

From logic to biology via physics: a survey

Giuseppe Longo, Maël Montévil

▶ To cite this version:

Giuseppe Longo, Maël Montévil. From logic to biology via physics: a survey. 2016. hal-01377051v1

HAL Id: hal-01377051 https://hal.science/hal-01377051v1

Preprint submitted on 7 Oct 2016 (v1), last revised 30 Nov 2017 (v2)

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers. L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



FROM LOGIC TO BIOLOGY VIA PHYSICS: A SURVEY

GIUSEPPE LONGO AND MAËL MONTÉVIL

Centre Cavaillès, République des Savoirs, CNRS, Collège de France et Ecole Normale Supérieure, Paris, and Department of Integrative Physiology and Pathobiology, Tufts University School of Medicine, Boston.

e-mail address: giuseppe.longo@ens.fr

IHPST, CNRS and université Paris I, Paris. Grant from île-de-France, DIM ISC.

e-mail address: mael.montevil@gmail.com

ABSTRACT. This short text summarizes the perspectives proposed in [LM14f], where we appreciate the unity of the organism by looking at it from different viewpoints: biological time, theoretical symmetries and singularities, critical transitions. We explicitly borrow from the conclusions in some key chapters and introduce them by a reflection, also proposed in the book, on "incompleteness", which we consider a pervasive notion in our forms of knowledge construction. Then we will introduce an approach to biological dynamics based on the integration of randomness in the theoretical determination: randomness does not oppose biological stability but contributes to it by variability, adaptation, and diversity. We see evolutionary and ontogenetic trajectories as continual changes of coherence structures, thus as symmetry changes within an ever-changing global stability.

Introduction

An analysis of biological phenomena requires multifold tools, thus, an approach at the interface of the discipline may help to gain insight. The construction of scientific objectivity at the core of physical theorizing is the main reference for our approach. However, in [LM14f], while borrowing from the methods of physics, we do not transfer techniques and tools from that discipline, or we do not do it passively: equations or evolution functions, for example, are used for clarifying theoretical concepts more than for deducing and computing consequences. Thus, this short survey will not focus on the tools, but on some key conceptual constructions that frame the theoretical work in [LM14f]. Our hope is that this will encourage the reader to refer to our book for a more detailed insight.

LOGICAL METHODS IN COMPUTER SCIENCE

DOI:10.2168/LMCS-???

© Giuseppe Longo and Maël Montévil Creative Commons

 $^{1998\} ACM\ Subject\ Classification:\ {\tt MANDATORY}\ {\tt list\ of\ acm\ classifications**}.$

 $[\]it Key\ words\ and\ phrases:$ Incompleteness, symmetries, randomness, critical transitions, biological evolution and ontogenesis.

An introductory survey of some themes in Perspectives on organisms.

1. A Definition of Life?

In the multisecular debate between physicalism and vitalism, the matter at hand was often to *define* what is life. A small but remarkable book by Schrödinger [Sch44] contributed to reviving the debate in a way we find to be relevant, at least in its second part, and on which we build in [LM14b]. Do we provide a "definition of life" in our book? Do we, at least, work towards such a definition? Let's better specify how we see this issue:

Primo: An "ideal" definition of life phenomena seems out of the question: there is no *Platonic idea* of life to be grasped in a definite manner or with the maximal conceptual stability and invariance specific to mathematical notions (as there is with the definition or *idea* of triangle, of Hilbert space or Turing machines . . .). It is rather a question of defining a few *operational notions* enabling to draw out concepts for a systemic understanding of biological phenomena. Analogously, physics does not define "matter" otherwise than using operative dualities or contrapositions with the notions energy, vacuum or anti-matter, or in the opposition between fermions and bosons, for example. Another, very rigorous, "provable impossibility to define the object of study" is presented in the next section. Note that Darwin's approach to evolution does neither use nor need a definition of life, but needs to refer to organisms and their variability.

Segundo: Any operational attempt, in our opinion, must be made with respect to the specific phenomenality of life. For example, it is possible that for any chosen finite list of "defining" properties of life, there would exist a sufficiently talented computer scientist able to create its virtual image and render it on a computer screen. It is quite simple to program a virtual "autopoietic" system [VMU74, Var89] or a formalized metabolic cycle in the manner of Rosen [Ros91] — see [MLS09], for example. However, any human being, but also the most simple-minded of animals would recognize it as a series of non-living "virtual images" (which are typically detectable through identical iteration, as indirectly suggested by Turing's imitation game, see [Tur50, Lon08]).

It is rather a question of proposing a sound intelligibility of phenomena in their constitutive history while keeping in mind the fact that any constitution is contingent — both the constitution (evolution) of life and of our historical understanding of it. That is, we stress the contingency of life phenomena and of our modest attempts to grasp its unfolding over a material evolution — better still: over one of the possible evolutions, taking place on this Earth, in these ecosystems and with this physical matter and history. Our point of view includes what biologists often express when they say that nothing can be understood in biology otherwise than in the light of evolution (Darwinian and in this world) and what historian claim to be the concrete historicity of science, as a non-arbitrary, but historical tool for constructing objectivity and the very objects of knowledge.

