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Fibonacci sequences, symmetry and ordering in biological patterns, their sources, information origin and the Landauer principle

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Abstract: Physical roots, exemplifications and consequences of periodic and aperiodic ordering (represented by Fibonacci series) in biological systems are discussed. The role and physical and biological roots of symmetry and asymmetry appearing in biological patterns is addressed. Generalization of the Curie-Neumann Principle as applied to biological objects is presented, briefly summarized as: "asymmetry is what creates a biological phenomenon". The "up-bottom approach" and "bottom up" approaches to the explanation of symmetry in organisms are presented in detail. The "up-bottom approach", implies that the symmetry of the biological structure follows the symmetry of media in which this structure is functioning; the "bottom-up" approach, in turn, adopt that the symmetry of biological structures emerges from the symmetry of molecules constituting the structure. A diversity of mathematical measures applicable for quantification of ordering in biological patterns is introduced. The continuous, Shannon and Voronoi measures of symmetry/ordering and their application to biology objects are addressed. The fine structure of the notion of "ordering" is discussed. Informational/algorithmic roots of ordering inherent for the biological systems are considered. Ordered/symmetrical patterns provide economy of biological information, necessary for algorithmic description of a biological entity. Application of the Landauer principle bridging physics and theory of information to the biological systems is discussed.

Keywords: biology; symmetry; asymmetry; periodic ordering; aperiodic ordering; Curie principle; information; Landauer principle; continuous measure of symmetry; Shannon measure of symmetry.

1. Introduction

Biology objects demonstrate remarkably repeatable patterns, governed by simple mathematical laws and regularities. Biological systems frequently exhibit symmetry and regularity on various spatial scales, starting from the genomic level and biomolecules and extending to entire organism [1-6]. A nearly universal observation, which was reported recently, states the subunits in protein assemblies are arranged in symmetric ways [7]. Ref. 8 hypothesized that the beautiful symmetries of biomolecules may reflect basic principles about the energy landscape in biology, just as symmetry relations do in particle physics. Symmetry is inherent for bodies of practically all animals (with rare exceptions); animals are characterized by some kind of overall body symmetry, and these are of only a few types: radial, bi-radial and bilateral symmetry [9]. Symmetry, in turn, represents a kind of ordering in physical and biological systems [10-11]. When we address symmetry of ordered pattern we usually restrict ourselves to mainly consider periodic order [12]. At the same time, order without periodicity has emerged to properly describe an increasing number of complex systems, and in particular biological ones [12]. Such kind of ordering, was referred in ref. 12 as *aperiodic ordering*. The outstanding example of the aperiodic ordering is supplied by the Fibonacci numbers, or Fibonacci series [13-16]. Fibonacci and

Lucas series appear in biological patterns [17]. Perhaps the most striking example of such samples is supplied by phyllotaxis, which is the arrangement of leaves on a plant stem [13-17]. These patterns are surprisingly regular, so regular in fact that a physicist can compare their order to that of crystals, however ordering in biological systems is usually not perfect, and quantitative measures of the deviation from the perfect ordering, which were introduced recently, will be discussed below in detail. It should be mentioned that non-ordered, asymmetrical biological systems exist. It is generally agreed that sponges are completely asymmetrical (see **Figure 1**), however, this thesis may be debated and will be addressed below in detail.

Figure 1. Calcareous sponges are depicted. Sponges are usually regarded as non-ordered biology objects/

Moreover, it was suggested that breaking symmetry is a prevalent process in biology [3, 18]. However, to be broken symmetry in biological patterns must first appear, and it appears on different levels of organization of biological systems [1, 2, 4, 18].

The reasonable question is: what is the biological reasoning of periodic and aperiodic ordering in biological systems? In other words: why nature prefers ordered patterns? The possible answers to this fundamental question may be classified as follows: i) Appearance of symmetry and other sample patterns are due to the external physical constraints implied on the biological system [5, 19-21]. This hypothesis adopts that just physical effects, which in many cases act as proximate, direct, tissue-shaping factors during ontogenesis, are also the ultimate causes (in other words) the indirect factors which provide a selective advantage – of animal or plant symmetry, from organs to body plan level patterns [19-21]. ii) The second idea explaining abundancy of the symmetric patterns in biology implies that symmetry of biological systems stems from the symmetry of molecules themselves and potentials describing interactions between molecules [22-23]. It was demonstrated, that symmetry of these potentials governs the symmetry of biological systems, such as actin, tubulin, and the ubiquitous icosahedral shell structures of viral capsids [22-23]. iii) The third approach relates appearance of mathematical ordering in biological systems to the pure survival reasons. For example, periodic cicadas emerge from their underground homes to mate every 13 or 17 years, which are primes [24-29]. The philosophy of the evolutionary-based explanation of the mathematical ordering is that if cicadas have 12-year cycles, all the predators with two, three, four, and six-year cycles will eat them, in other words, if the cicadas mutate to 13-year cycles, they will survive [28-29]. Let us quote ref.

