The complexity ratchet: stronger than selection
Vincent Liard, Jonathan Rouzaud-Cornabas, David Parsons, Guillaume Beslon

To cite this version:

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

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L’archive ouverte pluridisciplinaire HAL, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d’enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.
The complexity ratchet: Stronger than selection!

Vincent Liard, Jonathan Rouzaud-Cornabas, David P. Parsons, Guillaume Beslon
INRIA-Beagle team (INSA-Lyon), Lyon, France

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 solution and showed a strong negative selection along the 250,000 generations of the experiment. Importantly, simple organisms ended up with a very high fitness while complex genotypes ended up with a ≤10x lower fitness. This shows that, even in a simple environment, organisms engaged in this simplification process were never able to outcompete the simple ones, showing that selection is not able to invert the complexity ratchet.

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 makes it perfectly suited to study the evolution of complexity:

A. its genotype-phenotype map B. 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).

C. At each replication the genome may undergo mutations. Aevol implements a wide range of mutational operators including switches, InDels and chromosomal rearrangements. Mutations can change complexity at both genomic and functional levels.

Methods

Results

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.

Experimental design and 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).

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).

(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.

References