It should be clear that we do not discuss here how "life may have emerged from the inert", but rather we explore how to go from the current *theories* of inert to a sufficiently robust *theory* of the living. In particular, we proposed in [LM14f] an analysis of the physical singularity and the specificity of the living object. We proceeded by looking first at the properties we would want to have (or *not*) in any theory of the "living state of matter". It is indeed an *incomplete* (see next section) attempt at providing a conceptual framework guiding more particular analyzes.

In the following methodological reflection, we will borrow the role of incompleteness from Mathematical Logic to discuss "our theoretical endeavors towards knowledge" (to put it in H. Weyl's words) and of its relation to conceptual or formal "definitions", of life in particular.

1.1. **Interfaces of Incompleteness.** Do we need to have a definition of life to construct robust theories of the living state of matter?

Let's now answer this question by analogy with a frame where it may be dealt with in the highest rigor: Mathematical Logic.

Is the concept of integer (thus "standard" or finite) number captured (defined, characterized) by the (formal) theory of numbers? Frege (1884) believed so, as the absolute concept of number was, in his view, fully characterized by Peano-Dedekind theory. In modern logical terms, we can say that Peano Arithmetic (PA) was "categorical" for Frege. That is, PA was believed to have just one model, up to isomorphisms: the standard model of integers (the one which the reader learned about in elementary school, with 0, though, and formal induction). Thus, the theory was also meant to define uniquely "what a number is".

This viewpoint turned out to be blatantly wrong. Löwenheim and Skolem (1915-20) proved, by a simple proof, that PA has infinitely many non-isomorphic models and, thus, that it is not categorical. Moreover, a simple theorem ("compactness") showed that no predicate, definable in PA, may isolate (define) all and exactly all the standard integers (see [Mar02]). In short, any predicate valid on infinitely many standard integers must also hold for (infinitely many) non-standard integers (which cannot be considered properly "finite") — this is also known as the "overspill lemma". Gödel's incompleteness theorem reinforced these negative properties: PA is incomplete or, equivalently, it has lots of logically non-equivalent models, a much stronger property than non-categoricity.

A fortiori, there is no hope to characterize in a finitistic way the concept of a standard (finite) integer number, or, equivalently, (Formalized) Number Theory cannot define what a number is. One has to add an axiom of infinity (Set Theory) or proper second order quantification to do so, PA_2 , and these are infinitary or impredicative formal frames. Set Theory with an axiom of infinity and PA_2 are not only strict extensions but they are non-conservative extensions of PA: they prove propositions of PA, which are unprovable in PA (yet another consequence of Gödel's incompleteness).

As a side remark, whether the biological observables we focused on in our book and their theories are strict extensions or not of the related physical theories is surely an interesting question. However, it would be much more interesting if one of our theories or their conjunction were shown to be non-conservative with respect to a (pertinent) theory of the inert. For example, Pasteur's famous example of statistically non-balanced chirality of some macromolecules in cells is a property that can be stated in the language of physics, yet, as far as we know, it has not been derived from any physical theory. It would be fantastic if it could be justified within one of our frames, e.g. from a property of the phenotype at the cellular level, for example, extended criticality (see below).

In conclusion, despite its incompleteness, everybody soundly considers PA as the "natural" (formal) theory of numbers: it elegantly singles out the main relevant, and very robust, properties of numbers (0, successor, induction), even though it cannot define what a number is. In analogy to the impossibility of physics to define its object of study, physical matter, Logic is another example of a sound theoretical frame, which cannot define, within itself, its object of study, the object "natural number". Also, we do not see a way to get out from

the language of physics or of biology as Mathematical Logic can do as for PA, by using infinities: what would ever correspond to an axiom of infinity or higher order quantification? Perhaps: ... "take the point of view (and the language) of God"?

We encourage the reader to pursue her theoretical work in biology without the anguishing search for a definition of life and with the clear perspective of the intrinsic incompleteness of all our theoretical endeavors, [Lon11]. We can just hope to grasp explicitly and organize by theories some fragments of reality, whatever this latter word may mean. Let's try to do it to the best of our knowledge, in a sufficiently broad and robust way, and in full theoretical and empirical freedom. We should not necessarily feel stuck either to existing theories nor always searching for the "Ultimate (complete?) Theory" nor the "ultimate reduction". As we hint in the book and several papers, molecular analyzes are not useless, of course, nor wrong, a priori, they are just incomplete, in our opinion, as for describing phenotypes and their evolutionary or ontogenetic dynamics.

