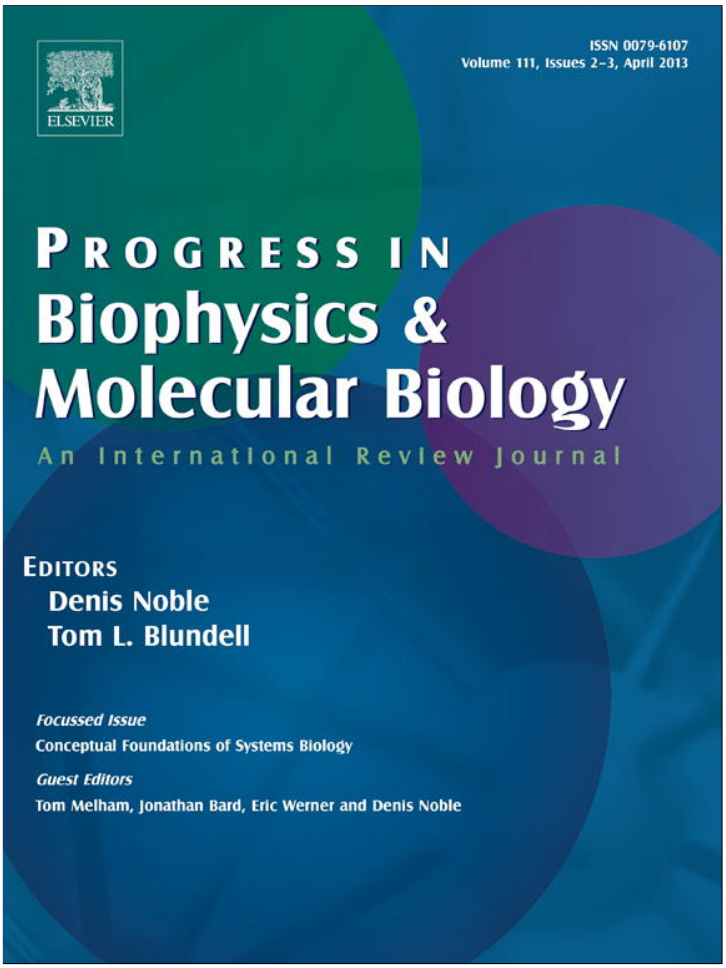

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Orginal research

Computing life: Add *logos* to biology and *bios* to physics

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ABSTRACT

This paper discusses the interrelations between physics and biology. Particularly, we analyse the approaches for reconstructing the emergent properties of physical or biological systems. We propose approaches to scale emergence according to the degree of state-dependency of the system's component properties. Since the component properties of biological systems are state-dependent to a high extent, biological emergence should be considered as very strong emergence – i.e. its reconstruction would require a lot of information about state-dependency of its component properties. However, due to its complexity and volume, this information cannot be handled in the naked human brain, or on the back of an envelope. To solve this problem, biological emergence can be reconstructed *in silico* based on experimentally determined rate laws and parameter values of the living cell.

According to some rough calculations, the silicon human might comprise the mathematical descriptions of around 10^5 interactions. This is not a small number, but taking into account the exponentially increase of computational power, it should not prove to be our principal limitation. The bigger challenges will be located in different areas. For example they may be related to the observer effect – the limitation to measuring a system's component properties without affecting the system. Another obstacle may be hidden in the tradition of "shaving away" all "unnecessary" assumptions (the so-called Occam's razor) that, in fact, reflects the intention to model the system as simply as possible and thus to deem the emergence to be less strong than it possibly is. We argue here that that Occam's razor should be replaced with the law of completeness.

1. Introduction

Contemporary biology rests on often precise information about the cell and its biomolecular components. In order to obtain such information one typically needs to interfere with normal cell functioning. For instance, the standard way of quantifying the intracellular transport of nuclear receptors (proteins which are activated by ligands and regulate transcription) requires that cells are transiently transfected with a plasmid over-expressing a receptor-GFP construct. In this way, one produces a cell with a high concentration of the receptor fused with a fluorescent marker (GFP molecule). This enables one to measure the intensity of fluorescence and to quantify the behaviour of the receptor in time and space (Kolodkin et al., 2010). One may add a ligand and observe the ligand-dependent shift of the receptor from the cytoplasm into the nucleus, quantifying the rate of its nucleo-cytoplasmic transport. One may then bleach a certain volume of the cell with a strong laser so that the GFP-fused receptors lose fluorescence and observe how the "bleached" receptor is replaced with the intact one, quantifying the motility of the receptor in the cell. One may perform various complicated experiments and get a plethora of data quantifying aspects of life.

