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Review of: "Micro- and Macroevolution: A Continuum or Two Distinct Types of Change?"

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Microevolution and Macroevolution

The theme addressed by the authors in this article is one of the most generous possible. Before making some considerations regarding the ideas in the reviewed article, in the face of the fundamental importance of the problem of describing the phenomenon of the transformation of biological material, I must recall another foundation on which human science generally rests and its weaknesses. The **word** is the tool through which human science communicates for the most part. There are other communication tools, but in current scientific problems with a dense theoretical character, the written word remains fundamental. There are many thoughts related to the word and words. They don't belong here. I just want to emphasize that any attempt to give definitions for the notions used in the reviewed article, and not only that, but in general, is doomed to failure in elementary logical analysis. I don't want to cancel the reasoning from the beginning, I just want to apologize for some criticisms that may appear at any time due to the language used, more precisely small or larger differences that may appear in interpretations due to the vague nature of the definitions of the concepts used. To avoid discussions related to language as much as possible, the definitions of the fundamental notions accepted by the authors must be given in the article or quoted from the source accepted by the authors. In this way, all readers will know (as much as possible) what notions we are talking about, and we will only comment on the definitions within the logic of the development of the subject and not on their content as accepted by the authors.

În contextul de mai sus, recomand autorilor să precizeze definițiile acceptate de aceștia asupra noțiunilor fundamentale de dezvoltare propuse în articol: evoluție, microevoluție, macroevoluție, biologie, biologie evolutivă și vector de stare al unui sistem biologic.

Afișarea unei liste (un tabel) cu aceste noțiuni fundamentale ar fi de mare folos cititorilor, ca reper pentru ca cititorii să poată reveni mai ușor la definiții, ori de câte ori simt nevoia. Un subiect precum cel din acest articol, mai ales pentru cei care nu sunt specialiști în biologie, matematică și informatică, va genera nevoia de multe astfel de retururi.

În esență, autorii prezintă un model matematic pentru fenomenele de evoluție biologică, Microevoluție și Macroevoluție. Exemplul concret al modelului matematic propus este amiba digitală. Ameba digitală este încă un model matematic, aș prefera să spun computer sau computațional (model computerizat) pentru amiba biologică reală? Care sunt limitele modelului (ameba digitală) pe care autorii își explică modelul (nu modelul biologic sau modelul real)?

To better understand what we are talking about, from my point of view, in chapter 2, according to the presented formulas, you should not only define the state vector, but give, for example, the state vector of the biological amoeba and the state vector of the digital amoeba, or at least explain the physicochemical significance of their components (mention characteristic properties of the biological and the digital amoeba, which will also show the similarity of the biological model with the digital one). I am particularly interested in the size of the vector space of the state vector of the amoeba - how many components do the vectors have, what are they called, what values can they take, are they real vector spaces or can they also be vector spaces over other number bodies (complexes, quaternions)? How many of the amoeba's characteristics are quantifiable? How many are quantified, and how many are not? Otherwise, everything just seems like a computer game. Computer simulation has become very common in all fields of science. However, computer simulation is useless and full of surprises if it is not complemented by experimental validation. In the sense of increasing the level of understanding and the value of the article, please insert a few lines about experimental validations (if they exist and are known) of the digital model of the amoeba, possibly indicating only the literature that contains such examples.

In chapter 3, the statement is made - The characteristic properties/dimensions of an organism (a biological system) are usually determined by assessing its size and traits. The subjectivity of this approach can be avoided by deriving the characteristic properties/dimensions directly from the nucleotide code of the organism. The well-studied protein-coding genes clearly represent characteristic properties/dimensions of an organism. You can give examples (even if hypothetical) of how the characteristics/dimensions are derived from the nucleotide code of the organism.

First-order evolution and second-order evolution from Table 1 can be mathematically modelled by the transformation operators between vector spaces of the same size, respectively with different dimensions?

We can write the evolutions from the "illustration" row in the form:

$$\begin{pmatrix} a_2 \\ b_2 \end{pmatrix} = T_{22} \begin{pmatrix} a_1 \\ b_1 \end{pmatrix} \quad (1)$$

respectively

$$\begin{pmatrix} a_2 \\ b_2 \\ c_2 \end{pmatrix} = T_{23} \begin{pmatrix} a_1 \\ b_1 \end{pmatrix} \quad (2)$$

where T_{22} and T_{23} are linear, affine, or non-linear transformations or applications. My question is if this is the model the authors had in mind?

Therefore, T_{22} -type transformations would mathematically model the biochemical driving mechanisms, and T_{23}-type transformations mathematically model – the expansion of the nucleotide code, the production of new genes and regulatory elements, and the antagonized by mutation repair?

If the answer to the previous questions is affirmative, can the authors give examples of such transformations found in experimental biological research? If they know such models, it would be good to at least give an example in the article or send it to the source.

In Chapter 4, it would be good for the authors to explain the correspondence between the elements of the digital amoeba component and the biological amoeba, possibly in the form of a table, on parallel columns, as in Table 1. In the first column, enter the components of the digital amoeba in each row, and in the second column, the corresponding elements of the biological amoeba. This recommendation is only valid if the digital amoeba is a (mathematical or computer) model of the biological amoeba. For example, the pair of input numbers in the program, the calculation program itself, the result obtained, and what elements of the life of a biological amoeba represent. This interpretation could facilitate biologists in better understanding the digital model and its limits. For example, in the digital amoeba, does the program of 32 instructions represent the transformations T_{22} and T_{23}, defined in (1) and (2)?

The modeller (mathematician, computer scientist, engineer) must explain the correspondences between the model and the modelled entity (in this case, the biological amoeba). Biologists or readers should not be left to guess the correspondence between the elements of the model and the modelled reality.

The idea of modelling micro and macroevolution through transformations between vector spaces of equal dimensions, and respectively of different dimensions, deserves to be published. For the idea to bear fruit, a minimum validation is necessary in the biological physical space, not only in the virtual space (digital amoeba). The limits of the models with the real, biological model must also be shown.

I wish success to the authors and remain available for dialogue because the subject is extraordinarily vast, and this observation makes me think of the statement of Saint Paul, Corinthians I, 13.12, "For now we see through a glass, darkly; but then face to face: now I know in part; but then shall I know even as also I am known." (King James Version (KJV 1900). Perhaps this article is also a beginning...

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