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## Toward a Post-Physicalistic Concept of the Organism

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### Abstract

The development of organisms shows an end-state-directedness at various levels of organization. The concept of “self-organization”, arising from the study of physico-chemical processes, has been used for the understanding of the nature and causality of this specific characteristic of organismic development. Based on that concept it is currently attempted to develop computational models of complex bio-molecular systems. We believe, however, that essential differences exist between physico-chemical and biological systems, which must be taken into account for future theoretical work. We discuss, e.g., the relationship between static and dynamic quantities, which limits the feasibility of mathematical modeling of the dynamics of organismic development. To grasp the logic of the organismic causality we outline a post-physicalistic concept of organisms based on the idea of an intrinsic nature, which is not static, but rather the process of the production of information.

### 1. Introduction

An end-state-directedness (*Endgerichtetheit*) can be observed in all organisms with respect to the dynamics of development at various levels of organization. Typical examples include embryogenesis, growth, regeneration of organs and cell division. The description of the intra-organismic causality that steers such processes is one of the central tasks of theoretical biology since its origin. End-state directed processes occur however in physical and technological systems. The development of fast computers since the 1960's has made possible the computation and simulation of physico-chemical systems, whose causality can be described only with the help of non-linear mathematics. Under certain conditions some non-linear systems can display end-state

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directed behavior, which is described in modern physics and systems theory as “self-organized.” Supported by the enormous computational power of modern computers, today’s biomathematicians, biophysicists, and systems biologists worldwide attempt to model the end-state-directedness of simple and complex bio-molecular systems as results of self-organization of dynamic physical-chemical systems.

We are convinced that these efforts have brought important insights about the causation of organismic processes and will continue to do so in the future. However we understand it to be problematic when physico-chemical models are applied to biological processes if the essential differences between the biological and the physico-chemical causality are ignored. The present article focuses on some of these differences that are particularly important for contemporary theoretical biology.

## **2. The Gradual Physicalization of Biology**

The theory of self-organization, i.e., complexity, chaos theory, and synergetics, often ascribed to the theory of dynamic systems, is not a trend, but rather the most important paradigm in various formally-operating natural sciences of the present. The models of these theories always imply certain ideas about *causality*, *system*, and *matter* borrowed from classical physics. Accordingly, biology cannot simply watch with indifference the invasion of such modelling in theoretical biology with the excuse that “they are just models.” Generally the conviction that organisms are nothing more than dynamic self-organizing physico-chemical systems prevails in the thinking of biologists, biophysicists and systems biology who have studied under the influence of the dynamic systems world view. With the great suggestiveness of this successful paradigm, it is difficult to think otherwise about organisms. Mathematical systems-theoretical thinking, which has prevailed since the 17<sup>th</sup> century in any case, has achieved in the last several decades such a great influence through the introduction of the computer that its ontology underlies explicitly or implicitly almost every natural scientific achievement.

It is not surprising that the so-called “whole cell simulations”<sup>1</sup> currently count as some of the most important goals of the natural sciences. The former director of the U.S. Institute for Human Genome Research, Francis S. Collins, predicted that it will be possible to construct a computer model of a cell that describes all its components including molecular interactions and that allows their reactions to stimuli to be predicted (Collins and Jegalian 1999). The well-known embryologist Lewis Wolpert argued that computer simulation of embryogenesis is possible in principle (1995) and

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<sup>1</sup> Tomita 2001; Normile 1999; Wayt Gibbs 2001.

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thought that it would be realized by the mid of the 21<sup>st</sup> century. The majority of biomathematicians and systems biologists scarcely reflect about the unclear boundaries between the pragmatic and ontological relevance of their models. This makes it practically impossible to determine to what extent they ascribe ontological significance to their system theoretical models and how explicitly they do this. Consequently this development is philosophically interesting. The talk about “systems,” both “dynamic” and “complex,” is viewed as obvious and unproblematic to such an extent that it is considered de facto ontologically relevant. Young biologists currently learn to think in systems theoretic terms and methods even when they have no reference to systems biology. They are not taught about the limits of this approach to biology, so that in the end they have no other choice than to view organisms as particularly complex dynamic systems. In this respect, the idea of dynamic systems is made into an ontology. Brian Goodwin is one of the most decisive exponents of the hidden, implicit ontologizing of the systems theory approach, since he speaks about the computer-based calculation of *possible* forms of life(!) that have not yet evolved, i.e., the computer-generated prediction of imaginable evolutionary results (1994, 102). “Evolution in silico” is no motto, but a reaffirmation of physicalism in the new century.

The physicalization of biological thought is not a new development; it has a prehistory of some hundred years. It is mirrored in the transformation of theoretical biology. This discipline began in the early 20<sup>th</sup> century with the works of Julius Schaxel and Jakob von Uexküll and pursued the goal of working out a philosophically-consistent foundation for biology. In the 1920s Alfred Lotka and Vito Volterra developed mathematical models of population dynamics; thereby, they became precursors to the systematic mathematicizing of theoretical biology that began in the 1930s with the work of Ludwig von Bertalanffy.<sup>2</sup> Theoretical biology became a mathematical discipline with the development of theories of nonlinear dynamic systems and the related approaches of self organization, chaos, and complexity that began in the 1960s and continue to the present. Theoretical biology thus became a mathematical discipline<sup>3</sup> that is often called “biomathematics.” The original breadth of the themes was sharply limited. In departments of theoretical biology today, mathematical models and computer simulations are employed to demonstrate and analyze processes in evolutionary theory, developmental biology, ecology, neurobiology, and epidemiology. This means that in practice the only branch of theoretical biology that has survived is the one that goes back to Bertalanffy. But even in this case, important philosophical

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<sup>2</sup> Alan Turing and Nicolas Rashevsky are the other important founders of the mathematical branch of theoretical biology.

