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. Moreover, organisms engaged in this competition for fitness even in a simple environment. This shows that, even in a simple environment, generations of the experiment. Importantly, simple organisms ended up with a very high fitness while complex genotypes came up with a ≈10x lower fitness. This demonstrates that, even in a simple environment, evolution leads to a complex genotype and was then stable for the rest of the experiment. The complex structures can flourish at both genomic and functional levels.

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 makes it perfectly suited to study the evolution of complexity:
A. Its genotype-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. Experimental design and complexity measures
The complex organisms evolve greater complexity (B); their fitness grows but remains far below simple organisms.

Results

A. Distribution of genomic complexity for complex (top) and simple (bottom) organisms. The higher the mutation rate, the lower the genomic complexity. Simple organisms approach the optimum fitness, f\textsubscript{opt} = 1.
B. Distribution of functional complexity for complex (top) and simple (bottom) organisms. The higher the mutation rate, the lower the functional complexity.

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).

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