In silico experimental evolution shows that complexity can rise even in simple environments
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Introduction
Systems biology, often viewed as reverse engineering of biological systems, deals however with objects that have not been designed. Neither do they have a predefined function nor do they follow engineering rules. Indeed, we don’t know what are the “design” rules that evolution imposes to biological systems while this knowledge would be a valuable interpretative framework for systems biology. One of the recurrent questions on that matter is the origin of the striking molecular complexity of biological systems. Answering this question requires deciphering the complex interactions between all the forces that drive evolution, including selective and non-selective ones. In this context, simulation is a valuable tool as it enables to observe how organisms grow in complexity (or do not) when they evolve in environments which complexity is perfectly controlled.

Methods
Aevol (www.aevol.fr) is an In Silico Experimental Evolution (ISEE aka digital genomics) 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-to-phenotype map mimics biology with a realistic genomic structure and a functional structure based on a graphical formalism. Proteins are represented by triangles which parameters are computed from the gene sequence. The evolution is simulated through 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. Evolution is simulated by a generational algorithm. The higher the mutation rate, the lower the functional complexity. The higher the mutation rate, the lower the fitness.

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.

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

Discussion
Our results show that, in such a simple constant environment, there is a decoupling between the molecular complexity of the organisms and the complexity of the environment. This shows that selection for complexity is not mandatory for complexity to evolve and that complex biological structures could flourish in conditions where complexity is not needed. Reciprocally, the global function of complex biological structures could very well be simple. We think this result is greatly significant for both evolutionary biology and systems biology.

References