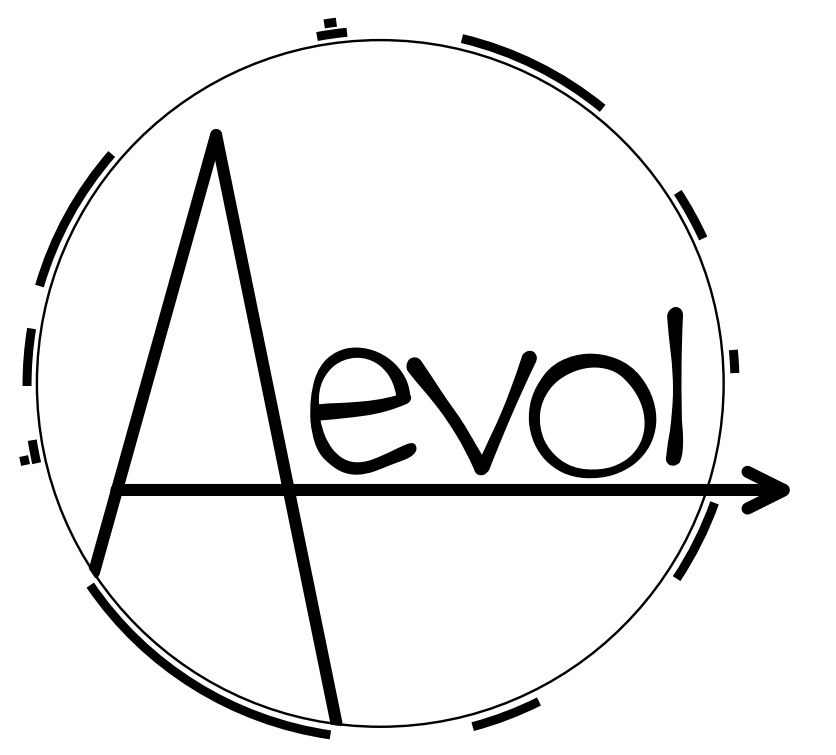




<http://frama.link/aevj16>

# Unexpected genome inflation and streamlining in variable environment



B erence Batut<sup>1</sup>, Guillaume Beslon<sup>2</sup>, Carole Knibbe<sup>2</sup>

<sup>1</sup>EA 4678 CIDAM, Universit  d'Auvergne, Clermont-Ferrand, France - <sup>2</sup>BEAGLE, Inria, LIRIS, CNRS, INSA Lyon, UCB Lyon, Universit  de Lyon, Lyon, France

Natural ecosystems undergo different levels of environmental perturbations from seasonal fluctuations to less frequent natural disasters and global changes. These different levels impact differently ecosystems, organisms and adaptive ability. Here we focus on stochastic environmental fluctuations and their effects on genome structure and genome evolution.