The above methodology comes with a big problem, however. To what extent does the nuclear receptor in a human body behave the same as in our experimental system? The receptor is over-expressed, so that its concentration is altered; the receptor is fused with a GFP molecule, giving it a different size and conformation and, perhaps, causing it to interact differently with the transport machinery; and, finally, the cell is isolated from its tissue and exposed to excitation light. Should one not expect these experimental procedures to affect the behaviour of the receptor? The likely answer is that one should. Admittedly, the example was

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chosen to be an exaggerated one; many experimental methods are much less invasive. Still, if we carefully look at the details, we can usually find at least one way in which they change at least something in the cell. Experiments such as the above determine properties of a cell which, during the process of experimentation, becomes a different cell. If the biological object of study is an entire elephant and one measures the temperature of its skin with a very small thermometer, the perturbation caused by the experiment may be minimized. However, if one tries to measure the behaviour of single molecules, the perturbation tends to produce an impact on the molecule that is of the same order of magnitude as the molecule itself. This presents a problem particularly in attempts to measure continuous molecular properties quantitatively.

This aspect of cell systems biology brings to mind the observer effect in quantum mechanics: "Once we have measured the system, we know its current state and this stops it from being in one of its other states" (Schommers and Espagnat, 1989). In other words, the laws of physics say that if we measure a system we have already changed the system. Does biology follow physics in this respect?

In this paper we shall examine this and a number of related issues, extending beyond the single scientific fields of Physics or Biology: in the next section we shall develop a more systemic, interdisciplinary, global and philosophical look at the concept of 'system' itself, and discuss implications for the emergence of new functional properties. Then, we shall introduce the concept of function and discuss its origin. This leads us to a link between stability and functionality, and thereby to proposing that physics may be more part of biology than biology is part of physics. The final section of this paper addresses the computability of the human body. It shows that by taking the natural organization of the body into account, the computation reduces from astronomical to large but feasible in a foreseeable timeframe. The consequence that emergence of biological function becomes computable removes the necessity of the strategy of sparsity from the life sciences. We conclude that this should be welcome since not Occam's razor, but rather its opposite may apply to Biology, and perhaps then also to Physics.

2. The concepts of system and emergence

Scientific interest in systems tends to be related to a desire to understand, to explain or, at least, to describe the behaviour of system components as well as the behaviour of the system as a whole, and, ideally, to deduce the properties of the system from the properties of the system's components. The latter ambition implies that one wishes to understand emergence (Rasmussen et al., 2001; Boogerd et al. 2005). For a property of a system to be characterised as emergent, it needs to satisfy three criteria: (i) the thesis or notion of being a systemic (organizational) property (a property that is not exhibited by elements in isolation), (ii) the thesis of physical monism, and (iii) the thesis of synchronous determinism. The thesis of it being a systemic property restricts what can be considered as emergent. The thesis of physical monism restricts the nature of elements. It states that the system should consist only of physical entities, denying any supernatural influences. The thesis of synchronous determinism restricts how systemic properties and the system's microstructure are related to each other: it states that there can be no difference in systemic properties without changes in the structure of the system or in the properties of the components (Stephan, 2006). Taken together, these theses constitute the minimal criteria for emergence.

It has become traditional to divide emergence into weak emergence and strong emergence, depending on whether specific behaviour of the system's components derive or not from the components' behaviour in isolation and in simpler configurations (Stephan, 2006). This separation has a deep intuitive background. Let us consider the classic example. A piece of diamond is hard and a piece of graphite is soft, because atoms of carbon are arranged differently in these two systems; the emergent property (hardness or softness) depends on the interactions between the system's components. If we consider a simpler configuration of the system, e.g. a small piece of diamond, we can find the way in which atoms of carbon should be arranged in order to give rise to hardness. In other words, systemic properties of a big piece of diamond can be deduced from the components' behaviour in simpler configurations. Consequently, the emergence would be classified as weak emergence. Let us consider now a live cell. Obviously, if we cut this cell into a hundred small pieces, each piece would be dead in isolation. From here, we can intuitively jump to the conclusion that the property of being alive is a strongly emergent property.