<sup>3</sup> Goodwin and Saunders 1992; Murray 1993; Kauffman 1993, 1995; Goodwin 1994; Frank 1998.

intuitions of Bertalanffy were lost from sight.<sup>4</sup> Thus, the transformation of theoretical biology into biomathematics led to a great gap among the theoretical reflections about the foundations of biology. This gap is filled today more and more by the philosophy of biology.

## 2.1 Organisms as Self-Organizing Dynamic Systems

For a theoretical biology reduced to biomathematics, the organism is a physico-chemical dynamic system whose end-state-directedness in embryonic and other processes results from an extremely complex structure of interdependent biomolecular reactions.

At this point it would make sense to introduce several “technical details” in the theory of dynamic systems: A system is defined as a *dynamic system* if its state at any given moment can be described as a limited set of time-dependent or state variables  $x(t) = [x_1(t), x_2(t), \dots, x_n(t)]$  for which a function  $F$  can be formulated stating mathematically the connection between states at times  $t$  and  $t + \delta t$ . The properties of this function reflect the *causal* relationships at work within the system.

The set of state variables  $[x_1(t), x_2(t), \dots, x_n(t)]$  spans an *abstract space*, the system’s so-called “state-space.”

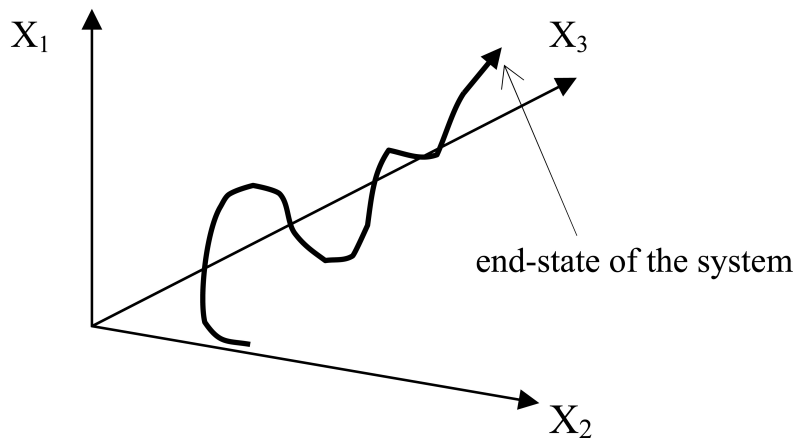


Fig. 1: State-space and trajectory of a dynamic system with three state variables.

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<sup>4</sup> In his book *Problems of Life*, Bertalanffy speaks of a new “non-quantitative’ or *gestalt* mathematics” for biology in which “not [...] the notion of quantity but that of form or order would be fundamental.” (1952, 159-160)

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It is important to keep in mind that the change or development of a dynamic system is not merely the result of the function  $F$ , but depends also on a group of externally fixed parameters. The most abstract formula for a dynamic system must therefore be/read as follows (Ebeling and Sokolov 2005, 40):

$$x(t + \delta t) = F(x(t), p, \delta t); p = [p_1, p_2, \dots, p_m]$$

The letter  $p$  represents a set of *parameters*. All parameters are externally defined constants. They represent either real constants or quantities assumed to be constant, the latter being the usual case.

In the paradigm of self-organization the end-state-directedness of physico-chemical processes is explained by the canalization of dynamics in definite very small regions of the corresponding “state-space.” The trajectories of system development seem to be attracted by these regions. The system runs through only an extremely small realm of possible states and then reaches an end-state. Such states that attract a system are called “attractors.” The end-state-directedness of such systems is steered internally, i.e., it is conditioned upon the interweaving of (nonlinear) relations only that prevail the elements of the systems. The concept “self-organization” denotes precisely the internally conditioned origin of order that does not require an external steering or an inner program.

Systems biology concentrates on the modeling of the dynamic of genetic, metabolic and signal networks and the conditions of their end-state-directedness through attractors. It also has experience with larger systems that come from the coupling of such networks. From the perspective of the theory of dynamic systems, the end-state-directedness of embryogenesis, cell cycles, and other end-state directed phenomena is reduced to the dynamics of an enormously complex system of positively and negatively coupled biomolecular reactions.