29: "a prey with a 12-year cycle will meet-every time it appears-properly synchronized predators appearing every 1, 2, 3, 4, 6 or 12 years, whereas a mutant with a 13-year period has the advantage of being subject to fewer predators". A second explanation, proposed by Cox, Carlton and by Yoshimura, concerns the avoidance not of predators but of hybridization with similar subspecies [25-27]. A genuine reasoning of the primes-shaped life cycle of cicadas remains debatable and the discussion of this reasoning gave rise to the deep philosophical discussion of the nature and roots of the notion of "explanation" of natural/biological phenomena in ref. 30. Survival reasons were also involved for explanation of symmetry appearing in the color of zebra finches, shown in **Figure 2.**

Figure 2. Zebra finch is depicted. Symmetrically banded males and females are preferred by an individual of the opposite sex

It was demonstrated that symmetrically banded males produced more offspring that survived past the period of parental care than males in either of the asymmetric treatments; this appeared to be the effect of female choice processes and female-based parental investment and not male intra-sexual dominance. Thus, it was shown, that symmetrically manipulated males gain reproductive advantages in controlled laboratory conditions and further supports recent theories indicating the evolutionary importance of symmetry in signalling-trait design [31]. Moreover, it was demonstrated that symmetric patterns are attractive not only to females, and it was found that males associated more with symmetrical than asymmetrical females, indicating a preference for symmetry [32]. iv) And, finally, we discuss the more hypothetic relation of an appearance of symmetrical patterns in biological systems to informational reasoning. It was suggested, that symmetric biological structures and patterns preferentially arise not just due to natural selection but also because they require less specific information to encode and are therefore much more likely to appear as phenotypic variation through random mutations [33]. This novel concept, which is well tailored to the general informational paradigm of exact sciences, was criticized recently in ref. 34, will be discussed below in its relation to the Curie-Minnigerode-Neumann and Landauer Principles [35-37]. In our paper we focus on the physical and informational reasoning of symmetry/ordering inherent for biological systems. We will also demonstrate that the notion of ordering has a "fine structure" and hardly could be quantified unequivocally with a single mathematical parameter.

2. Physical reasoning for the abundant symmetry of biological patterns

2.1. The "up-bottom approach" to the explanation of symmetry in organisms: symmetry is dictated by the properties of media in which the organisms acts

Physical reasoning involved for the explanation of symmetry of biological objects may be classified according to following main approaches:

i) The "up-bottom approach", implying that the symmetry of the biological structure follows the symmetry of media in which this structure is functioning

ii) The "bottom-up" approach assuming that the symmetry of biological structures emerges from the symmetry of molecules constituting the structure.

Let us start for "up-bottom" pure physical reasoning which may be responsible for symmetry abundant in the plants and animals realms. The two main symmetries that can be observed in the animal body plan are radial and bilateral, as illustrated with **Figure 3** [21, 38-39].

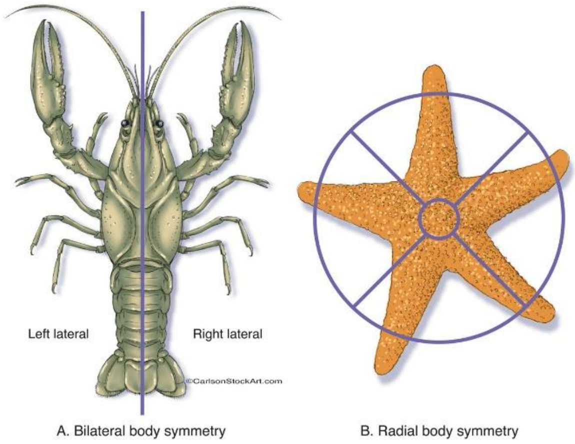

Figure 3. Bilateral (a) and radial symmetry (b) in biological objects.