However, we may also take a look from a different angle. The properties of carbon atoms in a diamond are the same in bigger or smaller pieces; component properties do not depend on the state of the system (e.g. the size and the geometrical shape of the diamond). On the contrary, properties of macromolecules in the cell, e.g. how macromolecules interact with each other, depend on the state of the cell. For instance, assume that we alter the concentration of just one component in the cell, e.g. an enzyme. This will change the concentration of the substrates and products of this enzyme. It is very likely that one of the substrates or products will be an activator, inhibitor or substrate for another protein. This second protein may be the transcription factor for a different enzyme or an activator for a third protein, and the effect of the initial change will carry on until, eventually, the properties (behaviour, concentrations, activity) of all components in the cell are altered. Components are fit to the system as a whole; their properties depend on the presence of other components, on the boundary conditions and on the initial conditions of the cell. The component properties of the pieces of diamond are not state-dependent. On the other hand, the component properties of pieces of the cell are state-dependent to a large extent. If we imagine a small piece of the cell with the same composition of amino acids, lipids, ribonucleotides and other molecules as the intact cell, some state-dependent information about interactions between molecules, e.g. the information about purposeful arrangement of these molecules as it was in the cell would be missing in cell parts. The reconstruction of the emergent property of the whole cell would require information about these state-dependent properties of molecules. The emergence in the diamond differs from that occurring in the cell by the degree to which component properties in these two systems are state dependent.

There is no emergence that is only weak or only strong; rather, emergence can be stronger or weaker, depending on how much we need to know about the component properties (how state dependent the component properties are) in order to reconstruct this emergence. This would also imply that, even if some properties might seem very strongly emergent, their emergence can still be reconstructed from the knowledge of component properties. The real question is whether we can know all the component properties that are engaged in the emergence.

3. Physics and stamp collecting

Many years ago, the Nobel laureate Ernest Rutherford reportedly said: "All science is either physics or stamp collecting." By "stamp collecting", Rutherford referred to chemistry, which he challenged to become physics – a "real" science based on the universal physical laws, rather than on the collection of more or less well-systematized information about the elements in the periodic system. Since then, we have stuck with the paradigm that all

sciences are developing towards physics. Shall biology become physics as well? When we say that *logos* ("word/theory", in Greek) should be added to biology, we are making a reference to the rational, natural laws that govern the universe, the collection of which comprises physics. In a first look, biology and physics have much in common. They both search for phenomenological relations between different emergent properties and intend to generalize those relations into laws. Often, emergent properties of a system are correlated as such, without digging into the underlying mechanism of interactions between system components. For example, in physics, the equation of state of a classical ideal gas formalizes the correlation between pressure, volume and temperature. The power of this phenomenological relation (the ideal gas law) is strong causality, e.g. we may definitely say that an increase of volume requires either an increase of temperature or a decrease of pressure. However, this kind of law gives only intuitive, very slight understanding of how pressure and temperature really emerge from interactions between molecules. Biology sometimes looks for similar generalizations, although it may still lag behind physics in this respect.

Another ambition for both physics and biology is to connect an emergent property of a system with underlying mechanisms of components' interactions. For example, in physics, temperature, as an emergent property of a whole system, may be deduced from the kinetic energies of the components (molecules). Biology also tries to connect biological emergent properties (e.g. the pumping activity of the heart) with underlying component properties (e.g. biomolecules forming a heart cell). However, compared to physics, functional properties in biology are much more strongly emergent. Consequently, more information is required to describe a biological system, and, therefore, it is more difficult to bring all information together in a single analytical expression. The complicated computer model is often the only way to reconstruct this type of emergence. As a result, it is difficult to depict clear mechanisms underlying biological emergence and to give explanations based on causal mechanisms.

The so-called design studies in biology are a combination of "stamp collecting" (arrangements of particular pictures depicting patterns) and searching for "universal laws" (Kolodkin et al., 2010). This may provoke the thought that biology is still somewhere in the midst of a journey towards physics. However, we would like to argue that, in reality, biological explanation is unique. In physics, the "main insight produced by causal-mechanical explanations is insight into how (e.g. by means of what causes and mechanisms) an event or regularity is brought about". Biological explanation is more related to the design question, i.e. to the question "why the mechanism consists of the parts of which it consists, and why those parts are organized the way they are in the context of the overall design of the organism" (Wouters, 2007). Design implies "*purposeful arrangement of parts*" (Behe, 2006) and intentionality is already inherent in the concept of design (Blecic and Cecchini, 2008). During a design study, we imply that the system is formed so as to enhance the emergence of useful biological functionalities.