Similarly, the issue of the emergence of life from molecules is a very relevant one, but as long as we do not have a sufficiently robust, yet incomplete, theory of organisms, what "objects", with what properties, should ever be shown to emerge from inert matter?

2. Symmetries breakings and randomness

Since ancient Greece (Archimedes' principle on equilibria) up to Relativity Theory (Noether's and Weyl's work on conservation properties) and Quantum Mechanics (from Weyl's groups to the time-charge-parity symmetry), symmetries have provided a unified view of the principles of theoretical intelligibility in physics. In our approach, biology requires a careful attention both to symmetries and to symmetry changes. In short, symmetry changes are symmetry breaking or formation (new symmetries may form) and, in particular, they relate randomness to the formation of new coherence structures, such as organisms, species, ecosystems.

In section 5 of chapter [LM14h], we propose a preliminary and informal remark, which may turn out to be significant when stressing the role of randomness in biology. Namely, we propose that each random event is associated with a symmetry change in all existing physical theories (see also [LMar]).

A random event is an event where the knowledge about a system at a given time does not cause its future description; thus, the event is unpredictable, relatively to the intended theory. In physics, though, the description before the event determines the complete list of possible outcomes. Thus, what is unpredictable is a numerical value in a pre-given space of observables — modulo some finer considerations as the ones we discuss in chapter [LM14c] as for quantum field theory and statistical physics. Moreover, in physical theories, the theory provides a metric or, more generally a measure (of probabilities or other measures) which determines the observed statistics. Then one may say: random or unpredictable, but not so much, as we know a probability distribution. Kolmogorov's axiomatic system for probabilities works this way and provides probabilities for the outcomes.

Our claim is that the various physical cases of randomness can be understood and compared in terms of symmetry breaking.

Quantum Mechanics:: measurement breaks the unitarity of the quantum evolution, which amounts to say that the quantum state space assumes privileged directions (a symmetry breaking).

Classical probabilities:: the intended phase space contains the set of all possibilities. Elements of this set are symmetric in the sense that they are possible. Moreover, the associated probabilities are usually given by an assumption of symmetry; for example, the sides of a dice or the regions of the phase space with the same energy, in the microcanonical ensemble of statistical mechanics. These symmetries break at the occurrence of the intended event, which singles out an outcome.

Algorithmic concurrency theory:: the theory gives the possibilities (a finite list) but does not provide probabilities for them. Probabilities may be added if the physical event forcing a choice is known (but computer scientists, in programming theory and practice, usually "do not care" — this is the terminology they use, see [LPP10]). The point here is to have a program that works as intended in all cases.

We thus related random events to symmetry breakings in the main physical frames (plus one of linguistic nature: networks' programming). In each case, we have several possible outcomes that have a symmetrical role, possibly measured by different probabilities. After the random event, however, one of the "formerly possible" situations is singled out as the actual result. Therefore, each random event that fits this description is based on a symmetry breaking, which can take different yet precise mathematical forms, depending in particular on the probability theory involved (or lack thereof). In this line of reasoning, randomness leads to a distinction between the possible and the actual result ("possible" and "result" have different specific meaning depending on the theory). The symmetry is then between the different possibilities, and this symmetry breaks when we obtain one result out of them. This scheme of randomness seems quite general to us.

In the case where probabilities are defined, let us better specify the symmetries we are discussing. Let us consider an event X, which can be either A, with probability p or B with probability 1-p. Then, we can consider $f_A(X)=1/p$ if X=A else $f_A(X)=0$ and $f_B(X)=1/(1-p)$ if X=B else $f_B(X)=0$. we see then that f_A and f_B have the same expectancy. It is precisely this symmetry that experimenters try to show empirically, and that legitimates the probability values.

Note that random situations following this pattern define a before and an after that the symmetry breaking separates. This before and after may be epistemic (for chaotic dynamics) or intrinsic (quantum mechanics).

Let's now review more closely, in a schematic way, how the random events are associated to symmetry breakings:

- **Quantum Mechanics::** the projection of the state vector (measurement); non-commutativity of measurement; tunneling effects; creation of a particle
- Classical dynamics: the randomness associated with chaotic dynamics stems from the equivalence between different initial conditions (because the classical measurement is not pointwise), and the exponential drift of the trajectories coming from these initial conditions.
- Critical transitions:: the point-wise symmetry change lead to a "choice" of specific directions (the orientation of a magnet, the spatial orientation of a crystal, etc.). The specific directions taken are the result of fluctuations. Also, the multi-scale configuration at the critical point is random and fluctuating.
- **Thermodynamics::** the arrow of time (entropy production). This case is peculiar as randomness and symmetry breaking are not associated with an event but with the microscopic description. The time reversal symmetry breaks at the thermodynamic limit.

Algorithmic concurrency:: The choice of one of the possible computational paths (backtracking is impossible).