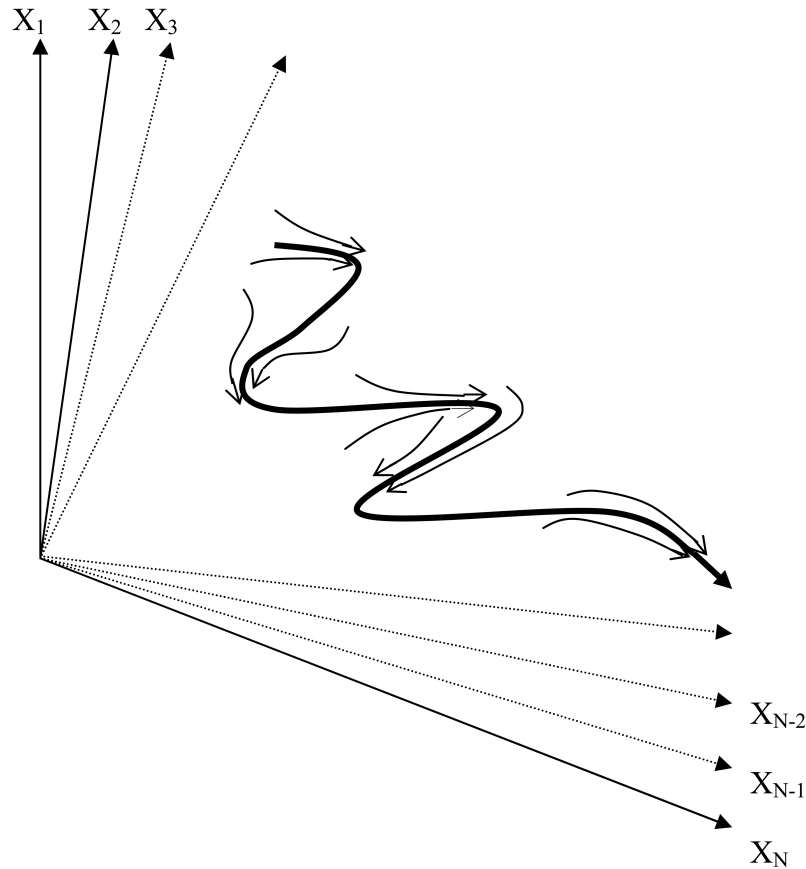


Fig. 2: An abstract depiction of embryogenesis: An end-state-directed process that is constrained by a series of attractors each developing out of previous state-spaces and the consequent attractors (indicated by the arrows convergent to the developmental trajectory).

In the figure above, the long curve represents a biologically meaningful development of embryogenesis, i.e., one that leads to a species-typical result and not to a malformation or a monster. The variables  $X_1$  to  $X_n$  represent important dynamical quantities (like concentrations of proteins and signal substances etc.), the coherent variation of which is characteristic for an organism. The long curve does not symbolize a single trajectory but rather bundles of these. The short lines on both sides of the embryogenetic curve show that accidental small deviations from the embryogenetic main path are corrected. This means that the entire curve represents a series of attractors (and not only the end-state).

The figure above is only intended to depict the logic of a hypothetical computer simulation that might be possible in a remote future – in other words: it depicts a thought experiment. To believe, however, that such a simulation is in principle feasible

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reveals overall a *metaphysical* preassumption to be fulfilled: I.e. that every organism is the result of a causal process that can be sufficiently described by the theory of dynamic systems.

The basic metaphysical assumptions for the foundation of theoretical biology are fundamentally more interesting than the others, epistemic and methodological.

### **3. Limits to the Understanding of Organisms as Self-Organizing Dynamic Systems**

We think that the metaphysical idea that organisms are complex systems whose causality can be understood in principle from the theory of self-organizing dynamic systems runs into two important limits: a mathematical and a physical.

#### **3.1 From a Mathematical Point of View**

The solving of differential equations, even with the help of computers, presupposes a particular condition: A sharp division is found in the biomathematical models used to date between dynamic and static quantities, i.e., between variables and parameters. The externally-determined parameters influence very sensitively the dynamics of variables, since they play a very important role in the canalization of this dynamic in a certain direction. Theoreticians determine the value of the parameters in the system so that the dynamic model can calculate the variables. This division between variables and parameters, i.e., between dynamic and static quantities, can be demonstrated in a great many texts of biological systems literature. To give just one example, a few years ago in a well-known journal, a model of the cell cycle of yeast had 36 variables and 143 parameters (ration 4:1) (Panning et al. 2007).

Some parameters represent the provision of the system with energy or material from the environment, others stand for the degree of activation of certain enzymes. Many parameters are abstract constructions that combine the influence of many quantities such as volumes of the organism, temperature, pressure, and pH value into the system dynamics as a single value, i.e., the parameter itself.

The sharp division between variables and parameters is not problematic within physics. It is obvious, however, that quantities whose causal influence on the system's dynamics in biomathematical models is summarized in parameters will vary continuously in real organisms. For example, the variation of cell volume during a real cell cycle would imply that some parameters that are connected to the concentration of

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many compounds and (osmotic) pressure can change. The same is true for an embryogenetic process. Hence, it is evident that even the most primitive organisms go beyond the physical dimension of self-organization. In sharp contrast to formal models, the quantities in real networks within organisms are highly dependent on the network's own inner dynamics. In order to preserve their own adaptation, organisms trigger multiple changes within themselves (Plaetzer et al. 2005). In modeling them as dynamic systems, these changes ought to be described as internally controlled changes of many parameters, especially if the model makers claim to have created a realistic model of the organism's causality. A model that realistically mirrors the organism's autonomy must be able, at least in principle, *to calculate a significant part of its parameters*, i.e., to dynamically represent those quantities which in current modeling are kept constant.

Therefore, with regard to the adequacy of self-organized dynamic systems theory to deepen our theoretical understanding of the organism, the crucial question is whether the sharp distinction between dynamic and static quantities, or variables and parameters, can be overcome or at least softened. That would be achieved if the model makers succeed in converting most of the parameters into variables and let the overall system's dynamics calculate its value. This would be real self-organization.

