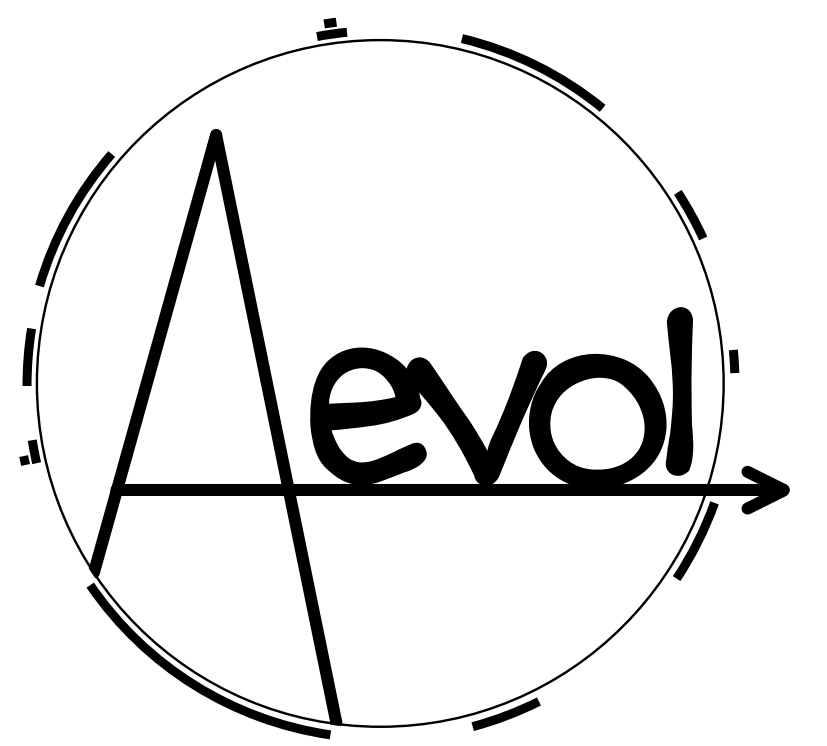




<http://frama.link/aevj16>

Unexpected genome inflation and streamlining in variable environment



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

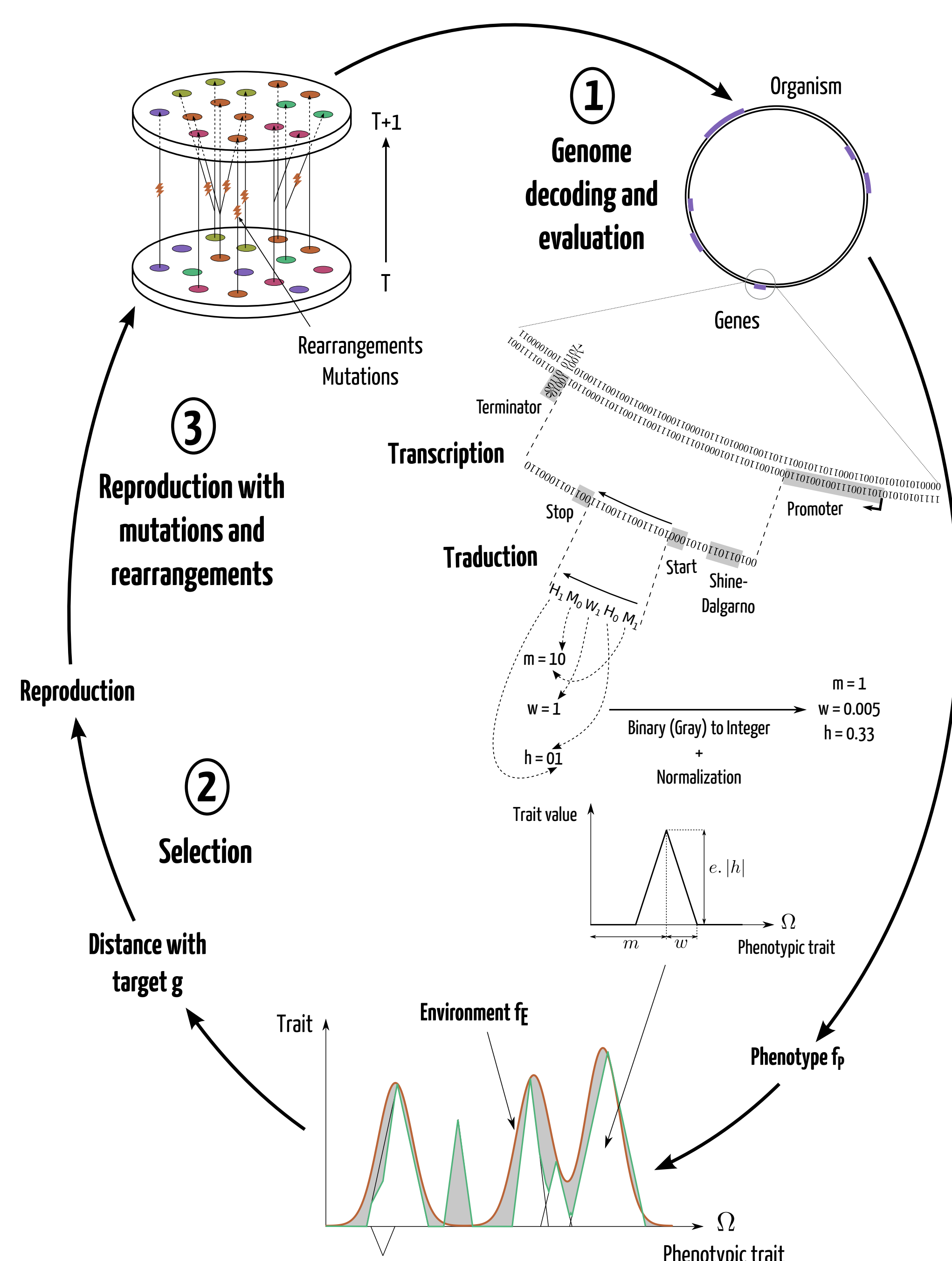
We used Aevol, an individual-based evolutionary model [1,2] to investigate the impact of environmental variation speed and amplitude on genome organization and evolvability.