If this list is exhaustive, as it seems, it is fair to say that random events, in physics, are associated with symmetry breakings (and programming follows this pattern). Note that in all these cases, one does not fit completely in our qualitative discussion and has a more complex structure: the case of thermodynamics. Indeed, from a purely macroscopic viewpoint, there is no particular form of randomness associated with the theory, and provided that a trajectory is defined, it will be deterministic (except for critical transitions or similar situations). Randomness appears at the microscopic level, either understood as chaotic classical dynamics or classical probabilities (statistical mechanics). Both correspond to the analysis of their respective categories. However, this does not explain the arrow of time, which is a particularly interesting symmetry breaking in this situation. The evolution of a thermodynamic system is towards a symmetrization of the system since it tends towards the macroscopic state to which correspond the greatest number of microscopic states (they are symmetric from a macroscopic viewpoint). That is, it tends towards the greatest entropy compatible with other constraints. In this case, randomness explains a dispersion in the microscopic phase space. Therefore, it is a process of symmetrization which breaks the time symmetry but does not lead to macroscopic randomness. On the opposite, it determines the macroscopic, mostly deterministic behavior of thermodynamic systems. Macroscopic randomness may still appear if there are different minima for the relevant thermodynamic potential, as in phase transitions.

All these symmetry changes and the associated random events happen within the intended phase space, or, in other words, within the set of possibilities given by the intended physical theory. The challenge we are facing in biology (see [LM14c] and below), is that randomness manifests itself at the very level of the observables. Critical transitions are the closest physical phenomenon to the needs of the theoretical investigation in biology, and we will discuss them in next chapter.

3. Symmetries and theoretical extensions of physical theories

On the grounds of the previous remarks, we claim now that some significant challenges for the proposal of mathematical and theoretical ideas in biology depend on the very different roles that symmetries play in biology when compared to physics.

The unifying theoretical framework in biology is neither associated with invariants nor to transformations preserving invariants (symmetries), like in (mathematical/theoretical) physics. It focuses, instead, on the permanent change of symmetries that per se modify the analysis of the internal and external Processes of life, both in ontogenesis and evolution, while preserving an ever changing structural stability. Note that adaptivity of an organism and diversity of a population or a species are consequences of variability, thus of randomness, and contribute in an essential way to the stability of an organism, a population, a species, by adaptivity and diversity. In a sense, thus, variability may be considered as the primary invariant of the living state of matter (yet it is not necessarily the only one!).

3.1. Extended criticality. To analyze variability, we proposed to consider the role played by local and global symmetry changes along "extended critical transitions". The notion of critical phase transition was first proposed in physics by Curie, at the beginning of the last century. It was then deeply revised and mathematized by the introduction of

renormalization methods which originated in quantum field theory [TPB77, ZJ07]. Critical transitions describe phase changes where a re-organization of the pertinent observables correspond to symmetry changes. In particular, a new coherence structure "emerges" by establishing previously non-existing correlations. Typically, the formation of a crystal or even of a snowflake, percolation, para-ferromagnetic transitions... may all be analyzed as critical transitions.

In our approach, extended criticality, dynamically changing coherent structures as global entities frame variability within a global, extended stability (extended with respect to all pertinent parameters). The coherent structure proper to critical phenomena also justifies the use of variables depending on non-local effects. Thus, an explicitly systemic approach may help in avoiding the accumulation of models and hidden variables. In conclusion, the notion of extended criticality provides a conceptual framework, to be further mathematized, where the dynamics of symmetries and symmetry breakings provide a new, crucial role for symmetries in biology by contrast with physics.

In short, in our perspective, the peculiar phenomenality of life deserves some new concepts and observables: we tried to propose such observables by the notions of extended critical transition, biological complexity, and organization, proper biological time, The point is the pertinence, if any, of these treatments, "per se". Those who claim that all these concepts should be reduced to physical (existing?) theories are welcome to try: we would be very pleased and proud if the competent reductionists were able to rewrite them fully and faithfully (derive or embed them) in (existing) physical frames. However, they should first look at the history of Physics itself, where novel theoretical frames stem from the invention of new perspectives as well as new concepts and observables (inertia, gravitation, entropy, anti-matter...). Their pertinence had to be judged "as such", within their domain of meaning, not on the grounds of their reducibility to existing, thus "safe", explanatory grounds. In any cases, should reduction or unification be performed, the first question is: what theory does one want to reduce to which theory? Reduction, as we learn from physics and logic, is an intertheoretical issue.

