time. The population size will be considered in discrete time steps: let N_t denote the number of individuals at time step t , and ΔN_t the increase in their number at this time step. Then

$$\Delta N_t = \sum z_i - \sum \delta_i \quad (2)$$

where z_i is the number of offspring produced by individual i in time step t , and δ_i is a function resembling the Dirac delta function: it equals one when an individual didn't survive time step t and zero if it survived. Both summations are made across all individuals present in the population at time step t ($i = 1, \dots, N_t$).

The first and second sum on the right-hand side of equation (2) represent the activity of individuals. This activity can be described quasi-mathematically only in the form of algorithms: if condition A is satisfied, then the individual enacts a , if B is satisfied, then it enacts b and so on. The word "enacts" should be considered symbolically. This may be real behavior, but also growth and development, reproduction, or many physiological processes, for example, metabolism. Also the structure of this algorithm will be more complex than that shown above. Such algorithms for all individuals present at time step t should be run concurrently to count newborn and dead individuals at regular time intervals. Of course, these algorithms should be not only concurrent, but also interrelated to take into account also interactions among individuals (for example, competition). This is a difficult task but possible to solve. There is a variety of numerical procedures for solving such problems. I would indicate here numerous models of the category of individual-based models recently designed and applied in ecology, which were shortly mentioned previously [Grimm, Railsback, 2005].

7. Costs and some advantages of the algorithmic approach

An algorithmic approach inevitably requires numerical analysis. In my opinion this is the highest cost of the awareness of the algorithmicity of biology. We lose all the easily attainable attributes of nature that were known from the analytic character of the Volterra models. These attributes may even be false, as we do not know if the picture of nature arising from the algorithmic paradigm will be the same as that produced by classical Volterra models. Yet, it was so easy to classify the dynamics of ecological systems based on the trajectories of sets of differential equations in the phase space. I suppose that the concept of stability of ecological systems, so much appreciated by ecologists and biomathematicians, will have to be redefined. My experience with individual-based models shows that it is much easier to generate population fluctuations there, — this dynamic always being difficult to attain in the Volterra models — if we ensure the biological correctness of our model assumptions [Finerty, 1980; Nisbet, Gurney, 1982]. Note that the domain of equation (2) is a set of natural numbers. The necessity to respect this restriction is a kind of formal hindrance, but it then frees us from unclear interpretations of variables in equations (1), which sometimes are numbers of individuals (natural numbers) and sometimes population densities (real numbers). Abandoning the Volterra models (most often analyzed in their differential form) also spares us the nightmare of the continuity of their solutions. Even populations of bacteria are not likely to satisfy this condition.

Indeed, taking equation (2) as the starting point, interpreted in the algorithmic sense, it can be shown [Uchmański, 2012] in which way, step after step, or rather assumption after assumption, added to its initial form and initial interpretation, we can arrive at equations of type (1) analytically interpreted. Some of these assumptions are purely formal and correct (they rely on calculating mean traits of individuals in a population or generation), but the most important ones, those changing the interpretation, raise grave doubts, as they replace the question (formulated in the algorithmic sense) about which individuals will reproduce at a given time moment or under specific conditions, and which ones will die (where individual variation is important) with the relation of a statistical character between the growth rate of population density and the density itself (where the individual variation of organisms disappears, and is replaced with average values). The Volterra models claim to be universal. Because they contain the assumption that individual variability can be replaced by average values, attempts are made to apply them to the description of number dynamics of all species (happily not of land plants). To me the basic attribute of living nature is its enormous diversity. It cannot be taken into account sufficiently through changes in the parameters of the Volterra models without changes in its general form. In addition, it is difficult to indicate at least one species that would, without any doubts, satisfy the assumptions of the Volterra model.

As it can be seen, my conviction that nature is algorithmic inclines me to think of individual-based models where the description of number dynamics of populations is concerned. In this case I am against the application of the Volterra models. Likewise, in my opinion, hybrid models emerging from time to time, that combine features of both the above approaches to the description of ecological systems, are a nuisance. This does not mean that I do not see the application of differential and difference equations in biology, and especially in ecology. These models, describing the cycling of elements or energy fluxes in ecological systems, can safely use these mathematical tools, as even in the worst case they provide very good approximations, which is indicated by the many very useful practical applications of these models.

The necessity of the application of the algorithmic approach can be seen not only in the case of the mathematical description of the dynamics of ecological systems, but also in other fields of biology. Many years ago, Przemysław Prusinkiewicz and Aristid Lindenmayer published a book with the significant title *Algorithmic beauty of plants* [Prusinkiewicz, Lindenmayer, 1990], in which they presented many models of the growth and development of the geometric structure of plants. The most important idea which the authors wanted to convince the readers of was the statement that the development of plants with the geometrical complexity of their above- and below-ground parts can be effectively and correctly described only by their respective fractal algorithms. Thus far, differential equations have been used to derive models of plant growth. They enabled, at best, the modeling the growth of plant mass, but did not provide tools for modeling the distribution of this mass in two- or three- dimensional space. Thus, we have had no tools to derive models of the development of the geometry of the multidimensional structure of plants. This constraint gave rise to doubts whether without these geometric peculiarities in plant development we could reliably model even only the growth of tree mass. The algorithmic approach with the use of fractal theory was later successfully applied to modeling the growth and development of a large class of modular organisms: in addition to plants, also corals, sponges, and, for example, colonies of bacteria and fungi [Kaandorp, 1994]. It should be emphasized here that this approach to the description of plant development with the use of fractal algorithms has no counterpart in the form of analytical models. This is not an approximate, numerical solution to a problem described with the use of a traditional method for modeling nature. This is an example of an exclusively algorithmic view of the modeling of biological processes.

8. Conclusions

I think that the most important reason why mathematical methods known from physics can't be applied in biology is the much greater complexity of biological systems and the different nature of this complexity in comparison with physical systems. So far, fractal modelling is only one mathematical

tool available to assess this complexity and to model its dynamics [Mandelbrot, 1982]. However, fractal modelling means building and later computer simulation of some algorithms.

The use of algorithms to solve problems that cannot be dealt with in any other way is not new in mathematics. There is a concept of the mathematical experiment [Tymoczko, 1979; Hofstadter, 1981; Lemańska, 1994; 1997], the application of which is, in principle, close to that proposed in this paper with reference to biology. Ecology seems to provide many examples of processes and events, the hidden nature of which can be disclosed just by the application of the method of mathematical experiment by means of computer simulations of respective algorithms.

What can we expect from the algorithmic approach in biology for the future? At present, the individual-based approach in ecology involves a wide variety of models developed for the needs of the moment [DeAngelis, Grimm, 2014]. They certainly require a greater degree of standardization (standard models for standard ecological situations) and appropriate methods for their generalization. The first step in this direction has already been taken. A so-called ODD protocol has been proposed, introducing a standard method for the description of the goal, attributes, and use of individual-based models [Railsback, Grimm, 2012]. Also so-called pattern oriented modelling [Grim et al., 1999, 2015] can focus these efforts properly. On the other hand, despite some optimism (see for instance [Grimm, Berger, 2016] or [Grimm et al., 2017]) it is difficult to predict all aspects of the future development of this new view on the application of mathematical methods for the description of living nature.

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