There is a reason why it is very probable that models resting on today's principles of the theory of dynamic systems cannot handle the required level of dynamical complexity (Deacon and Koutroufinis forthcoming): The role of parameters in the theory of dynamic systems is to *constrain* the development of the state variables  $x(t)$ . Through the choice of parameters, the modeler can construct a certain attractor of the dynamics of a system of coupled differential equations. If the parameters or relations between parameters are changed above a certain value, the dynamics of the system will be qualitatively changed, i.e., attractors of a new kind arise: A "mono-stable" system can become "bi-stable" or even chaotic (Ebeling et al. 1990, 118). The determination of the parameters results from the hierarchically higher level of the one who models, just as in cybernetic machines, the target state is determined by the engineer who by definition is at a logical level which is higher than that of the operations of the system. But a dynamic model which is supposed to capture the organism's autonomy must be to a high degree a self-constraining model. If we consider that the parameters (or relations between the parameters) constrain the dynamics, it is questionable whether on the basis of the theory of dynamic systems, dynamics could be constructed that constrain themselves. Of course, we can imagine that in systems of a hundred or more coupled differential equations, the modelers could succeed in dynamizing some parameters, i.e., calculate their values with the help of other equations. But it would not suffice to marginally reduce the number of parameters in contemporary models – *they would have*



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*to be distinctly smaller than the number of variables.* The question is, however, whether the steep reduction in the number of parameters to a *fraction* of the number that the contemporary models have would lead to an enormous increase in the instabilities, i.e., to chaotic behavior (Koutroufinis forthcoming; 2007, 124-128; 1996). In this case, the development of the modeled organism would derail into areas of the state-space which are biologically not expedient (e.g., malformations, monsters, death).

This has the following significance for the large projects of systems biologists who believe that it is in principle possible to simulate the whole process of embryogenesis: Every advanced dynamic model of embryogenesis that had to operate without the foundation of the external determination of most parameters, would in the best case simulate teratogenesis or the origin of malformations, i.e., the derailing of embryogenesis into unlivable monsters. However, even less ambitious projects, like for example the whole cell simulations run into limits in principle when they see in the theory of dynamic systems a means for the understanding of organismic causality. For cells cannot be described as systems, most of whose quantities are not internally regulated.

### **3.2 From a Thermodynamic Point of View**

Systems serving as models of self-organization require *gradients* of energy and/or material. A typical example of such a gradient is the difference of temperature in the so-called Bénard convection. This effect appears when the lower layer of a fluid is heated and the upper layer is kept at a cooler temperature. At a certain difference of temperature between the bottom and the top of the fluid the heat flux reaches a critical value and convection occurs. Coherent macroscopic movements emerge in the fluid and form a highly structured pattern of hexagonal cells. In all mathematical models of dynamic systems, gradients are represented by a number of parameters.

There is a fundamental finding in thermodynamics with consequences for the applicability of the theory of complex dynamical systems to biology. These consequences have barely been understood. It states that every form of self-organization of a physico-chemical system amounts to a *decrease* in the gradients which are imposed on the system and which move it away from the thermodynamic equilibrium, that is, from the state of total lack of physical action. *Each self-organized system tends to return to equilibrium.* The hexagonal Bénard cells transport heat upwards faster than simple heat conduction, thus *increasing the rate of gradient destruction.* Two well-known physicists got to the heart of this finding:

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As systems are removed from equilibrium, they will utilize all avenues available to counter the applied gradients. As the applied gradients increase, so does the system's ability to oppose further movement from equilibrium. [...] No longer is the emergence of coherent self-organizing structures a surprise, but rather it is an expected response of a system as it attempts to resist and dissipate externally applied gradients which would move the system away from equilibrium. (Schneider and Kay 1995, 165)

All self-organized structure-formations conceivable in physics occur only because the higher the order of the system's actions, the more efficient the degradation of the causes of this order, i.e., the degradation of the gradients. This essential property of dissipative (i.e. entropy producing) dynamic systems is also well known as the *principle of maximum entropy production*.

A dynamic system which is suggested as a model of an organism must be able to independently calculate and adjust also – but not only – those parameters which describe the organism's self-supply with energy and materials from its environment, as this is something all organisms do constantly. Accordingly, the modeling of real biological self-organization would demand of systems with an ability to establish the self-imposition of energetic-material gradients by their dynamics. But within current physics this is *impossible*, primarily because all dissipative dynamic systems organize themselves in order to reduce the gradients imposed on them, hence not in order to maintain them (Koutroufinis forthcoming). Thus we cannot expect from a system the capacity to determine its own parameters – especially those representing energetic-material openness – such that it would impose gradients upon itself.

There is also experimental evidence indicating that the causal order of organisms evades a physicalistic understanding of self-organization. For example, biologists have known for a long time that the exchange of energy and material between real (not virtual) organisms and their environment does *not* follow the principle of maximal entropy production. This is logical, of course, since a high production of entropy means a high degradation or waste of energy. The experimental and theoretical research of Gernot and Renate Falkner clearly shows that the metabolic exchange between cyanobacteria and their environment only exhibits a high production of entropy if the adapted states of the bacteria have been disturbed by an environmental alteration. The cells then readjust their energy utilization to the new environmental conditions, such that an entirely new stationary state of minimum entropy production is attained (Plaetzer et al. 2005). Thus, the act of physiological re-adaptation, as they described it,

is aimed at minimization of entropy production, which is in contrast to the physico-chemical theory of self-organization that predicts a maximization. Only the transition of one optimally adapted state to the next seems to be in accordance with the physicalistic conception of self-organization in that it produces – in a state of flux – a lot of entropy. But as soon as re-adaptation has been accomplished, the organism is in a state of low entropy and low entropy production as well. This indicates that only during the onset of an act of physiological adaptation the organism behaves as if it follows the laws of a merely physical dynamics, whereas in the subsequent stages it proceeds in a manner that can only be explained in biological terms. Considering the fact that the energy dependence of other metabolic processes also obeys linear flow-force relations in regions far from thermodynamic equilibrium (see, for example, Stucki, 1980), it seems plausible to assume that all organisms aim at the minimization of entropy production. Physiologic re-adaptation is a biological act that requires the *internally conditioned* coordinated variation of many dynamic quantities or variables which, in the models of systems biologists, are described as parameters (i.e., as non-variables).