Pure physical "demystification" of animal symmetry was suggested in refs. 19-20. Let us quote ref. 19: "symmetry is a response in the geometry of the "living matter" to physical forces". As an example of such pathway of thinking, consider the directed locomotion of sea inhabitants. The most comprehensive idea which explains how directed locomotion is favored by bilateral symmetry comes from a theoretical paper [18], which argued that bilateral symmetry is favorable for manoeuvrable locomotion in the macroscopic world (in which inertial forces dominate over viscous forces, i.e., in the high Reynolds numbers' realm, because bilateral is the only type of symmetry which is streamlined in only one direction while being non-streamlined in others [18]. Symmetry of biological entities which inhabit water and air becomes more clear when the ideas developed in ref. 40 are taken into account. It was concluded in ref. 40 that a large proportion of fish species have developed compressed, elliptical body cross-sectional shapes. This shape is justified from the hydrodynamic point of view, as the basic issue of minimizing drag for a given volume would result in a body of revolution [40]. Thus, this adaptation must have had very significant advantages, to have reappeared so many times. One such advantage is clear from the use of the body as a propulsor, as the sideways oscillations of a vertically compressed body will produce much larger forces but this also reduces rolling, which would, in turn induce yawing moments due to the difference in angle of attack on the pectorals and the angle of attack on the caudal and dorso-anal fins produced by rolling. Thus, vertical compression is a stabilizing development [40-41].

We propose following development of the suggested pure "physical explanation" of symmetry inherent for fishes and birds. The observed symmetry is to a much extent explained by the isotropy of physical properties of gases and liquids, in which fishes and birds act. Gases and some of liquids are essentially isotropic media. Gases are isotopic due to the random molecular motion of molecules, constituting the gaseous phase, also called the molecular chaos hypothesis, implying that the velocities of colliding molecules are uncorrelated, and independent of position [42-45]. The hypothesis of molecular chaos also implies the equipartition theorem serving as a basis for the classical thermodynamics and statistical physics, which states that in thermal equilibrium energy is shared equally among all of its various forms [46-50]. The equipartition theorem, in turn, is grounded on two main assumptions: (1) the classical version of the canonical probability distribution is applicable and adequate; (2) the classical expression for the total energy of the particle splits additively into two parts: one part depends quadratically on a single variable (say x), and the other (denoted U_{other}) is entirely independent of that variable $U = ax^2 + U_{other}; a = const$. It is easily seen that the equipartition of energy holds whatever is the value of the constant a; moreover the equipartition theorem for a broad class of potentials $U = ax^2 + bx; a, b = const$, as discussed in ref. 51. Thus, symmetry of bodies of birds, possibly emerges from isotropy of air accompanied by equipartition of energy, which is true for air molecules. This "physically grounded" approach may be stretched even further: actually conservation laws appearing in physics arise from the fundamental symmetries of space-time; thus, symmetry recognized in physical systems reflects these fundamental symmetries; hence, it is plausible to suggest, symmetry of biological systems also arises from the fundamental space-time symmetries.

The situation with liquids is much more complicated; indeed, liquids may by isotropic and non-isotropic (liquid crystals) [52]. However, the most important biological liquid is water, which is considered isotropic in biophysical models, which deal with water and water inhabitants. This assumption as a matter of fact is far from to be trivial. It was demonstrated that the state of water in the body constituents of living organisms and in the vicinity of biological macromolecules differs significantly from the state of water in solutions of simple molecules and in pure water [53-54]. Biological macromolecules induce a characteristic water structure in their close vicinity due to weak macromolecular-water interactions [53-54]. Anyway, considering water as an isotropic medium is justified at the macroscopic level of treatment of biological system. On the other hand, aqueous solutions of DNA govern their chirality, i.e., the lack of mirror symmetry of the solutions, which already brings us to the "bottom-up" approach to the symmetry of biological objects, implying that the symmetry of biological structures emerges from the symmetry of molecules constituting the structure [55-60].

2.2. "Bottom-up" approach to the symmetry of biological systems, mathematical measures of order in biological patterns and the Curie-Neumann Principle

2.2.1. Mathematical measures of symmetry and ordering in biological patterns

As we already mentioned in the previous sections that DNA constitutes the symmetry properties (chirality) of aqueous solutions [55-59]. Not only DNA but also tobacco mosaic virus governs lyotropic liquid crystalline behavior of the ensemble of these viruses. Thus, we come to the "*bottom-up*" approach to the symmetry of biological structures and patterns, adopting that the symmetry of large scale, macroscopic biological structures emerges from the symmetry of molecules constituting the structure. High symmetry assemblies of proteins, resembling those inherent to the geometries of the Platonic solids were discussed in ref. 7. Symmetry of biological macromolecules in its comparison with the symmetry of nuclei, atoms and elementary particles was deeply analyzed in ref. 8. Let us quote from ref. 8: "The role of symmetry in the physics of atoms, nuclei, and elementary particles is different from its role in the biological world. In microphysics, it has been fruitful to postulate symmetry as being fundamental, thereby severely constraining the form of the underlying laws. Furthermore, the consequences of symmetry for dynamics and stability are profound in the subatomic world. General treatment of these symmetry effects, based on group theory, allows a nearly complete classification of states and transitions. Indeed, even the deviations from exact symmetry have their own quantifiable consequences. In the biological world, symmetry exists too, but it often appears to be an accident. While accidents still can have significant consequences, rationalizable on a case-by-case basis, there has been no general unifying theory of symmetry in biology. Exact symmetry in biology would even seem to be antithetical to the notions of complexity, variety, and metamorphosis that are central to the idea of life, as we know it. Nevertheless, as in microphysics, life requires stability and sameness as well as change"… For a particular protein, biomolecular symmetry will not be exact unless it is the result of gene duplication. It is a quantitative issue how much the forces leading to minimal frustration, partially determined by symmetry considerations, are dominant over the aspects of the landscape arising from randomness".