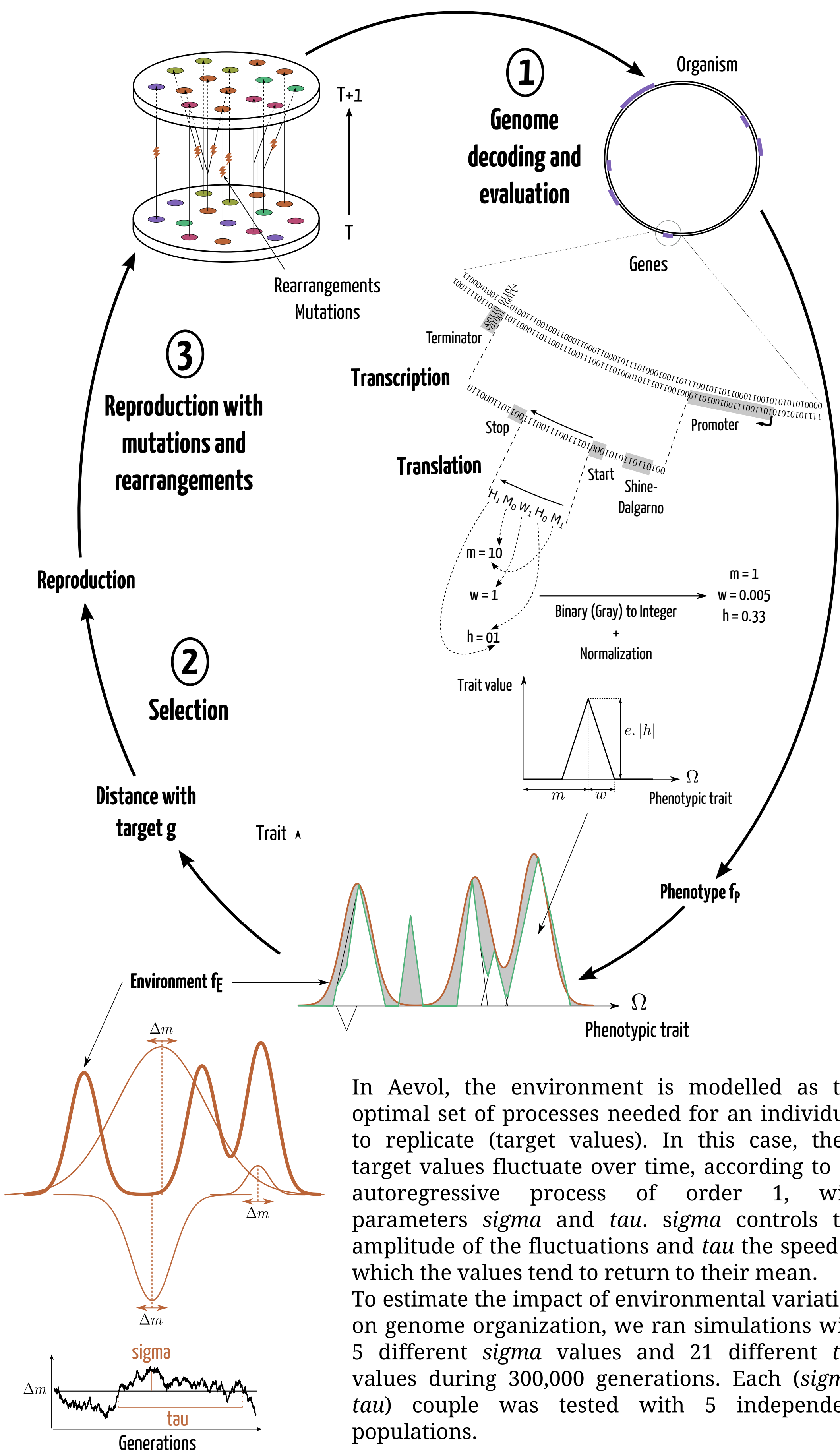
We used Aevol, an individual-based evolutionary model [1,2] to investigate the impact of environmental variation speed and amplitude on genome organization and evolvability.

Our simulations show that evolved genome size and gene density strongly depend on the speed and amplitude of environmental fluctuations.

This behavior can be explained by indirect selection for evolvability when the speed is low to moderate, and by indirect selection for robustness when the speed is so high that the selection becomes stabilizing rather than directional.