There is also experimental evidence that a process of minimization of entropy production also takes place during embryonic development. The results of numerous measurements in several studies led to the conclusion that the entropy production “indeed decreases at separate stages of the ontogenesis (if early stages of development are excluded).” (Martyushev and Seleznev 2006, 40)

To sum up: both theoretical considerations and experimental evidence make clear that *the theory of self-organization of physics is too weak to account for real biological self-organization*. There is much to be said for the fact that biological end-state-directedness cannot be understood with contemporary and even contemporary imaginable physics, operating with differential equations. Consequently, one cannot claim that it is possible in principle to reduce organisms to dynamic systems.

#### **4. About the Need of a Post-Physicalistic Concept of the Organism**

The main regions of theoretical physics – mechanics, electrodynamics, relativity theory, thermodynamics, quantum theory, etc. – are based on certain fundamental equations, like Newton’s Second Law, the Maxwell equations, the Einstein field equations, the Schrödinger equations, etc. With the exception of Newton’s Second Law, these equations presuppose direct or indirect infinitesimal calculus.<sup>5</sup> In addition to these

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<sup>5</sup> The general theory of relativity requires differential geometry which is carried out with infinitesimal calculus.

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fundamental equations, these disciplines have their typical objects, like the harmonic oscillator, the solar system, electromagnetic waves, the atomic model, etc. These objects are basically designated as “systems.” By “system” is meant in the formal languages of various sciences the collection of strongly interacting/interdependent elements and the relations between them (Bertalanffy 1971, 55; Bertalanffy et al. 1977, 17). The relations between the elements of the above-mentioned objects are represented by differential equations that are developed with the help of fundamental equations. By integration of these derived differential equations, one attempts to define the dynamics of a system of a certain constitution as an unambiguous function of time, which succeeds in simple dynamic systems.

In complex dynamic systems of self organization theory, an analytic solution is not possible, as a rule, and the behavior of systems is reckoned with computers, i.e., simulated. The relations between the elements in non-living physico-chemical dynamic systems can be described adequately by differential equations, i.e., there is no basic break between the causality of real systems and the models. This is possible because in the real non-living systems, casual factors have a constant value. No one would expect from a model of harmonic oscillators that the constants of the spring are altered by the behavior of the system itself. Nor that a model of the solar system calculates the mass of the sun or the gravitation constant. In the real world these magnitudes cannot be variables altered by the system’s dynamics. These factors can be represented by parameters in the models without any problem.

The situation with organisms is quite different. When one claims that important processes of an organism can be reduced to dynamic systems, or something similar like networks (Kauffman, 1995, 99-111), then one states that the causality of the organism can be reduced to the elements and the relations subsisting between them which can be described by differential equations. But to describe the organism means at least to describe its metabolism, i.e., the dynamics of self-supply, the anabolism and catabolism. If the causality of these processes cannot be reduced in principle to the causality of the models, then it is impossible to grasp the logic of the organismic causality by means of mathematically-conceived causality of models. As explained in section three, a good model of organismic causality would allow the division among parameters and variables in a much smaller degree than is the case in present-day models. This difficulty seems from a contemporary perspective to be impossible to overcome. On the contrary, there is much to be said for a unique nature of organismic causality, that cannot be understood by the main mathematical methods of physics since the 17<sup>th</sup> century, infinitesimal calculus. This means that causality of real organisms follows a logic that is *essentially* different from the logic of biomathematically computed, i.e., simulated

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causality. This speaks for the necessity of a post-physical (in the literally sense of the word) turn in theoretical biology.

#### 4.1 Intrinsic Nature vs. a Bundle of Features

This post-physical understanding of the organism derives from the fact that all living creatures engage in processes that are effectively ‘outside’ that which can be modeled in the mathematics of contemporary systems physics. In present-day models, the model makers take on the function that every actual organism engages in: i.e. determining the values of the parameters of their own dynamics. In other words they work according to the paradigm of modern physics.

This internalization of model parameter-setting can be designated by the concept of the *intrinsic nature* of the organism. For Aristotle the *soul* (psyché) was the intrinsic nature of the organism. For the vitalists, it was the *vis vitalis*, the entelechy, etc. In the 20th century it was conceived as a “genetic program,” (however if one thinks this through to the end, this could only function if it shows vitalistic attributes that contradict the properties of a program). In the present contribution, this concept is used to construct a contrast between any future organism conception and the methodology of modern physics. The abstract entities of physics – i.e., quantities like mass, elasticity, electrical charge, impulse, spin, intensity of the magnetic field, viscosity, etc. – symbolize features of real entities, i.e., of planets, macroscopic bodies, electrons, magnetic fields, fluids, etc. But the essence, i.e., intrinsic nature or ground of being of real entities does not interest most physicists. In physics, the real entities are solely defined as a bundle of properties, while further thoughts about the essence of these real entities do not appear to be necessary. This applies not only to derivative equations, describing the dynamics of the systems, but also to the basic equations of the various major domains of theoretical physics. The quantities in all equations (basic and derived) of mechanics, electrodynamics, quantum mechanics, etc., are abstract entities that symbolize the features of actual entities. The expression “actual entities” does not have the same meaning as in the metaphysics of Alfred North Whitehead, but rather it serves solely to delimit the concept from “abstract entities,” a philosophical terminus technicus.