According to Anokhin's theory of functional systems (TFS), "a system can be called a complex of selectively involved components where all interactions are produced by mutual cooperation of components focused on obtaining a useful result" (Anokhin, 1975). The useful result as a system-forming factor may play a serious role in systems that give rise to very strongly emergent properties (e.g. involving consciousness) and where selection for function is engaged. For less complex systems, the role of the useful result as a system-forming factor may be substantially smaller. In addition, the definition that "the goal always precedes its realization by the organism" might be confusing (Anokhin, 1975). It is still a controversial topic in the current theory of functional systems (Khitrov and Saltykov, 2003). Curiously, this "difficult" topic has migrated into the design studies concerning artificial systems and is discussed by various authors, sometimes in direct analogy with the old concept of Plato's *noema* (428/427 BC) (Losev et al., 1993), which can be translated from Greek as "meaning". According to that concept, future (not yet realised) *noema* becomes a current *noema* in the process of *noesis* (realisation via the interaction with the environment). Since current *noema* would be different from planned, future *noema*, the future *noema* must be readjusted and the loop continues (Toshiharu et al., 2009). The theory of functional systems does not operate with the term *noema*, but it does imply *noesis* when discussing reverse afferentation ("reverse afferentation" meaning here a kind of "feedback"; the concept was introduced into physiology by Anokhin). Biology took one step further when enabling the system to select (by trial and error from all possible combinations) those degrees of freedom of components that lead towards a useful result (Anokhin, 1975).

What is a useful result for a physical system, and how may this useful result become a system-forming factor? We propose that the answer is that the useful result of a physical system is its stability. From this point of view, the current physical universe (with its universal laws) may be considered as a system which has already passed the tests of stability. Countless "trial and error" universes may have already been eliminated by stability selection, and we would never notice the earlier existence of most of them. Functional biology is a system that is stable in terms of evolutionary changes, which can be seen as fluctuations on a long time scale. Such fluctuations challenge and thereby bring about the stability of physical systems (Westerhoff and Van Dam, 1987). The implication is that the observable and hence also the observed physical systems may need to or have evolved to a persistent state, and thereby have acquired (been selected for) a design that enables them to persist vis-à-vis the fluctuations challenging their state. Function, useful result, adaptation, and many other "biological" criteria, may thereby not be extraneous to physics. All these concepts have been inspired in some measure by biology. We therefore suggest that it is not biology that is becoming physics. It is rather *bios* ("life", in Greek) that is being added to physics; it is physics that is on its way to become biology.

4. Computing life

4.1. Emergence of the silicon human

There is perhaps one fundamental difference between physical and biological systems: the components of many physical systems are rather homogeneous, and thereby follow the same law in the system. Consequently, physical systems can be described in terms of rather simple equations, written on the back of an envelope. In contrast, in a biological system, the diversity of components is much higher and many "laws" exist that govern the interactions between these components, which complicates the reconstruction of biological emergence.

In fact, we can simplify biology, taking into account that the same property of a biological system might be viewed as having different strengths of emergence, the strength of emergence being related to the way in which we model the object, or the complexity of the components we use within the model. We can describe an object in such a way that the property of interest is as weakly emergent as possible. Doing this used to be considered the "art" of good modelling: the less the component properties are state dependent, the easier it should be to deduce them from the knowledge of elemental properties in isolation, the less one needs to know about the system as a whole, and the easier it should be to parameterize the model. The model would then also be more robust against the

changes of initial and boundary conditions (e.g. concerning moiety-conserved properties such as enzyme levels at the time scale of signalling), more universal and less state-dependent.

We believe that such a reductionist approach is flawed from the perspective of the fundamental aim of biology, i.e. to understand Life, and must therefore be challenged. Let us discuss the modelling of a disease. We consider a certain symptom of the disease, which might emerge from interactions in a gene regulatory network. At one extreme, we may consider this network as a whole, with all 25,000 human genes and with thousands of mRNA and protein molecules. In the other extreme, we can simplify reality to a system with a single gene encoding one single enzyme with one single substrate and one single product; the mutation of this single gene causes malfunctioning of an enzyme and might cause accumulation of the enzyme's substrate, and be responsible for a certain symptom. The model based on the simplest scenario is more comprehensible and gives more straightforward predictions. In fact, for many monogenic diseases, such a simple picture works as a fair approximation.

