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

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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-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. Long-term evolution of functional complexity in a complex organism. Functional complexity and fitness continuously grow during the 250,000 generations but the fitness remains far below that of simple organisms.

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:

• To unravel the origin of molecular complexity, we evolved populations in the simplest possible environment: the Aevol target is a triangle. By repeatedly evolving populations of organisms in an environment designed to allow survival of the most robust organisms, we were able to outcompete the simple ones, showing that complexity for complex organisms:

- The higher the genome complexity, the lower the fitness. Simple organisms approach the optimum if the mutation rate, the lower the functionality.

1. Simple organisms are those encoding only proteins with the same m and w values.

2. Functional complexity: quantity of information encoded on the proteome (number of different parameters).

3. 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.

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