The metaphysical foundation of physicalistic procedures stands in opposition to the basic idea of the metaphysics of Aristotle, who defined the relation of essence and properties clearly and definitively for the philosophical tradition. For Aristotle the *ousia*, which in the Latin tradition was translated inaccurately as “substantia,” is more

than the sum of its properties. The *ousia* is the *intrinsic nature* of an actual entity that constitutes its properties. In contrast to this, physics ascribes no intrinsic nature to actual entities as the basis of their properties (Russell 1927, 270, 402; Eddington 1920, 200; Brüntrup 2011, 45). Physics need not distinguish between actual and abstract entities, since it defines the latter by their role, i.e., function in highly complex formalisms. The more complex the formalism and the experimental apparatus of physics, the less clear and important it becomes whether there are actual entities to which the abstract entities refer.

Bertalanffy took over these positions and introduced them explicitly in theoretical biology. His anti-metaphysical perspective on natural science is particularly important for the understanding of modern biomathematics: Natural laws are only “symbolic representations of formal relations between phenomena” and “not factors causing the course of events.” (1952, 170) Similarly, “ultimate physical entities are not ‘material atoms’ as a metaphysical reality, but *they can be described only formally by mathematical expressions, and physics tells nothing about their ‘inner nature’.*” (ibidem, italics from the authors) On the basis of this anti-essentialism, Bertalanffy thought that his theory “overcomes the mechanism-vitalism alternative at a higher level” (ibidem): The “organismic conception,” by which he meant his mathematically-oriented theoretical biology, “says everything the scientist is entitled to announce. He makes no statements about the ‘nature’ of things and hence also about the question of an ‘essential’ difference between the living and the non-living. [...] The task of the vitalist is different: what he tries to do is to understand the ‘inner nature’ of things.” (ibidem, 171)

The difficulties posed by the mathematization of organismic causality shown above (which oppose the program of Bertalanffy) lead us to question whether theoretical biology can overcome its anti-realistic position without becoming vitalistic. Biologists must ask themselves what the idea so beloved in physics means for them, namely, that indispensable general concepts like atom and electron are merely names for logical terms in formalisms: Ought their science distinguish itself from the methodology of physics that views universal concepts like “electron” as complex abstract entities – i.e., as combinations of simple abstract entities like load, mass, spin, etc. –, for which no real entities need to correspond? The acceptance of this anti-realistic position in biology would reduce the organism of a certain species to abstract entities, or rather universals, e.g., to protein concentrations, whose relations a system of differential equations could describe. The uniqueness of a particular species would then consist in a specific combination of certain universals. But a combination of abstract entities is still an abstract entity. The conviction that something abstract can represent something real like

individual organisms of a concrete species without a high loss of descriptive/explanatory adequacy rests on the metaphysical assumption that the causality of the real can be completely conceived by an abstract *mathematical* logic. This assumption is unavoidable, since mathematics operates only with abstract entities. This fundamental assumption of physics since the 17<sup>th</sup> century was more or less successful in physics, although it led to large aporias with regard to the nature of our cosmos since the question of the nature (essence) of the cosmos and its elements was consciously ruled out. In biology it runs rather quickly into great difficulties, as we did indicate in Section Three.

Theoretical biologists ought to attend in addition to the fact that ignorance of the question about the intrinsic nature of actual entities goes hand in hand with the position of *ontological relationalism* that is so widespread in modern physics. This position negates the idea of intrinsic features of entities that refer relationally to one another, and it develops an ontology whose basis is the relations themselves. According to *ontological relationalism*, the relata have no actual, i.e., intrinsic nature because they “are no more than that which stands in relation.” (Esfeld, 2002, 76) This general position can be applied to the question of the nature of abstract entities: In this case it would state that quantities in equations, i.e., the relata, are abstract entities whose nature consists in their function in a formalism that expresses relations between them. It has often been claimed that important quantities of base equations are defined circularly as interdependently: The concept of mass in the Second Newtonian Law is not definable without the concept of force and vice versa. Similarly, it is often claimed that it is not possible to speak of electrical charge without introducing the concept of electric field and vice versa. To what extent the basic quantities of physics are abstract entities that are only definable circularly and interdependently is a difficult and controversial question under discussion. But the position of ontological relationalism can also be raised in relation to the elements of various physical theories without touching on the problem of circular interdependence of abstract entities of physics in base equations: The derived equations describe the relations of elements of a certain system, e.g., the forces between electrons. It is often claimed that the nature of complex abstract entities, e.g., the concept of “electron” consists solely in its function in formal relational nets, i.e., in derived equations in which they occur. From this people claim that the concepts of electron and all other elementary particles are merely concepts whose nature is defined by the relations that they have in mathematical formalisms to other concepts of similar complexity.

But even if physicists should succeed in reducing the abstract entities that occur in the highly complex formalisms of quantum theory, describing kinds of elementary



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particles, to the knots of the mathematical relations existing between them, the following question remains open: Do constants or other static quantities, i.e., parameters, occur in the equations (derived equations and base equations) that are not relationally defined, since they possess an unchanging value that, as such, is not determined by the relational nets in which they occur? If yes, then we must raise the question whether the relational-functionalist ontology of modern physics has systematically ignored the intrinsic nature of the relata or rather hidden it in the parameters. If this is the case, then the idea of the intrinsic nature lives on unrecognized in the parameters, and indeed, in the sense of the substance concept of medieval metaphysics, in which the essence of entities is considered equal to static being, since the parameters are constants.

