

Darwin Theory Visited by Long-Term Experiments using Bacteria and Digital Organisms

"Dynamics of Phenotypic and Genomic Change in a Long-Term Evolution Experiment with *Escherichia coli*"

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Professor of Microbial Ecology at *Michigan State University*,
Hannah Distinguish Pr

"*In Silico* Experimental Evolution, a Modelling Insight into the Complexity of Biological Systems"

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Lundi 18 Novembre 2019 à 14h

Amphi Sup Sud - Bât Jean Roget
Faculté de Médecine, La Tronche

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Richard E. Lenski

Professor of Microbial Ecology at Michigan State University,
Hannah Distinguished Professor,
Member of the US Academy of Sciences.

"Dynamics of Phenotypic and Genomic Change in a Long-Term Evolution Experiment with *Escherichia coli*"

Abstract: Evolution is an on-going process, one that can be studied experimentally in organisms with rapid generations. We have watched 12 populations of *Escherichia coli* evolve in a simple environment for over 30 years and 70,000 generations. The aims of this experiment are to characterize the tempo and mode of evolution, and to examine the repeatability of the phenotypic and genomic changes. With students and collaborators, we have quantified the dynamics of adaptation by natural selection, documented many cases of parallel evolution, observed changes in the underlying mutation rate, and seen the appearance of a new metabolic function that transcends the usual definition of *E. coli* as a species. We have sequenced hundreds of complete genomes to find the mutations in time-series of samples from the populations. These genomic data provide insights into the dynamic coupling of phenotypic and genotypic evolution during periods of optimization and innovation.

About the author:

Professor at Michigan State University, Richard E. Lenski is the founder of the longest experience of ongoing developments in the world, the LTEE 'Long-Term Evolution Experiment' using *Escherichia coli* bacteria. The main focus of Lenski's is to study experimental evolution in the context of experiments that are replicated and performed under controlled conditions. In order to study evolution as it happens requires organisms that replicate, mutate, and evolve very fast, so that any changes can be detected on a reasonable time scale. Two different fast-evolving systems are being explored by Lenski: the first deals with the *Escherichia coli* bacteria, and the other uses digital organisms in the Avida system which are computer programs that self-replicate, mutate, compete, adapt and evolve in the computational world in which they live. In both systems, the dynamics of evolution, including genomic as well as phenotypic changes, are investigating.





Guillaume Beslon

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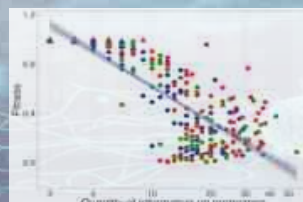
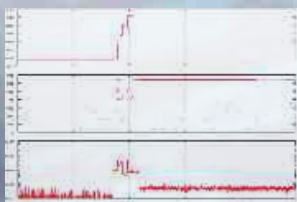
"*In Silico* Experimental Evolution, a Modelling Insight into the Complexity of Biological Systems"

Abstract: The evolutionary origin of the complexity of biological systems is an issue that has been intriguing the scientific community for decades. Two main hypotheses have been proposed to explain the apparent trend toward complexity increase. According to the first one, the complexity of biological systems is due to selective factors (the more complex organisms having a higher fitness). According to the second one, the mutational process is the sole responsible (complexity being mechanically due to the accumulation of mutations). The debate is difficult to resolve because it is essentially based on thought experiments and no simple assay makes it possible to address this issue. In such a context, the modeling appears as a middle way: more rigorous than a thought experiment, it makes it possible to carry out "impossible experiments" by testing parameters settings (or situations) that would be intractable in practice.

In the context of Darwinian evolution, we have developed the Aevol model with the objective of performing virtual experiments to isolate the evolutionary mechanisms impacting the molecular structure of biological systems. Using Aevol, we are able to evolve virtual organisms into different environments, some favouring simple organisms, some favouring complex organisms. Our results show that complexity increases in both situations but also that this increase is not due to the sole mutational process. These results open the way to a third explanation: the existence of a "complexity ratchet" rooted in the historical nature of the evolutionary process.

About the author:

Guillaume Beslon is a recognized specialist in numerical evolution modeling. His activity deals with computational biology, artificial life and *in silico* experimental evolution. Beslon has developed the *aevol* model, which is a digital genetics platform specifically designed to study the evolutionary dynamics of microorganisms. *Aevol* uses a fine grained model which enable to study the molecular evolution. The ongoing projects focus on the evolution of complexity at the genomic, proteomic and phenotypic levels, the evolution of genome size, the prediction of evolution, the evolution of genetic regulation networks, and benchmarking of bioinformatics tool like phylogenetic software.



Translational Innovation in Medicine and Complexity

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of Escherichia coli evolve in a simple environment
for over 30 years and 70,000 generations !"*