Indeed, the exact, perfect symmetry (in the rigorous mathematical sense) is rare in a realm of biology. It is sparse on different levels of biological structures, and even on the molecular level, it is not abundant. Now we come to the novel ideas, which appeared in the theory of symmetry in last decades. Until now, it was usually latently accepted that symmetry changes abruptly or intermittently, i.e. symmetry is an exact feature of the pattern. In other words, symmetry is usually viewed, as a binary feature, when an object is considered as either perfectly symmetric or asymmetric. Despite this, a fundamentally new approach to quantifying symmetry as a continuous measure of a pattern was suggested and tested recently by Avnir, Zabrodsky and co-workers [61-65]. The notion of "continuous measure of symmetry" was introduced and developed in refs. 61-65. Continuous measure of symmetry is a fundamentally new approach to quantifying symmetry [61-65]. Continuous measure of symmetry is quantified by the sum of minimum squared distances that are required to move the points of an original shape in order to obtain a symmetrical shape [61-65]. The continuous measure broke the binary "yes-no" paradigm traditionally used for the analysis of symmetry of patterns [61-65]. This approach was successfully exploited for quantification of the symmetry of electronic wave functions [66] and quasicrystals [67]. The continuous measure of symmetry was recently applied to the analysis of symmetry of proteins [68-69]. It was revealed that symmetry deviations of proteins are by far higher in solution, compared to the crystalline state [69]. However, only first results in the field of the continuous analysis of symmetry of biological objects were reported, and it seems, that the mathematical apparatus of continuous measure of symmetry has an enormous potential in mathematical biology.

It should be emphasized that the continuous measure of symmetry is not a single mathematical value enabling quantification of ordering in the biological patterns. The alternative measure of order in the biological patterns emerges from the Voronoi tessellation (or Voronoi diagram). A Voronoi tessellation of an infinite plane is a partitioning of the plane into regions based on the distance to a specified discrete set of points (called seeds or nuclei and shown with black squares in **Figure 4**). For each seed, there is a corresponding region, consisting of all points closer to that seed than to any other [70-77].

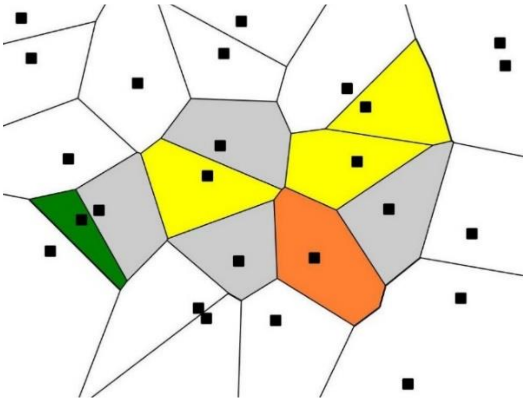

Figure 4. Voronoi diagram (tessellation) emerging from the initial 25 randomly placed points, also called seeds, represented with black squares); green polygon is a quadrangle; yellow polygons are pentagons; grey polygons are hexagons, the orange polygon is an octagon. Are the seeds ordered? The answer to this question is supplied by calculation of the Voronoi (shannon) entropy of the pattern.

The Voronoi (Shannon) entropy of a given set of points located in a plane is given by:

$$S_{vor} = -\sum_i P_i ln P_i, \tag{1}$$

where P_i is the probability of finding *n*-sided Voronoi polygon within a given Voronoi tessellation and *i* is the total number of polygon types with different numbers of edges [24,25,26]. The summation in Equation (1) is performed from *i* = 3 (the smallest possible polygon—a triangle) to the largest coordination number of the polygon, e.g., for an octagon, the largest value of *i* is 8. Consider the Voronoi diagram built of pentagons only, in such a diagram $P_5 = 1$ and consequently $S_{vor} = 0$. It is reasonable to relate to such a diagram the maximal degree of ordering; in contrast, the Voronoi entropy of the random pattern of seeds was established as $S_{vor} = 1.71$. Seeds may be displaced continuously from their initial locations, and the Voronoi entropy, in turn, will be changed continuously. Voronoi tessellations were already successfully applied for the analysis of ordering in the biological systems, namely: proteins [73], cell dynamics [74] and ordering of GABAA receptors in hippocampal inhibitory synapses [75],

