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To cite this version:

HAL Id: hal-01938802
https://hal.archives-ouvertes.fr/hal-01938802
Submitted on 28 Nov 2018

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The complexity ratchet: Stronger than selection!

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Abstract

Using the Aevol digital genetics platform we designed an in silico experiment to study the relationship between molecular complexity and phenotypic complexity: We evolved populations of digital organisms in an environment designed to allow survival of the simplest possible organism: one which genome encodes a single gene. By repeatedly evolving populations in this experimental framework, we observed that >1/3 of the lineages quickly found this simple genotype and were then stable for the rest of the experiment. At the same time, most lineages were not able to find this simple genotype and were then stable for the rest of the experiment.

Methods

Aevol (www.aevol.fr) is an In Silico Experimental Evolution (ISEE – aka digital genetics) platform developed by the Beagle team to study the evolution of genome structure. Aevol is based on three principles that make it perfectly suited to study the evolution of complexity:

A. Its genotype-to-phenotype map. Evolution is simulated by a generational algorithm. Organisms’ fitness is based on a curve-fitting task: the protein triangles are summed to compute the organisms’ phenotype that is compared with a target function (red curve below).

B. Complex organisms accumulate more information at the genomic and functional levels

Genomic complexity is strongly bounded by mutation rates (A) due to robustness constraints on the genome (Knibbe et al., 2007; Fischer et al., 2014). Mutation rates also constrain the functional complexity (B) but this effect is less stringent at the functional level.

C. Experimental design and complexity measures

Complexity measures:

• Qualitative measure: “simple” organisms are those encoding only proteins with the same m and w values.
• Genomic complexity: quantity of information encoded on the genome (total amount of coding sequences).
• Functional complexity: quantity of information encoded on the proteome (number of different parameters).

Results

(1) Organisms evolved complex functional structures in 66% of the simulations

Whatever the mutation rate, >1/3 of the simulations led to “simple” organisms with few genes and a low functional complexity (A). >2/3 of the simulations led to “complex” organisms despite the simplicity of the target function (B).

(2) Complex organisms accumulate more information at the genomic and functional levels

Genomic complexity is strongly bounded by mutation rates (A) due to robustness constraints on the genome (Knibbe et al., 2007; Fischer et al., 2014). Mutation rates also constrain the functional complexity (B) but this effect is less stringent at the functional level.

(3) Simple organisms are fitter than complex ones

Whatever the complexity measure, we observe a clear trend for simple organisms to be fitter than complex ones after 250,000 generations. This demonstrates that in our simulations complexity is not driven by selection. On the opposite, complex functional structures have evolved in spite of selection.

(4) Despite the advantage of being simple, complex organisms evolve greater complexity on the long term

The simple/complex identities are determined early on in the simulation and generally conserved thereafter (A). Complex organisms evolve greater complexity (B); their fitness grows but remains far below simple organisms.

Discussion

The emergence of complex organisms in a simple environment is a strong argument in favor of a complexity ratchet, i.e. an irreversible mechanism that adds components to a system but that cannot get rid of existing ones, even though this could be more favorable. Indeed, in our experiments this ratchet clicks and goes on clicking despite the selective advantage of being simple. Evolution of fitness in complex organisms shows that the ratchet is empowered by negative epistasis. Our results show that complex biological structures can flourish in conditions where complexity is not needed and that, reciprocally, the global function of complex structures could very well be simple.

References