Bertalanffy's above-mentioned anti-essentialism converges strongly with the functionalism and ontological relationalism of modern physics. The direction of theoretical biology in this tradition emphasizes that it has overcome the substantialism of genetic determinism, i.e., the metaphor of genetic programming: Genes cannot steer the construction of the organism by means of "instructions," and they are not the bearers of genetic information. Much more interesting than this correct position is its justification: gene and proteins are nothing more than the material elements of networks of biomolecular relations that are equally justified with the other elements – a position that is well known as "parity thesis" (Griffith and Gray 2005, 423; 1997, 474; 1994, 275). The genome can even be seen as a limiting factor (in the sense of a canalization) for the developmental potential of a cell (Wessel 2009). One can argue about this understanding of genes, but the nature of the gene is not the theme of this article. However, if the functional whole of such networks is portrayed as a system of  $x$  coupled differential equations with  $m \cdot x$  parameters, the question necessarily arises: are the parameters anything other than moments of a new tacitly imported (static) substance, like the genetic program was previously? The parameters are nothing but a reflection of the intentions of the person modelling. They reflect their will to calculate something specific through directed determination of parameters, i.e., to create a dynamics of definite end-state directedness.

It is typical for physicists that they produce their systems experimentally and conceptually by themselves. "System" means finally "composite." But in biology we face ourselves with organisms. Something similar occurs for biological universals like species of organisms, proteins, genes, viruses, etc. They are not at all constructed like physical universals, which are merely bundles of features. In striking contrast to physics, we are faced in biology with an enormous, confusing diversity of kinds of entities. Each of these entities contains further sub-entities and at the lowest level there



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are typically no two identical members, since real biological entities reveal a certain variety. It is apparent that we cannot define the essence of these abstract entities in biomathematical equations – e.g., what are specific kinds of molecules – on the basis of their role in a mathematical formalism of our own construction. The enormous qualitative multiplicity of life compels entirely different ways of conceptual construction of entities such as these, which are permissible in physics. For this reason, a biomathematically-oriented theoretical biology can never achieve the high degree of functional dependency between mathematics and ontology that theoretical physics has – i.e., to produce the definition of the nature of its abstract entities (ontology) from their role in formalisms (mathematics). In biology we encounter at every step the fact that the organisms have something that can be designated as intrinsic nature. This is shown by their capacity to regulate all kinds of values of their dynamics by themselves. It is also indicated by the fact that organisms are active agents of interaction with their environment.

#### **4.2 Intrinsic Nature and Information**

The easiest way to define the intrinsic nature of the organism is as that which cannot be grasped by a net of coupled differential equations. More precisely, the intrinsic nature of the organism is that causal factor that could only be described by a mathematic dynamics that does not need a division between dynamic and static quantities, i.e., between variables and parameters. This however is a negative definition. To deliver a positive definition of the intrinsic nature of the organisms is immeasurably more difficult, since it requires an organismic theory emancipated from physics.

We are convinced that a positive resolution of this problem is dependent on clarifying the concept of information. It is for the moment unclear what is to be understood by “biological information.” But many philosophers of biology are currently working on the foundation of a new concept of information (see e.g., Deacon 2012, Deacon and Koutroufinis forthcoming, Knappitsch and Wessel 2011). The concept of information is not the subject of the present article, however, two points are important in view of a critique of physicalistic theoretical biology.

First, informational causes do not correlate with the amounts of energy and matter that are transported from a source to a receiver. The answer of the receiver does not depend upon this amount or magnitude (Jablonka 2002, 580f.). There is an uncoupling of energy and information amounts, since only information allows of making distinctions (Collier 2008, 776). This is important because all biomathematical

statements are fashioned according the model of physics, which operates only with energetic and material quantities.

Secondly, mathematical information (more precisely communication) theory, invented by Claude Shannon in 1948, possesses only a syntactic aspect, and not a semantic one (Deacon 2012, 372, 381-386; Jablonka 2002, 579f.; Godfrey-Smith and Sterelny 2007). Shannon's concept of information rests at least implicitly on some key concepts of statistical physics such as "state," "uncertainty," "probability," "entropy," and "order." These concepts presuppose the physicalistic idea of a system. This rests upon the idea stated above that the physicist determines experimentally and theoretically what makes up a system in general. The system with which physicists operate is an abstract model in that they only take up those features of a real entity that interest them, or which they can conceive mathematically. It is clear that such an abstract construction only possesses semantic aspects for the physicists themselves. For physical systems, features of their surrounding or their own elements have no significance.

In sharp contrast, philosophers of biology attempt to conceive the concept of biological information such that it can comprehend the meaning that the inner structures of the organism (genetic material, signal molecules, neuronal excitations) and external influences of the environment (*Umwelt*) (language, signal molecules) have *for the organism itself* (Deacon 2012, for the concept of "dynamic information" see Knappitsch and Wessel 2011). In his recent book *Incomplete Nature* Deacon introduces a new form of biological naturalism<sup>6</sup> that clearly goes beyond physicalism without attempting, however, to exclude physics from biology (Koutroufinis forthcoming). Deacon suggests a variety of re-foundations of fundamental biological notions. In his approach, a thought experiment called *autogen* takes on a key role. Initially created as a model for the explanation of the emergence of life out of inorganic matter the autogen introduces a new way of thinking about the relation of physics, biology, and information theory. The autogen model is the most elementary form of a dynamic organization that can be considered to be a real *self* since it goes beyond essential shortcomings of self-organization theory. The autogen's selfhood is the result of a dynamics that emerges out of at least two coupled self-organized processes (Deacon 2012, 302-305; Koutroufinis forthcoming). These processes mutually constrain themselves in such a way so that the emerging dynamics does not obey to the principle of maximum entropy production that characterizes all self-organized systems of physics.<sup>7</sup> Although depended on physical

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<sup>6</sup> For several reasons that cannot be expounded here Deacon's approach can be described as a *neo-naturalistic* one (Koutroufinis forthcoming).