Thus, we already have two alternative continuous measures of ordering in biological systems, namely the continuous measure of symmetry [68-69] and Voronoi Entropy (and this is not an exhaustive list) [73-77]. And the reasonable question immediately arises: are these measures correlated? It was recently demonstrated that the continuous measure of symmetry and the Voronoi entropy of the pattern are not necessarily correlated; moreover, anti-correlation of these values was registered [67, 78]. Alternative measures of ordering in biological patterns, such as Minkowski functionals were also introduced [79-80]. Shannon (informational) measure of symmetry was also suggested recently [81]. Consider a 2D pattern built of 1D and/or 2D shapes or lines, demonstrating a number of symmetry elements (rotational symmetry, centers of symmetry, axes of symmetry, etc.), denoted G_i, i = 1,2 ... *k*, where *k* is a number of non-identical symmetry operations [81]. Elements G_i form the symmetry group of the shape *G* (which should be clearly distinguished from the symmetry group of the entire pattern). Thus, the informational measure of symmetry of the pattern $H_{sym}(G)$ is defined in a Shannon-like form (compare with Eq. 2) as:

$$H_{sym}(G) = -\sum_{i=1}^{k} P_i(G_i) ln P_i(G_i), \tag{2}$$

where $P_i(G_i)$ is the probability of appearance of the symmetry operation G_i within the shapes (lines) constituting the pattern, defined as:

$$P_i(G_i) = \frac{m(G_i)}{N_G} \leq 1, \tag{3}$$

where $N_G = \sum_{i=1}^{k} m(G_i)$ is the total number of symmetry elements (operations) appearing in the 1D or 2D shapes, recognized in a given pattern, and $m(G_i)$ is the number of the same symmetry elements (operations) $\mathrm{G_i}$, calculated for a given pattern. The normalization condition given by Eq. 4 takes place:

$$\sum_{i=1}^{k} P_i(G_i) = 1 \tag{4}$$

The informational (Shannon) measure of symmetry, defined with Eq. 2, is applicable for the the mixed patterns built of curves and shapes, thus it is suitable for the analysis of the biological patterns (such as those, depicted in **Figure 5**). Thus, we necessarily conclude that the notion of "ordering in biology patterns" has a fine structure, and the correlation between various mathematical measures of order remains an open problem and should be elucidated in a future research.

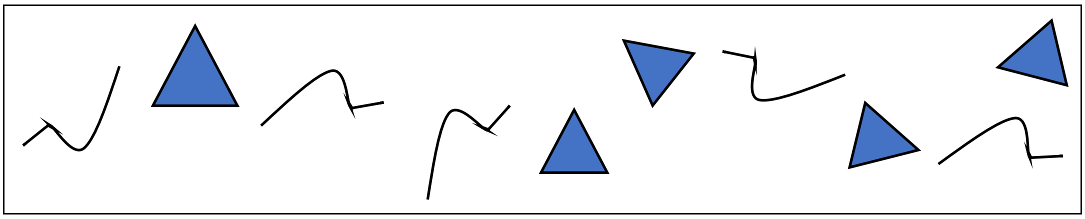

Figure 5. Mixed pattern built of $p=5$ irregular non-symmetric curves and $p=5$ equilateral triangles. The symmetry group of the equilateral triangle is the dihedral symmetry group D_3 containing $3p$ symmetry axes and $3p$ rotations (including the 2π rotation, denoted G_1). One more G_1 operation comes from the irregular curves; thus, we have in total $7p$ symmetry operations in this pattern. The IMS is easily calculated, according to Eq. 2: $H_{sym} = -\left(\frac{2}{7} ln \frac{2}{7} + \frac{5}{7} ln \frac{1}{7}\right) = 2.23$.