Note that, among our proposals, the concept of extended critical transition, in association with ubiquitous symmetry changes, leads to radical methodological changes, based on the specificity of objects and genericity of trajectories, in biology. In short, in physics and mathematics, objects are generic, they are invariants of the theory and experiment: a triangle, a Hilbert space... are used in proofs as generic, by their very definition. Similarly, for Galileo's falling stones or an electron: they are invariants for the theoretical and experimental frames (they are fully interchangeable, in their class). On the opposite, trajectories are specific, that is they are optimal in the suitable phase spaces (in the case of the electron, the "trajectory" is given by Schrödinger's equation thus by the trajectory of a probability amplitude in a Hilbert space). In contrast to this, we analyze biological (phylogenetic, but also ontogenetic) trajectories as generic: they are possible ones, within a phase space co-constructed with the trajectory (see below). Biological objects, instead, are specific, in the sense that they are defined by a history and not by generic features. They are mostly not interchangeable (or not mathematically invariant) both for the theory and for experiments (a major challenge for the interpretation of in vitro experimental work).

This notion is probably the most radical change of perspective we propose. By comparison with physics, it alters the very theoretical nature of the scientific object as for proper biological observables: organisms and phenotypes. As a result, physical notions like the space of theoretical determination (phase space) cannot have the same meaning and use.

One of the main and maybe the main notion at the core of these changes is historicity. In evolution and development, biological objects organize themselves, and they do so in a never identical manner, as long as their organization allow them to survive. We want to emphasize again that the specificity of biological objects, associated with this historical determination and the unstable mathematical symmetries, calls for a change of perspective in the understanding of biological phenomena. Physical objects, even the most complex ones, are understood by their regularities (invariants and associated symmetries), while one of the most stable features of biological objects is their variability, which engenders diversity and contributes by this to biological structural stability, at all levels of organization. It is the reason we put variability, understood as symmetry changes, at the core of our approach to biological phenomena.

3.2. More on critical phase transitions. We have seen that symmetry and symmetry breaking have fundamental consequences for the determination of the behavior of objects. Theoretical symmetries correspond to conserved quantities, which are the properties of physical objects and allow their theoretical determination.

On the contrary, at a spontaneous symmetry breaking point, the loss of the determination of *both* phases behaviors leads to a particular determination, which is associated to the non-analyticity of the partition function. More precisely, the critical point constitutes a singularity in the determination of the system because it is between two different behaviors, characterized by different relevant macroscopic phase spaces.

The strength of these singularities can be of different magnitudes; depending on the Ginzburg criterion [ANB77, LM14d] an original method, renormalization, can be required. This criterion qualitatively corresponds to a more averaging nature of models in higher spatial dimensions since the higher the dimension of space, the more neighbors a point has. When this averaging is insufficient, renormalization methods [Fis98] are necessary to take into account the global structure of determination of the system that results from the coupling between fluctuations and local averages.

3.3. Variability and stability. It should be clear that when we focus on symmetry changes and variability as core notions for understanding life adaptivity and diversity, we do not forget biological structural stability and autonomy, under ecosystemic and internal constraints. No extended criticality would ever be possible without the integrating and regulating activities proper to an organism and its relations to the ecosystem. The main motivation we initially had to look at criticality is the role of the coherent structures characteristic of critical transitions in physics. Even though these structures change along all control parameters in a biological organism, these structures are the mathematical representation of the organismal (changing) stability, its internal and external coherence.

This issue is a major turning point for our perspective. It directly concerns the nature of the mathematical accounts that we can provide on biological organizations, by the instability of biological symmetries.

4. Remarks on reductionism and renormalization

In critical transitions and quantum field theories, the use of renormalization methods is required. These methods use the recursive calculation of interactions on ranges of scales. The aim is to show asymptotically scaling properties of the system without trying to solve

the whole set of interaction taking place at all scales. These methods are based on the stability of the equational determination when one changes the scales. The intelligibility of the phenomenon still has an "upward" flavor. That is, the understanding of larger scales come from smaller scales. The global situation may seem to be given by its (elementary) components, but the system is never understood as a combination of its parts. Renormalization analyzes a recursive flow of models. The "locus of the objectivity" is not in the description of the parts but in the stability of the equational determination when taking more and more interactions into account. This rationale also holds for those critical phenomena, where some parts, atoms, for example, can be objectivated extrinsically to the renormalization and have a characteristic scale. In general, though, only scale invariance matters and the contingent choice of a fundamental (atomic) scale is irrelevant. Actually, in quantum fields theories, there is no known relevant elementary scale. Again, such a scale would not play a significant role since the objectivity of the approach lies in its inter-scale relationships, see for example [ZJ07].

In short, even in physics, there are situations where the whole is not the sum of the parts because the parts cannot be summed on. This issue is not unique to quantum fields as it is also relevant for classical fields. In these situations, the intelligibility is obtained by the scale symmetry. This symmetry is why fundamental scale choices are arbitrary concerning these phenomena, see [LMP12] for further discussions.