<sup>7</sup> The simplest type of autogen is an autonomous molecular system consisting of two coupled, non-linear, self-organizing processes: *autocatalysis* and *self-assembly*, which *mutually support and constrain each*

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self-organization autogenic dynamics manifests an end-state-directedness which defines a higher order form of self unattainable in contemporary physics. This specific kind of end-state-directed dynamics, which Deacon calls *teleodynamics*, protects the system from exhausting its energetic and material gradients. In addition, teleodynamic organization is capable of a form of evolution which may endow autogens with the increasing capacity of representing and even anticipating their environment (*ibidem*, 442-462). Thus the idea of teleodynamics opens the way to a new access to the concept of biological information that includes semantics.

## 5. Summary and Conclusion

Theoretical biology delimited by mathematical modeling reduces organisms, explicitly or implicitly, to dynamic physico-chemical systems and describes their dynamics by means of differential equations. It applies an instrument, therefore, that is one of the most important foundations of all realms of theoretical physics. However, the organismic dynamics rests upon a causality that cannot be encompassed by mathematic methods that require a sharp division between dynamic and static quantities. Current biomathematics also ignores the entanglement that exists between differential calculus and the fundamental ontologies of theoretical physics, since the nature of the quantities contained in equations of physics is defined by their function in the respective formalism of basic equations. Such a functionalistic connection between ontology and

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*other*. In rare cases, an autocatalytic process produces a molecular form susceptible to self-assembling into an enclosing structure, as a byproduct. In these cases, enclosure is likely to encapsulate the very molecules that in proximity with one another tend to produce this containment. The persistent generation of a high local concentration of like molecules by autocatalysis is a necessary boundary condition, or *constraint*, required for self-assembly, and that the prevention of the diffusion of reciprocal catalyst molecules is the necessary boundary condition, or *constraint*, required for persistent autocatalysis. Thus *autocatalysis* and *self-assembly mutually support and constrain each other*. Both coupled processes require a gradient. Both deplete that gradient, and in the process, produce more regularity, more catalysts, and more enclosing structure. Moreover, if such an enclosed structure is broken up by external factors in an environment with supportive conditions, then the whole complex will tend to reform or even produce replicas from the partially diffused components. The dynamics of an autogenic process does not merely use the constraints that enable the utilization of local gradients—*autogen closure halts both of its component self-organizing processes before supportive local energetic and substrate gradients are destroyed*. Cessation of these processes halts depletion of the conditions that make them possible. An autogen thereby preserves the potential for future autocatalysis and self-assembly when external factors break them up. Thus, an autogen acts like a ratchet: it produces something when active, and preserves it from getting lost when it is not active. So, *autogens do not fully deplete essential environmental conditions, e.g., energetic and/or material gradients, in the way that ordinary self-organizing systems do*. This is the most essential feature of autogenic dynamics, since it goes beyond the principle of maximum entropy production that characterizes all kinds of self-organized dynamics. Dynamic systems that lack this reciprocity thus exist at the whim of extrinsic parameters, whereas autogenic systems actively generate parameters (constraints) critical to their existence.

mathematics is currently unthinkable in theoretical biology. However, from the fact that it is neither possible to conceive the logic of organismic causality with the theory of dynamic systems, nor to define biological abstract entities upon a mathematical foundation, biology ought to gain something positive – its self-understanding as a post-physicalistic science: organisms cannot be reduced to a bundle of characteristics like actual entities of physics, since they possess an autonomy that is not conceivable physically and mathematically, since this emerges from their intrinsic nature.

In the history of philosophy, the essence of the organism has been conceived in terms of different ontologies. To name just three of them, Aristotle used the concept of *ousia*, Leibniz the concept of *monad*, and Whitehead the concept of *actual occasion*. The language of intrinsic nature of the organism does not mean, however, a return to the medieval or Cartesian ontology of substance, but rather *a turn away from functionalism and ontological relationalism of theoretical physics*.

The intrinsic nature of the organism can serve as an important basis for understanding all biological universals. The intrinsic nature of a real entity is its essence. The concept “essence” means however not necessarily something that exists in and for itself without any relations – only in the substance metaphysics of Descartes is this limitation of the concept of “essence” permitted. The intrinsic nature or essence of an entity can also be understood as a process that emerges from relations with other entities. Even if we follow an ontology that assumes *internal relations* between the relata,<sup>8</sup> this does not mean that the actual entities (the relata) lack their own essence, as the ontological relationalism of modern physics claims. Leibniz’s “monads” and the “actual occasions” of Whitehead are the best examples of actual entities whose essence is logically equal with their internal relations.

A possibility to introduce the idea of intrinsic nature into modern biology is to bring it into connection with the concept of biological information: Intrinsic nature, i.e., the essence of an organism, is nothing static, but rather the process of production and reworking of information of all kinds (genetic, epigenetic, hormonal, neuronal, referred to the environment/Umwelt, etc.). The idea that information is not simply transported and stored like a piece of matter and called up like a finished text, but rather co-constructed by the organism (Deacon 2012, 372ff) compels us to ponder the semantic value of information: Biological information has a value that is not adequately represented by notions like “probability” and “uncertainty.” The semantic content of information for a concrete organism has to do with its value for the survival, prospering, and benefit conferred to the evolution of its species.

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<sup>8</sup> Internal relations are the “strongest” form of relations. The existence of internal relations claims that the relata are not capable of existence without their relations.

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