2.2.2. *"Bottom-up approach to the symmetry" of biological systems and the Curie-Neumann Principle*

Obviously properties of biomolecules influence properties of macroscopic biological objects. But what is the interrelation between symmetry of biomolecules and eventual properties of macroscopic structures? In the realm of crystallography this interrelation is constituted by the Curie-Minnigerode-Neumann Principle, which in its simplest form was formulated by Minnigerode "The group of the structure of a crystal is contained in the group of each of its physical properties", or in other words: all elements of symmetry of a crystal are at the same time elements of symmetry of its macroscopic properties [82-83]. This statement may be mathematically expressed, as:

$$G_{object} \subseteq G_{property}, \tag{5}$$

which is understood as follows: in order that a physical property is allowed to exist within an object it is a necessary but not sufficient condition that the group of the symmetry operations of the object G_{object} be at least a subgroup of the group of the symmetry operations of the physical property $G_{property.}$, or alternatively: the tensor describing a physical property (the so-called "property tensor") has to be invariant against all symmetry operations of the object (crystal), or alternatively: the symmetry elements of the causes must be found in their effects, but the converse is not true; that is, the effects can be more symmetric than the causes. [82-83]. However, Curie already clearly understood the role of asymmetry in constituting the physical phenomena. The phenomenon of piezoelectricity just emerges from the symmetry breaking in certain crystals [83]. This idea was aphoristically formulated by Curie as follows: "Asymmetry is what creates a phenomenon". And it seems that this approach may be extended to biology; however, there is a long way ahead in order to understand the role of asymmetry in constituting biological phenomena.

3. Informational Reasoning for Symmetry in Biological Systems

3.1. Symmetry and ordering in biological system has informational/algorithmic roots

Alternative reasoning for abundance of symmetrical patterns in biological systems was suggested in ref. 33. The authors of ref. 33 noted that it is plausible to assume (by a certain analogy to engineering design) that symmetry may stem from natural selection, as discussed in Section 2.1, in which it was demonstrated that bilateral symmetry of sea inhabitants is favorable for their manoeuvrable locomotion in water [19]. However, evolution, unlike engineers, cannot plan ahead, and so these symmetrical features must also afford some immediate selective advantage which is hard to reconcile with the breadth of systems where symmetry is observed. It was suggested in ref. 33 that the symmetric structures preferentially arise not just due to natural selection but also because they require less specific information to encode and are therefore much more likely to appear as phenotypic variation through random mutations. Arguments from algorithmic information theory enabled formalization of this hypothesis, leading to the prediction that many genotype–phenotype maps are exponentially biased toward phenotypes with low descriptional complexity (preference for symmetry is a special case of the bias toward compressible descriptions). The authors of the aforementioned hypothesis validated this idea predictions with biological data, showing that protein complexes, RNA secondary structures, and a model gene regulatory network all exhibit the expected exponential bias toward simpler (and more symmetric) phenotypes [33]. The authors of ref. 33 supplied arguments, supporting their concept, rooted in the algorithmic information theory, in which it is well-accepted, that when the space of algorithms is considered, outputs that can be generated by short programs are exponentially more likely to be produced than outputs that can only be generated by long programs. It was demonstrated in ref. 33, that formalism developed in the algorithmic information theory may be successfully applied for the analysis of genotype–phenotype maps. Thus, symmetry, appearing in biological systems emerges from the "informational arguments", providing economy of biological information, necessary for description of a biological entity [33].

The "informational biological paradigm" introduced and developed in ref. 33 was recently criticized in ref. 34, in which the role of symmetry breaking in biological systems was stressed. It was noted that, while symmetry may arise more commonly in biological structures with low complexity, there is evolutionary pressure to develop asymmetry in many biological structures with high complexity. The emergence of symmetry cannot be fully understood without considering the emergence of asymmetry as well [34]. Consider, for example, the human brain, one of the most complex and mysterious biological structures [34, 86]. While the two halves of the brain look roughly symmetric at first glance, a recent large-scale neuroimaging demonstrated that structural left–right asymmetries are the rule, rather than the exception, for cortical brain areas [86]. Importantly, the human central nervous system is not the only one that shows such striking asymmetries. Breaking symmetry is therefore a crucial step in the development of all nervous systems [34]. This statement is in the striking correspondence with the Curie-Minnigerode-Neumann Principle, formulated by Curie as follows: "Asymmetry is what creates a phenomenon" [83], which may re-shaped as follows: "Asymmetry is what creates a biological phenomenon".

Anyway, explanation of symmetrical patterns, abundant to biological systems with arguments rooted in the algorithmic information theory seems deep and promising. We propose to stretch this approach to grounding of other kinds of periodic and aperiodic ordering appearing in biological systems, such as Fibonacci series and Archimedian and Lucas spirals [13-17, 87]. Indeed, the Fibonacci series found in phenotypic structures of plants and animals, defined by Eq. 6

$$F_n = F_{n-1} + F_{n-2;} F_0 = 0;\ F_1 = 1 \tag{6}$$

and Archimedian spiral, defined by Eq. 7

$$r = a + b\theta, a = const; b = const \tag{7}$$

represent an examples of simple, and informationally effective mathematical regularities, which may be specified by short algorithms. Ref. 87 reported created a model of the cell division implying asymmetric cell division. In the model cells divide asymmetrically to generate a mature and an immature cell [87]. Model output on the number of cells generated over time fits specific Fibonacci p-number sequences depending on the maturation time [87]. Thus, the relation of the Fibonacci series to asymmetry of biological processes became elucidated [87].