Broadly speaking, the theoretical principles that we propose in [LM14f] constitute an extension of existing physical theories since they address observables and quantities unique to life phenomena. They preserve the same formal mathematical structure and, if we set the value of the considered observables or parameters to 0, they lead us back to the case of the inert. That is, if there is no protention [LM14g], no second temporal dimension [LM14a], no extension of criticality [LM14e], zero anti-entropy [LM14b], one returns to physical frames. Our theoretical propositions are thus compatible, although they may be irreducible to "existing physical theories". That is, they are reducible to physics as soon as they are outside the extended critical zone having its own temporality and its anti-entropy, or as soon as these specific quantities go to 0.

In the next section, we will explore the consequences of our analysis on the notion of phase spaces, discuss causality and introduce the concept of enablement.

5. Phase spaces and enablement

We recalled the role of invariance, symmetries and conservation properties in physical theories, as presented in chapter [LM14h]. Our aim, here, following chapter [LM14c], is to hint that the powerful methods of physics, which allowed to pre-define phase spaces on the grounds of the observables and the invariants in the "trajectories" (the symmetries of the equations), do not apply as such to biology.

In biology, symmetries at the phenotypic level are continually changed, beginning with the least cell reproduction, up to the "structural bifurcations" which yield speciations in evolution. Thus, there are no biological symmetries that are *a priori* preserved, except and for some time, some basic structures such as bauplans (still more or less deeply modified during evolution). There are no sufficiently stable mathematical regularities and transformations to allow an equational and law like description entailing the phylogenetic and ontogenetic trajectories. These are cascades of symmetry changes and thus just cumulative historical dynamics. Moreover, each symmetry change is associated with a random event

(quantum, classical or due to bio-resonance, see [BL13]), at least for the breaking of symmetries, while the global shaping of the trajectory, by selection say, is also due to non-random events. In this sense biological trajectories are generic: they are just possible ones and yield a historical result, that is an individuated, specific organism (see [BL11, LM11, LM14e]).

In other words, this sum of individuals and individualizing histories, co-constituted within an ever-changing ecosystem, does not allow a compressed, finite or formal description of the space of possibilities, that is, of the actual biological phase space (functions, phenotypes, organisms). These possibilities are each the result of an unpredictable sequence of symmetry breakings. This situation is in contrast to the invariant (conservation) properties which characterize physical "trajectories", in the broad sense (including for Hilbert's spaces, in Quantum Mechanics).

An immense literature has been tackling "emergence" in life phenomena. In the technical analyzes, the strong and dominating theoretical frames inherited from mathematical physics (or even computing) do not seem to have been abandoned. In approaches from Artificial Life to Cellular Automata and various very rich analysis of dynamical systems, the frame for intelligibility is a priori given under the form, often implicitly, of one or more pre-defined phase spaces, possibly to be combined by adequate mathematical forms of products (Cartesian, tensorial products ...). A very rich and motivated frame for these perspectives is summarized in [DFZG07]. Well beyond the many analysis which deal with equilibrium systems, an inadequate frame for biology, these authors analyze interactions between multiple attractors in dissipative dynamical systems, possibly given in two or more phase spaces (the notion of attractor is a beautiful mathematical notion, which requires explicit equations or evolution functions — solutions with no equations — in pertinent phase spaces in order to be soundly presented). Then, two or more deterministic, yet highly unpredictable and independent systems, which interact in the attractor space, may "produce persistent attractors that are offsprings of the parents.... Emergence, in this case, is absolute because no trajectories exist linking the child to either parent (p. 158) ... [The] source of emergence is the creation, evolution, destruction, and interaction of dynamical attractors (p. 179)".

This analysis is compatible with ours, and it may enrich it by a further component, in pre-given interacting phase spaces. Yet, we go somewhat beyond pre-given phase spaces, from a critical perspective, which, per se, is a tool for intelligibility. Below, we will hint again to further possible (and positive) work, besides negating the possibility of an a priori and compressed mathematical description of (combined) spaces of evolution.

In summary, in our approach, the intrinsic unpredictability of the very *Phase Space* of phylogenetic (and ontogenetic) dynamics is due to:

- (1) physical and properly biological randomness, including bio-resonance, due to interacting levels of organization, as a component both of integration and regulation, in an organism, as well as of amplification of random fluctuations in one level of organization through the others;
- (2) extended criticality, as a locus for the correlation between symmetry breaking and randomness;
- (3) cascades of symmetry changes in (onto-) phylogenetic trajectories;
- (4) enablement, or the co-constitution of niches and phenotypes, a notion to be added to the physical determination.

These phenomena are also crucial to understand life persistence, as they are at the origin of variability, thus of diversity and adaptability, which are an integral part of life

stability. Our theoretical frame, in particular, is based on reproduction with variation and motility as the proper default state for the analysis of phyllo- and ontogenesis. Selection shapes the bubbling forth of life by excluding the incompatible.

