



A resonance based model of biological evolution

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HIGHLIGHTS

- A model relies on forced harmonic oscillator for evolution is proposed.
- Macroevolution is described as a resonance phenomenon.
- It presents a hypothesis for the so-called Cambrian Explosion.
- The model provides also an explanation for periods of evolutionary stasis.

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ABSTRACT

We propose a coarse grained physical model of evolution. The proposed model 'at least in principle' is amenable of an experimental verification even if this looks as a conundrum: evolution is a unique historical process and the tape cannot be reversed and played again. Nevertheless, we can imagine a phenomenological scenario tailored upon state transitions in physical chemistry in which different agents of evolution play the role of the elements of a state transition like thermal noise or resonance effects. The abstract model we propose can be of help for sketching hypotheses and getting rid of some well-known features of natural history like the so-called Cambrian explosion. The possibility of an experimental proof of the model is discussed as well.

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1. Introduction

According to established theory, random genetic mutations and natural selection are the phenomena that act as the core engine for the evolution of the species [1].

Random mutations are modifications along the sequence of the DNA, mainly due to replication errors, so that 'random' means that they are the product of individual causes that we ignore and cannot have control on it and, still more important, are unrelated with the organism fitness.

In addition to these two (classical) factors, epigenetic phenomena are rapidly gaining momentum [2,3]. We can roughly define epigenetic changes as variations of the phenotype of an organism due to a modification of the gene expression pattern without modifications of the DNA's sequences.

Random mutations, natural selection and epigenetic changes have been taken under consideration to generate a theoretical frame to the 'saltation-and-stasis' phenomenology suggested by fossil records [4,5].

Fossil records show a highly non-linear trend of the evolution, made of long period of standstill interrupted by relatively fast appearances of many species. The Gould and Eldredge 'Punctuated Equilibria' theory interprets the alternation between

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'saltation' and 'stasis' keeping the idea that evolution is characterized by the combined effect of random mutations and natural selection, although in some situations its speed may be very low [5].

Nowadays, the discovery of the lack of bi-univocal character of the genotype–phenotype relation [6,7] and the overwhelming combinatorial complexity of molecular interaction (Tompa and Rose in their paper [8] gave a gross estimate of 10^{7200} molecular interaction constraints to be satisfied in a relatively simple system like yeast) push to try to face evolution non-linearity with a fresh perspective.

Here we try to sketch a plausible frame of evolution building upon the three basic evolution pillars: stochastic nature of DNA mutations, epigenetic changes and selective pressure. Our goal is to insert these three pillars in the frame of the physical theory of forced harmonic oscillators. We do not propose a 'definitive mathematical theory of evolution' but we hope this exercise can be useful for hypothesis generating.

We build upon the universal character of state transitions displaying some largely invariant features across different fields of application such as cell differentiation, finance and physical chemistry (see for example Refs. [9–12]). The exercise to fit evolution into the general frame of state transitions allowed us to accommodate both stochastic and directional effects and to generate some implications on evolutionary biology.

2. Evolutionary model

The main actor of this proposed model is a biological species defined as a vector in a N -dimensional space, where N is the number of characters that describes that species. We associate to each of the N characters an axis representing all the possible expressions (not only those actually observed) of that character. We call X the coordinate of a species on one of these axes. A given X will correspond to the value taken for one (out of the N defining the space) character by a species that, in turn, is a point associated to a unique configuration in the N -dimensional space. Thus, the value of X corresponds to a certain phenotype. Each species encompasses many individuals, so we intend the X of a given species as the 'average' phenotype.

It is worth focusing on the abstract nature of our model so, at this point, we give for granted the mutual independence of the variables spanning the space.

The phenotypic N -dimensional space must be intended as the co-domain of a domain Z represented by the genotype. The vector points in this space thus correspond to the single individuals that belong to the species.

Since every living organism by definition eats, grows and reproduces, the configuration of a particular character that best ensures a species in its habitat to perform these functions will be a point X which we will call X_0 , i.e. X_0 is the point of maximum fitness.

If we add another dimension which indicates the allelic frequency f of a certain character set, namely the number of times it appears in a population divided by the number of individuals of that population, then we can build an allelic frequency distribution. Such allelic frequency will follow a Gaussian; that is, if we consider the N -dimensional space of the characters as the domain of f (which is a function in N variables, i.e. $f = f(X_1, X_2, \dots, X_N)$) we expect the top of the distribution (the maximum of f) corresponds to a particular point of the N -dimensional space. In the case of considering only one character, that point is X_0 . This corresponds to say that the 'optimal configuration' tends to be the most frequent.

In the following, we will introduce the hypotheses at the base of the proposed theoretical model.

2.1. First hypothesis: harmonic oscillator

Now let us assume, for one character, that the typical effect of random mutations and natural selection is an oscillation of the actual point X around the peak of allele frequency, so that point generally will not be in X_0 but at a coordinate we will call X_{MAX} . X_{MAX} in turn will swing around X_0 with a harmonic motion given by

$$X(t) = A_0 \cos(\omega_0 t) \quad (1)$$

In (1), $X(t)$ is the coordinate of X_{MAX} at time t , A_0 is the amplitude of the oscillation and ω_0 is the frequency of the oscillation (i.e. the frequency by a constant factor equal to 2π , for which hereinafter we will call the frequency ω). Such ω_0 is given by

$$\omega_0 = \frac{2\pi}{T_0} \quad (2)$$

with T_0 oscillation period of X_{MAX} . In turn

$$T_0 = \frac{m}{\lambda}$$

where m is a positive integer that represents the number of mutations that result in an oscillation of X_{MAX} while λ is the rate of mutations, which is by definition given by

$$\lambda = \frac{1}{n\tau}$$

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