3.2. Symmetry and ordering in biological systems and the Landauer principle: informational paradigm of biology

The idea that symmetry in biological patterns is deeply rooted in informational basic structure of the reality fits with ideas, introduced by John Archibald Wheeler, who suggested that fundamentals of physics should be re-built on the informational groundings and assumed that the main notions of physics are deeply rooted in the "bit-based" scientific paradigm [88]. This approach was may be very briefly and aphoristically summarized as follows: "all things physical are information-theoretic in origin", aphoristically reduced to "it from bit" [88]. The idea was developed recently within the highly debated and controversial Landauer principle, suggesting the thermodynamic equivalent of information, establishing the lower theoretical limit of energy consumption of computation. It holds that "any logically irreversible manipulation of information, such as the erasure of a bit or the merging of two computation paths, must be accompanied by a corresponding entropy increase in non-information-bearing degrees of freedom of the information-processing apparatus or its environment" [35-36]. In other words, there is a minimum possible amount of energy E required to erase one bit of information, known as the Landauer limit and supplied by Eq. 8:

$$E = k_B T ln2, \tag{8}$$

where $k_B = 1.38 \times 10^{23} \frac{J}{K}$ is the Boltzmann constant and T is the absolute temperature of heat sink [89-92]. The Landauer Principle was experimentally tested in refs. 93-94. Extension of the Landauer Principle to the realms of quantum mechanics [95] and general relativity [96] were reported. The Landauer Principle applied to mechanical motion demonstrates that dissipation of energy is the key process through which mechanical motion becomes observable [97]. The analysis of performance of photon detectors (such as eyes) brings to the conclusion that just efficiency that is limited the Landauer energy bounds on information gain and information erasure [98]. Estimation of information contained in molecular motion based on the Landauer Principle was performed in ref. 99. The Landauer Principle restricts the informational capacity of biological systems; thus, it closely related to the abundance of ordering in biologic systems; indeed, periodic and aperiodic ordering enable saving of memory, available for the organism. The Landauer Principle bridges between the informational and thermodynamic paradigms of life, which explains an ability of organisms to maintain low levels of entropy that explain order [100]. The informational paradigm of life enabled the analysis of the SARS-CoV-2 virus using Shannon's information theory [101]. A relationship between the information entropy of genomes and their mutation dynamics was established. In particular, it was revealed that genomes undergo genetic mutations over time driven by a tendency to reduce their overall information entropy [101]. Let us estimate with the Landauer Principle roughly the informational capacity of living cells. Consider that the characteristic spatial range of living cells, namely, $l \cong 1-100\mu m$ spans the dimensions of a majority of prokaryotic and eukaryotic cells [101]. Thus, maximal informational capacity of a living cell may be estimated, according to the Landauer Principle according to Eq. 9; if we speculate that information exchange occurs only *via* the surface of a living cell we estimate:

$$\xi \cong \frac{E_S}{k_B T ln2} \cong \frac{\gamma_{int} l^2}{k_B T ln2}, \tag{9}$$

where E_S and γ_{int} the total and specific interfacial energies of a cell. Assuming $\gamma_{int} \cong 1.0 \times 10^{-3} \frac{J}{m^2}$ yields $\xi \cong 3.5 \times 10^5 - 3.5 \times 10^9$ [102]. (This value should not be confused with the genomic capacity of a cell [103-104]). Thus, we may estimate the informational interfacial capacity of a small micro-scaled cell a $\xi \cong 3.5 \times 10^5$ bits; compare with the DNA-based code, which enables the storage of 5.2×10^6 bits of information [105]. Thus, the informational capacity of DNA and cells is restricted; hence, assessing the thermodynamic efficiency of the computations performed by organisms becomes crucial. Ref. 106 posed and addressed following fundamental question: how close life has come to maximally efficient computation (presumably under the pressure of natural selection)? The answer suggested in ref. 106 is summarized as follows: despite inevitable shifts across the architectures of life, the authors revealed a surprising consistency in the efficiency of translation, one of the most universal types of computation carried out in biological systems [106]. The analyses demonstrated that as bacteria become larger their overall translational efficiency converges on that of a single ribosome [106]. In addition, this efficiency is maintained for unicellular eukaryote and mammalian cells [106]. Astonishingly, this efficiency is only about an order of magnitude larger than the Landauer bound, supplied by Eq. 8 (see ref. 106). And it should be emphasized that symmetry and ordering (periodic and aperiodic) inherent in biological systems improve the efficiency of biological computation, indeed, when an *n*-fold symmetry is present, the single computation act governs the location of a number of *n* "spots" in the biological pattern. An interface between artificially created digital information and information produced by organisms was addressed in ref. 107. It was demonstrated that human-related digital information has reached a similar magnitude to information in the biosphere [107].