By the lack of mathematically stable invariants (stable symmetries), there are no laws that entail, as in physics, the biological observables in the becoming of the biosphere. In physics, the geodetic principle mathematically forces objects never to go wrong. A falling stone follows exactly the gravitational arrow. A river goes along the shortest path to the sea, and it may adjust its path by nonlinear well definable interactions as mentioned above, but it will never go wrong. These are all optimal trajectories. Even though it may be very hard or impossible to compute them, they are unique, by principle, in physics. Living entities, instead, may follow many possible paths, and they go wrong most of the time. Most species are extinct, almost half of fecundations in mammals do not lead to a birth, and an ameba does not follow, exactly, a curving gradient — by retention it would first go on the initial tangent, then it corrects the trajectory, in a protensive action. In short, life goes wrong most of the time, but it "adjusts" to the environment and changes the environment, if possible: it is adaptive. It maintains itself, always in a critical transition, that is within an extend critical interval, whose limits are the edge of death. It does so by changing the observables, the phenotypes, and its niche — in the sense of Darwinian correlated variations of organisms and ecosystems. Thus, it is the very nature and phase space of the living object that changes, in contrast to physics.

We must ask new scientific questions and invent new tools, for this co-constitution by organisms as they co-evolve and make their worlds together. We should see this feature as a central component of the biosphere's dynamics. The instability of theoretical symmetries in biology is not, of course, the end of science, but it sets the limits of the transfer of physicomathematical methods to biology. Kant already doubted of the applicability of physicomathematical reasoning to biology, [Kan81]. In biological evolution, we cannot use the same very rich interaction with mathematics as in the core of physical theories. However, mathematics is an adaptive human construction: an intense dialogue with biology may shape for it new scientific paths, concepts, structures, as it did with physics since Newton.

By providing some theoretical arguments that yield this "negative result", in terms of symmetries and critical transitions, we hope to provide also some tools for a new opening. Negative results marked the beginning of new sciences in several occasions: the thermodynamic limit to energy transformation (increasing entropy), Poincaré's negative result (as he called his Three Body Theorem), Gödel's theorem (which set a new start to Recursion Theory and Proof Theory) all opened new ways of thinking, [Lon12]. Limits clarify the feasible and the nonfeasible with the existing tools and may show new directions by their very nature if these limits have a sufficiently precise, scientific content.

The scientific answer we propose to this end of the physicalist certitudes is based on our analysis of symmetry changes in extended critical transitions and the notion of "enablement" in evolution (and ontogenesis). Enablement concerns how organisms co-create their worlds, with their changing symmetries and coherence structures, such that they can exist in a non-ergodic universe.

Our thesis is that evolution, as a "diachronic process" of becoming (but ontogenesis as well), "enables", but does not cause, unless differentially, the future state of affairs. Moreover, Galileo and Newton's entailed trajectories mathematized Aristotle's "efficient cause"

only. Instead, in our view, in biological processes, such entailed causal relations must be enriched by "enablement" relations, plus differential, physical, often quantum indeterminate, causes.

Life is caught in a causal web but also lives in a web of enablement and radical emergence of life from life, whose intelligibility may be largely given in terms of symmetry changes and their association to random events at all levels of organization.

As hinted in section 5 of [LM14c], a long term project would be to better quantify our approaches to two-dimensional time for rhythms, to extended criticality and to antientropy (see chapter [LM14b]), to construct from them an abstract phase space based on these mathematically stable properties. The analysis should follow the nature of Darwin's evolution, which is a historical science, not meant to "predict", yet giving a remarkable understanding of the living. Thus, the dynamics of extended criticality or anti-entropy should just provide the evolution of these state functions, or how these abstract observables may develop with respect to the intended parameters, and over time. And this, without being "projectable" on specific phenotypes, even not in probabilities, as it is instead possible for Schrödinger's state functions in Quantum Mechanics. To this purpose, one should give a biologically interesting measure for extended criticality and describe in a quantitative way, in the abstract space of extended critical transitions, the qualitative evolution of life. In a preliminary way, we have been able to do so, by following Gould's analysis of increasing biological complexity, that is in the analysis of the evolutionary dynamics of a global observable we will call anti-entropy, [LM14b].

ACKNOWLEDGMENT

The authors wish to acknowledge our preliminary joint work with Francis Bailly and many fruitful discussions with Carlos Sonnenschein, Ana Soto, Matteo Mossio, Arnaud Pocheville.

