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

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I find the paper very interesting. The authors support the idea that macroevolution and microevolution are fundamentally different. They propose to use the genotype of an organism instead of its phenotype in the mathematical formalism of evolutionary biology. At each time step, a state vector is associated with the organism. The dimension of the state vector is determined by the protein-coding genes and regulatory elements in the nucleotide code. Hence, they distinguish between first-order change, where only the parameters that define the state vector change, and second-order change, where new dimensions are added. In particular, one may associate many state spaces with a population.

The authors explain the mechanisms that drive first-order evolution and those that add new dimensions. They illustrate their ideas by simulation, using a population of digital amoebas.

They discuss different methods of simulation of evolution and compare them with their approach. Below are some questions and suggestions.

1) I understood from the illustration that the number of state spaces that one can associate to a population depends on time. Is there any limitation on this number?

2) What is known about the mathematical transformations between different state spaces? How should they be? For instance, how to model mathematically "the alternative food" used for the survival of the digital amoeba population?

3) I think that the authors should distinguish between the mathematical model that describes second-order evolution and the mathematical tools used to simulate it. For instance, here the authors use a C++ program, Excel, standard Excel operators, ... and, as they explained in this paper and in reference [25], they could not simulate this type of evolution by changing bits of the digital code of the amoeba. The mathematical tools may add new limitations that are not due to the mechanisms that drive macroevolution.