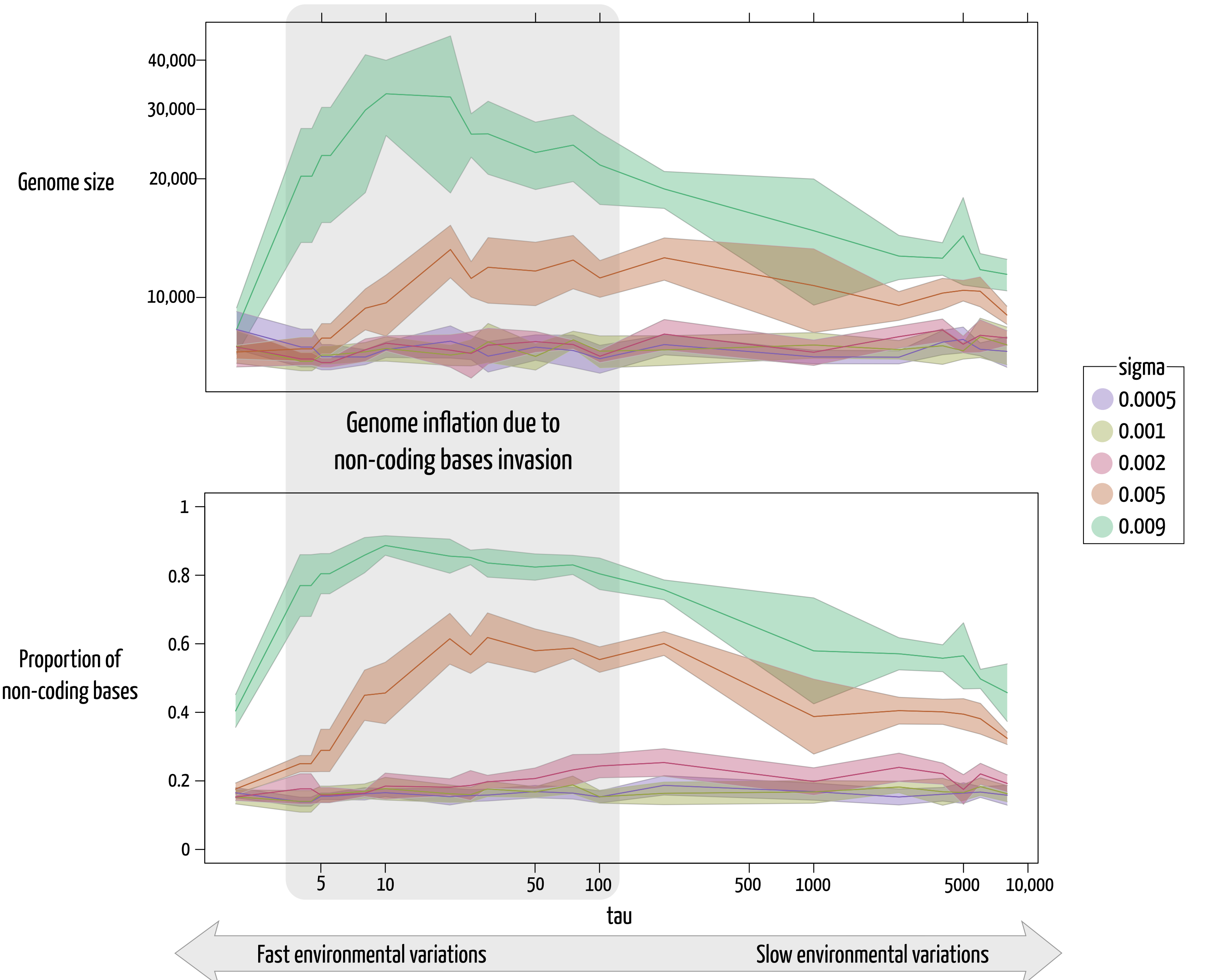
## Material and methods

Aevol [1,2] model simulates the evolution of a population of  $N$  artificial organisms using a variation-reproduction cycle. The population size is constant and the population is completely renewed at each time step.