References

- [ANB77] J. Als-Nielsen and R. J. Birgeneau. Mean field theory, the ginzburg criterion, and marginal dimensionality of phase transitions. *American Journal of Physics*, 45(6):554–560, 1977.
- [BL11] F. Bailly and G. Longo. Mathematics and the natural sciences; The Physical Singularity of Life. Imperial College Press, London, 2011. Preliminary version in French: Hermann, Vision des sciences, 2006.
- [BL13] Marcello Buiatti and G. Longo. Randomness and multilevel interactions in biology. Theory in Biosciences, 132(3):139–158, 2013.
- [DFZG07] J.A. Drake, M.M. Fuller, C.R. Zimmermann, and J.G.P. Gamarra. From energetics to ecosystems: the dynamics and structure of ecological systems. Springer, 2007.
- [Fis98] M.E. Fisher. Renormalization group theory: Its basis and formulation in statistical physics. Reviews of Modern Physics, 70(2):653–681, 1998.
- [Kan81] I. Kant. Critique of Pure Reason. transl. N. Kemp Smith, Palgrave Macmillan, this edition published 1929, 1781.
- [LM11] G. Longo and M. Montévil. From physics to biology by extending criticality and symmetry breakings. *Progress in Biophysics and Molecular Biology*, 106(2):340 347, 2011. Invited paper, special issue: Systems Biology and Cancer.
- [LM14a] G. Longo and M. Montévil. A 2-dimensional geometry for biological time. In *Perspectives on Organisms*, Lecture Notes in Morphogenesis, pages 75–97. Springer Berlin Heidelberg, 2014.
- [LM14b] G. Longo and M. Montévil. Biological order as a consequence of randomness: Anti-entropy and symmetry changes. In *Perspectives on Organisms*, Lecture Notes in Morphogenesis, pages 215– 248. Springer Berlin Heidelberg, 2014.

- [LM14c] G. Longo and M. Montévil. Biological phase spaces and enablement. In *Perspectives on Organisms*, Lecture Notes in Morphogenesis, pages 187–213. Springer Berlin Heidelberg, 2014.
- [LM14d] G. Longo and M. Montévil. Critical phase transitions. In Perspectives on Organisms, Lecture Notes in Morphogenesis, pages 137–160. Springer Berlin Heidelberg, 2014.
- [LM14e] G. Longo and M. Montévil. From physics to biology by extending criticality and symmetry breakings. In *Perspectives on Organisms*, Lecture Notes in Morphogenesis, pages 161–185. Springer Berlin Heidelberg, 2014.
- [LM14f] G. Longo and M. Montévil. Perspectives on Organisms: Biological time, symmetries and singularities. Lecture Notes in Morphogenesis. Springer, Dordrecht, 2014.
- [LM14g] G. Longo and M. Montévil. Protention and retention in biological systems. In *Perspectives on Organisms*, Lecture Notes in Morphogenesis, pages 99–119. Springer Berlin Heidelberg, 2014.
- [LM14h] G. Longo and M. Montévil. Symmetry and symmetry breakings in physics. In Perspectives on Organisms, Lecture Notes in Morphogenesis, pages 121–136. Springer Berlin Heidelberg, 2014.
- [LMP12] G. Longo, M. Montévil, and A. Pocheville. From bottom-up approaches to levels of organization and extended critical transitions. *Frontiers in Physiology*, 3(232), july 2012. invited paper.
- [LMar] G. Longo and M. Montévil. Comparing Symmetries in Models and Simulations. Springer, to appear.
- [Lon08] G. Longo. Laplace, turing and the "imitation game" impossible geometry: randomness, determinism and programs in turing's test. In R. Epstein, G. Roberts, and G Beber, editors, *Parsing the Turing Test*, pages 377–411. Springer, 2008.
- [Lon11] G. Longo. *Interfaces of incompleteness*. downloadable english version, 2011. original in Italian in "La Matematica", vol. 4, Einaudi, 2010.
- [Lon12] G. Longo. On the relevance of negative results. In Conference on Negation, duality, polarity, Marseille 2008, November 2012. (proceedings inInfluxus, electronic journal, http://www.influxus.eu/article474.html).
- [LPP10] G. Longo, C. Palamidessi, and T. Paul. Some bridging results and challenges in classical, quantum and computational randomness. In H. Zenil, editor, Randomness through Computation. World Scientific, 2010.
- [Mar02] D. Marker. Model theory: an introduction. Springer Verlag, 2002.
- [MLS09] M. Mossio, G. Longo, and J. Stewart. A computable expression of closure to efficient causation. Journal of Theoretical Biology, 257(3):489 – 498, 2009.
- [Ros91] R. Rosen. Life itself: a comprehensive inquiry into the nature, origin, and fabrication of life. Columbia U. P., 1991.
- [Sch44] E. Schrödinger. What Is Life? Cambridge U.P., 1944.
- [TPB77] G. Toulouse, P. Pfeuty, and G. Barton. Introduction to the renormalization group and to critical phenomena. Wiley, London, 1977.
- [Tur50] A. M Turing. Computing machinery and intelligence. Mind, 59(236):433–460, 1950.
- [Var89] F.J. Varela. Autonomie et connaissance. Seuil, Paris, 1989.
- [VMU74] F.G. Varela, H.R. Maturana, and R. Uribe. Autopoiesis: The organization of living systems, its characterization and a model. *Biosystems*, 5(4):187 196, 1974.
- [ZJ07] J. Zinn-Justin. Phase transitions and renormalization group. Oxford University Press, New York, 2007.