There are at least three serious problems with such an approach, however. First, this simplification might not work if a disease is caused by multiple factors, both genetic and environmental, and the neglect of the state-dependency of the component properties could change the modelling results. In essence, the simplified model is then simply too far from reality. Second, the simplification might not work because the substrate of the one enzyme is not the metabolite causing the disease, but belongs to a pathway that is impacted upon by the disease-causing mutation; we thus need to determine cause versus consequence associations. Third, reduction of the model will prevent the identification of the important underlying design principles for the network, meaning that we might miss potential therapeutic targets to restore the network to normal homeostasis.

On the other hand, we should note that the more component properties that need to be integrated are added to the model, the bigger the model will become. With respect to a human organism, this approach would lead to a mechanism-based computer replica of a whole body – the so-called silicon human (Westerhoff, 2001; Snoep et al., 2006; Hunter et al., 2008; Westerhoff et al., 2009a; Kolodkin et al., 2011a,b; Kolodkin et al., 2011a,b; Westerhoff et al., 2011).

The main concerns are usually associated with the "astronomical" number of interactions involved in the entire human body (Noble, 2006). However, because of the modular organization of the organism, the number of interactions may be large, but not quite "astronomical". Let us show what difference modularity makes for the numbers. If we talk about a human being, and think about the interactions between the 25,000 genes in each of the 10^{14} cells of the whole body (2.5×10^{18} genes per body), then the number is pretty high, i.e. $2.5 \times 10^{18}\,!/2 \approx 10^{2\times10^{19}}$, i.e. a 1 with 2×10^{19} zeros, much larger than the number of atoms in the universe ($\approx 10^{80}$). If we only envisage binary interactions, the number is smaller ($(2.5 \times 10^{18} \times (2.5 \times 10^{18} - 1))/2 \approx 3 \times 10^{36}$) but still enormous. However, taking into account the modular organization of the body and the fact that not everything may interact with everything else, the number of interactions becomes much smaller. Let us start with a single cell. If a cell contains about 1000 metabolic enzymes ('enzyme types' really, but we assume that all enzymes defined by the same gene(s) behave as a single ensemble) and about 500 metabolites ('metabolite types' really, but we again assume ensemble behaviour), maximally 5×10^5 binary enzyme-metabolite interactions are possible. These are the current numbers for yeast (Herrgard et al., 2008; Smallbone et al., 2011; Heavner et al., 2012), but although the yeast genome is approximately 5 times smaller than, e.g. the human genome, we do not expect much difference between organisms in terms of the number of catalysed reactions in a single cell. In addition, 5×10^5 interactions are an overestimation, since in reality not every enzyme can interact with every metabolite. It is much more likely that an enzyme interacts on average with at most 5 metabolites, bringing down the number of metabolic interactions to only 5000. Continuing this line of thought, there are about 3000 human transcription factor genes. If every transcription factor binds to 100 different genes, then there are about $3000 \times 100 = 3 \times 10^5$ interactions. If the average factor is much more specific, then this number could be only 10,000. Together with metabolic interactions, we approach the order of 10^4. The addition of tens of thousands of interactions on the level of transporters, receptors and so on would not change this order of magnitude of the number of interactions in a cell substantially. Now let us go to the intercellular level where 10^{14} cells are organized in tissues and organs, with perhaps 5 cell types per organ. Let us say that each cell type interacts with 100 neighbours via maximally 50 metabolites (25 000 interactions), and that one organ interacts with all other 71 organs via another 50 metabolites (a little more than 3500 interactions). If we sum all interactions mentioned above, there would be still in the order of 10^5 interactions. This is indeed not a small number, but taking into account increasing computational power, it should not constitute cause for any principal limitation.

The essence of these calculations is that, if one foregoes the natural organisation of living systems, the number of interactions appears astronomical, but with a bit of realism, these numbers turn out to become manageable within a few decades. Building the silicon human will eventually break the barriers of a single science and overcome the limitations of the human mind, delegating the reconstruction of emergence to the computer. These days, partial animal and bacterial silicon cell models (computer replicas based on experimentally determined rate laws and parameter values of the living cell; http://www.siliconcell.net/) have already helped industry. The whole-body human silicon cell model will revolutionize medicine in similar ways (Lehrach et al., 2011).