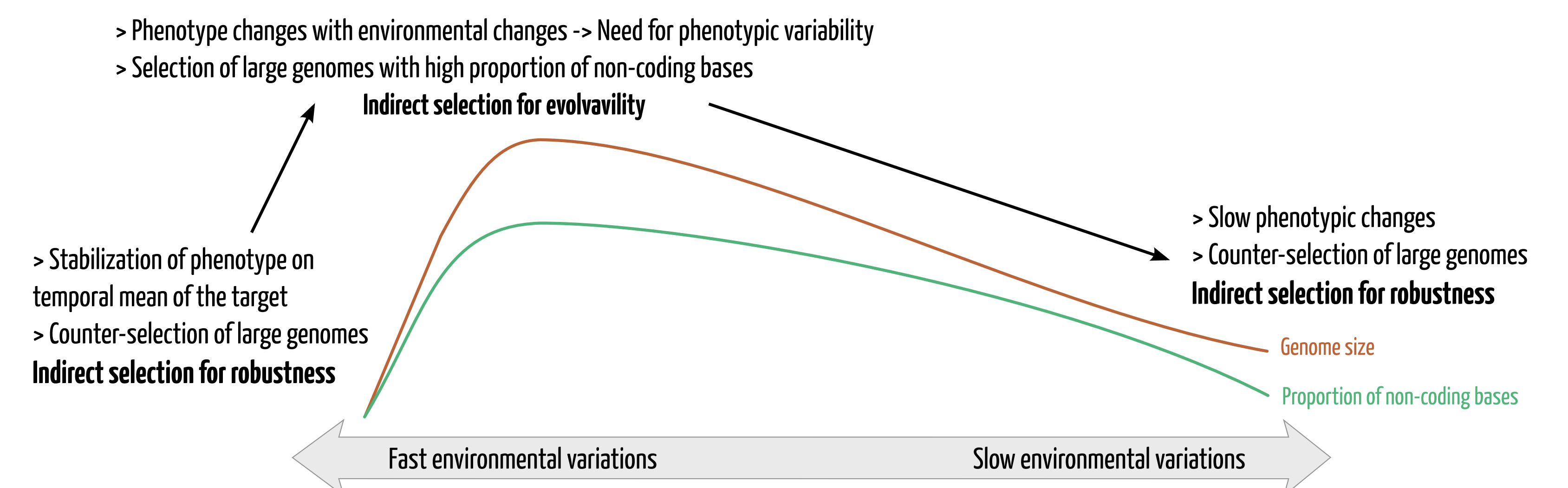


## Results

For all  $\sigma$  values, variation speed (inverse of  $\tau$ ) has a non-linear impact on genome structure:



Intermediate speeds of environmental fluctuations yield genomes with the lowest gene densities. Non-coding DNA could play a role in adaptation to environmental fluctuations when these fluctuations occur at intermediate speeds. This relation between speed of environmental variation and genome size may be driven by evolvability and indirect selection of mutational variability level.



## Conclusion

This work shows the non-intuitive but strong influence of environmental variability on genome architecture.

As mild speed varying environments require more phenotypic variability, they promote the indirect selection of variability and the genome inflation through the accumulation of non-coding sequences. Without effect on the phenotype, these non-coding sequences are indirectly selected. However, they increase global genetic variability and thus help organisms to face environmental variations.

On the other hand, in too quickly or too slowly varying environments, genetic variability is more deleterious than beneficial. Non-coding sequences are then washed-out from the genome and genome streamlining is observed.

## References

- [1] Batut, B. *et al* (2013) *In silico* experimental evolution: a tool to test evolutionary scenarios. *BMC Bioinfo*, 14, S11
- [2] Knibbe, C. *et al* (2007) A long-term evolutionary pressure on the amount of noncoding DNA, *Mol Biol Evol*, 24, 2344-2353

## Acknowledgments

We would like to thank Vincent Daubin and Gabriel Marais for the discussions. This research has been partly funded by the European Commission through the FP7 EU-FET grant EvoEvo (ICT-610427).



## Contacts

B erence Batut: [berence.batut@gmail.com](mailto:berence.batut@gmail.com)  
Carole Knibbe: [carole.knibbe@univ-lyon1.fr](mailto:carole.knibbe@univ-lyon1.fr)