4. Conclusions

Biological systems demonstrate remarkable symmetry and ordering which may be periodic or aperiodic [1-2, 4, 12]. These ordering and symmetry span all of biological spatial scales starting from biomolecules [7, 8] up to entire organisms and biological patterns, created by organisms [9, 19-21]. The symmetry may be even regenerated with time as it occurs with damaged jellyfish [108]. The challenging and fundamental questions are: what are the physical and biological reasoning of periodic and aperiodic ordering in biological systems? In other words: why living nature prefers ordered/symmetrical patterns? The possible answers to this fundamental question may be summarized as follows: i) Appearance of symmetry/ordering is due to the external physical constraints implied on the biological system [5, 19-21]. ii) The second hypothesis explaining abundancy of the highly ordered patterns in biology adopts that symmetry of biological systems emerges from the symmetry of molecules themselves and potentials describing interactions between molecules [22-23]. iii) The third approach relates appearance of mathematical ordering in biological systems to the pure survival, evolutionary reasons [24-29]. iv) The most recent hypothesis relates an appearance of symmetrical patterns in biological systems to informational reasoning. It was suggested, that symmetric biological structures and patterns preferentially arise not just due to natural selection but also because they require less specific information to encode [33]. We addressed this approach within the general informational scientific paradigm, proposed by John Archibald Wheeler, who suggested that fundamentals of physics should be re-built on the informational groundings and assumed that the main notions of physics are deeply rooted in the "bit-based" scientific paradigm [88]. The ideas discussed in ref. 33 stretch this approach to the "bit-based" biological paradigm, which may be formulated as follows: economy of information is essential in the constituting of biological patterns. Thus, it becomes understandable why just the simplest mathematical regularities such as Fibonacci series [13-17, 87] and symmetrical patterns are abundant in biology; these regularities decrease the algorithmic complexity of biological systems [33]. The informational paradigm of biology is closely related to the Landauer Principle bridging theory of information of physics and suggesting the thermodynamic equivalent of information, under establishing the lower theoretical limit of energy consumption of biological computation [35-37, 89-99]. The analyses of the computational efficiency of bacteria demonstrated that as bacteria become larger their overall translational efficiency converges on that of a single ribosome [106]. Moreover, this efficiency is universal for unicellular eukaryote and mammalian cells and it only about an order of magnitude larger than the Landauer bound [35-37, 89-99, 106]. Thus, the Landauer briefly formulated as "information is physical" may be re-shaped to "biological information is physical and strictly speaking thermodynamically-rooted". Symmetry and ordering increase essentially computational/informational effectivity of biological systems.

It should be emphasized that the role of symmetry in biological systems is very different from that in physics (such as symmetry of crystals). Symmetry in the biologically-rooted patterns is never perfect. Thus, mathematical methods enabling quantification of symmetry and its deviation from the mathematically perfect symmetrical patterns were suggested [61-69]. It turns out that the notion of ordering has a fine structure, and may be quantified mathematically with essentially different mathematical measures such as the continuous measure of symmetry, Voronoi (Shannon) entropy and Minkowski functionals [61-81]. Thus, a unique mathematical measure quantifying "order" in biological systems does not exist. It was demonstrated that the maxima and minima of the Shannon entropy and continuous measure of symmetry are not necessarily correlated; moreover, in certain cases, maxima of the continuous measure of symmetry may correspond to the minima of the Shannon entropy [78]. Accurate quantification of ordering and symmetry in biological patterns is well-expected to be a hot theme of the nearest future mathematical biology investigations. Consider, that "physical ordering", as quantified by the Boltzmann entropy, and symmetry are in the intimate relation: symmetry usually decreases the Boltzmann entropy of systems [10, 11].

Moreover, breaking of symmetry and asymmetry are crucial for understanding biological phenomena [34, 86-87]. For example, breaking symmetry is a crucial step in the development of all of biological systems [34]. Thus, the Curie-Minnigerode-Neumann Principle, may re-shaped for biological systems as follows: "Asymmetry is what creates a biological phenomenon" [82, 83]. Thus, we conclude that symmetry and ordering, abundant in biologically rooted patterns, could be hardly related to a single, unique physical or evolutionary reason. We conclude that general unifying theory of symmetry in biology does not exist, and, perhaps, has no chance to be developed. However, the role of symmetry/asymmetry reasoning in understanding biological phenomena is crucial.

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