However, on the way towards the silicon human we will encounter several fundamental problems. We have touched upon some of them earlier. Now let us deal with them in detail.

4.2. In the light of emergence: Occam's razor, the observer effect and other challenges in computing and (or) understanding life

Above, we concluded that for biology one should assume emergence to be strong rather than weak. If ones wishes to reconstruct an emergent property, one should take into account all knowledge about component properties. This can be formulated as the law of completeness: "If entities A, B, C and D (e.g. proteins) have been discovered in a living system S (e.g. cell, organism, ecosystem) for the fitness of which A, B, C, and D are all known to be essential, and if some properties of system S can be equally well explained either via A, B and C or via A, B, C and D, then the more complex explanation is most likely the correct one": "One should not remove things without necessity" (*Pluralitas non est eliminanda sine necessitate*) (Kolodkin and Westerhoff, 2011).

This contradicts the principle of parsimony, which suggests that, if one considers a phenomenon that can be explained in two different ways, the first explanation requiring entities (terms, factors, transformations etc.) A, B and C, and the second explanation requiring entities A, B, C and D, and if one observes that both explanations give the same result, then, entity D is unnecessary and the simpler explanation is most likely the correct one. The parsimony principle basically suggests to "shave away" all assumptions that are unnecessary to explain the phenomenon under study. The axiom is known as Occam's razor in the memory of William of

Occam (1285–1349) who suggested the following: "One should not postulate (pose) more things without necessity" (*Pluralitas non est ponenda sine necessitate*). William of Occam was a Franciscan friar and used his razor as a tool for demythologization of the cosmology of antique times. He worked actively to shave away the "soul" and the "will" of cosmic elements and his legacy has cleared an avenue for modern science. For instance, shaving away the sacred status of stars liberated astronomers from the fear of being killed by star worshipers and led to the discoveries of Nikolaus Kopernikus. In later times, the statement of Occam was somewhat modified: "Entities should not be increased (multiplied) without necessity" (*Entia non sunt multiplicanda praeter necessitatem*) (Thorburn, 1918). This provided a good motivation to start viewing the behaviour of physical objects as being determined by simple physical laws rather than by divine intervention and thus became very important for the development of physics.

However, Occam's Razor has always been a heuristic method rather than a universal law. There is no proof of the principle: if the simpler explanations are true, this does not imply that those explanations are more realistic because of any universal tendency towards simplicity. On the contrary, the second law of thermodynamics advocates that there is a tendency to complexity rather than to simplicity (Westerhoff et al., 2009b). And there are many examples where the more complex explanation turned out to be true: chemiosmotic coupling (Mitchell, 1961), the control of metabolic fluxes (Groen et al., 1982), and general relativity (Einstein, 1961) are but a few of them.

Coming back to biology, some years ago it became almost a paradigm that all cellular information is stored in DNA, assuming consequently that if one knows the DNA sequence one can deduce all the properties of the organism. Today it is obvious that this is not true; to show this we use the same example used by Denis Noble in his plenary lecture of the Oxford Seminars: if one takes a carp's nucleus and puts it into the fertilized but enucleated egg cell of a goldfish, then, in most cases the hybrid will die. In the rare cases that an embryo manages to develop to an adult organism, the new organism will look like a goldfish (Sun et al., 2005). The reason behind this is that it is the cell as a whole, with all its components including various cytoplasmic molecules (especially proteins) that is responsible for the emergence of life. It is not downward causation but circular causality that is at play in living systems (Boogerd et al., 2007).

We conclude that one should not deem emergence to be less strong than it is in living systems. One should allow component properties of the system to be as strongly state dependent as possible, and, most importantly, one should allow all the components of the system to be crucial for the *in silico* reconstruction of the system's emergent properties. Only experimentation and modelling should then deliver data that demonstrate that certain components or interactions are not important. This principle may apply both to internal and to external players: since biological systems are semi-open, e.g. open to some molecules and closed to others, and, even more remarkably, the openness is controlled by the system itself, it is not so easy to distinguish which molecule is external and which is a component of the system (Westerhoff and Van Dam, 1987).

Now let us return to the problem mentioned in the introduction concerning the idea that if one has measured a system, one has already changed it. A corollary is that measurement of a system also tends to fixate it in its state and thereby transform its dynamics: "once we have measured the system, we know its current state and this stops it from being in one of its other states" (Schommers and Espagnat, 1989). This concerns quantum mechanical objects and is closely related with wave-particle duality, particularly with the impossibility of measuring properties of a particle as both a wave and a particle at the same time. We will not go into details of quantum mechanics theory and the remarkable debates between Niels Bohr and Albert Einstein. We simply mention that the debates themselves started from Albert Einstein's objections to Max Born's explanations of quantum physics events as being based entirely on probability without any causal explanation. Interestingly, the observer's problem in quantum physics inspired Niels Bohr to introduce the principle of Complementarity, according to which items could be separately analysed as having several contradictory properties, but each property is analysed in independent experiments and, consequently, "cannot be comprehended within a single picture, but must be regarded as *complementary* in the sense that only the totality of the phenomena exhausts the possible information about the objects" (Bohr and Einstein, 1949). It is remarkable that this may go much further than quantum physics and may address the fundamental concerns related to the understanding of reality. Besides the classical Copenhagen interpretation and the de Broglie–Bohm theory, there are also theories about transactional interpretation, objective collapse, quantum information, time-symmetric and branching space-time, M-theory, many worlds, many minds. Perhaps, the discussion is also related to the concept of emergence in biology, discussed above. For example, does the realization of a certain emergent property (from all the stochastically possible properties) and the knowing (measuring) of this property, stop the system from being able to exhibit other incompatible emergent properties? Does the observation of a cell in a certain state preclude it from exhibiting the properties of other states?

4.3. The limitation of the human brain

The complexity of interactions even in bacteria might be higher than the complexity of neuronal connections in the human brain. Therefore, without the aid of a computer it may simply be impossible for a single human to understand biology. Although we can reconstruct *in silico* some behaviour of biological systems and manipulate them, it is still problematic and it may be impossible for any individual human to understand the system rationally and completely, because again it would require that the brain understands the complexity of a model that is as complex as the real system. This implies that the computer aided understanding facilitated by the Silicon Human, should be different in nature, from traditional understanding by the human brain. The mathematical model would function as a successful predictor that can be interrogated by the human brain for anything it requires explaining, not for explaining the total behaviour all at once. Perhaps the explaining would be that of only part of the system.

Nowadays, our world is perceived as a system composed of related components, with each component also being a system, composed of the next layer of components, and so on. This is our reality, the world we live in. This viewpoint also constitutes the foundation of our paper. Undoubtedly, this view is helpful for industrial and medical applications. Nevertheless, we should note that this view of the world is just a model. Whether this view provides a real understanding of reality is an open question, perhaps an issue for metaphysics (to discuss this in detail is thereby out of the scope of the current paper). We brought up this issue only in relation to the following. One might say that the reconstruction of the emergence of life in a computer model leads one away from understanding life, simply because one may lose the overview of a total model. However, why would reconstructing this emergence in one's own brain (the type of modelling that everyone is undertaking in everyday interaction with the outside world) give any better understanding of reality than just reconstructing this reality *in silico*?

5. Instead of conclusions

If in 1930 A.D. somebody would have suggested that one should be able to understand the molecules, or at least to deduce their properties, from the interactions between hypothetical elementary particles, the argument against this could have been the following. 'The particles are too small to be measured and experiments are too difficult ever to become affordable.' Now we realize that all these measurements have materialized and that the real challenge was in a "different plane": heisenberg's uncertainty principle, and the fact that one cannot measure both the impulse and the location of an electron in space with unlimited precision. The challenge led to a new level of understanding of reality by approaching the problem with quantum mechanics equations. In many ways, challenges experienced by current biology resemble the challenge related to the observer effect deriving from Heisenberg's uncertainty principle in physics. This should perhaps lead biology into a systemic change of the approaches by which it aims to understand its systems. The challenge to compute Life and to understand what Life is, is becoming a hot topic in science. As an example, we would like to refer to vast debates around this topic in a special issue of the journal "Origin of life and evolution of the biosphere" (Gayon et al., 2010), to the book of Robert Rosen (Rosen, 1991) and to some recent publications (Letelier et al., 2011). Perhaps the computing of Life would require that the approach of Occam's razor should be replaced with the law of completeness deriving from the concept of emergence that we have discussed.

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