Our simulations show that evolved genome size and gene density strongly depend on the speed 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 has a constant size over time and is completely renewed at each time step

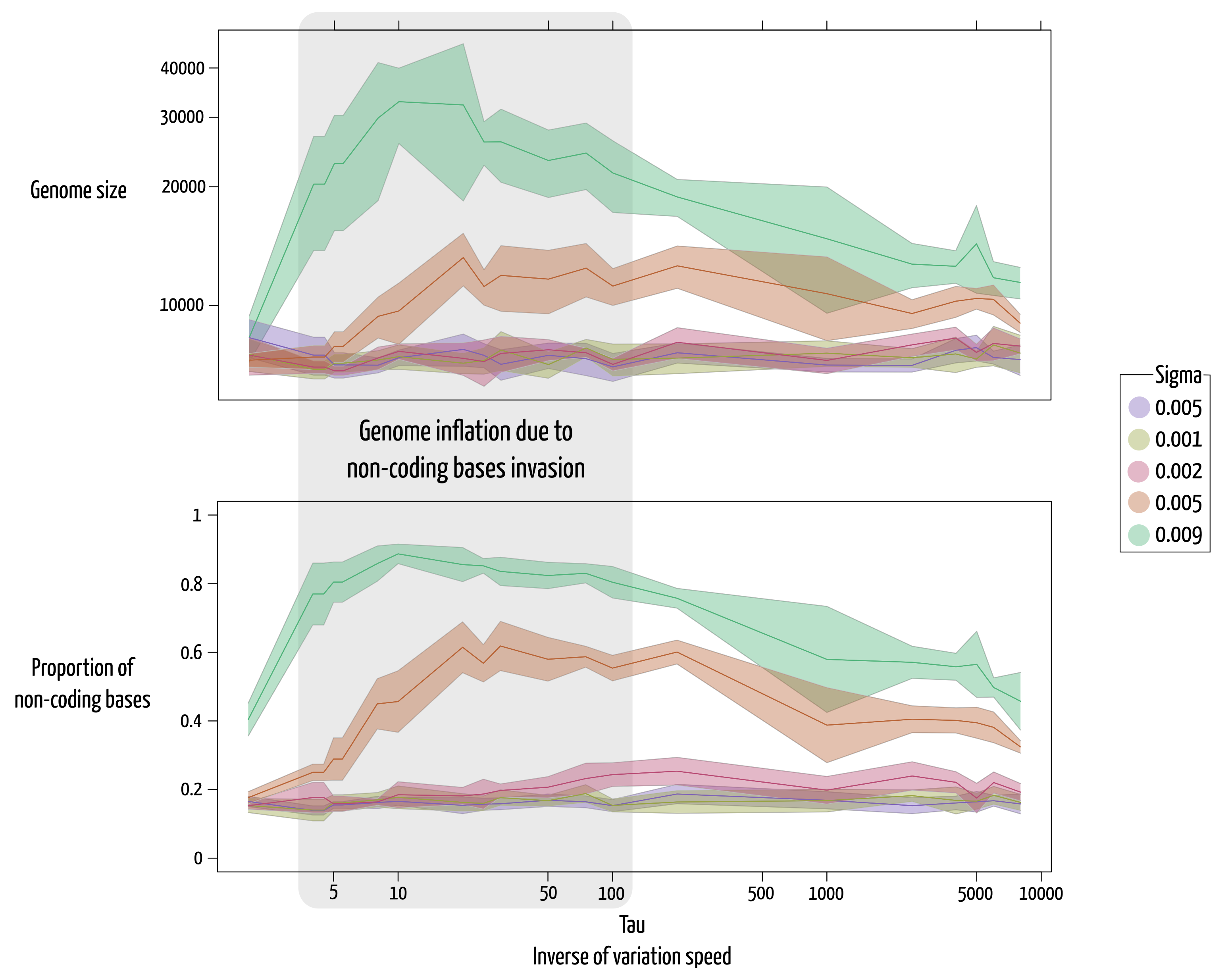


In this model, the environment is modelled as the set of processes needed for an individual to survive. These target values fluctuate over time, according to an autoregressive process of order 1, with parameters σ and τ . σ controls the amplitude of the fluctuations and τ the speed at which the values tends to return to their mean.

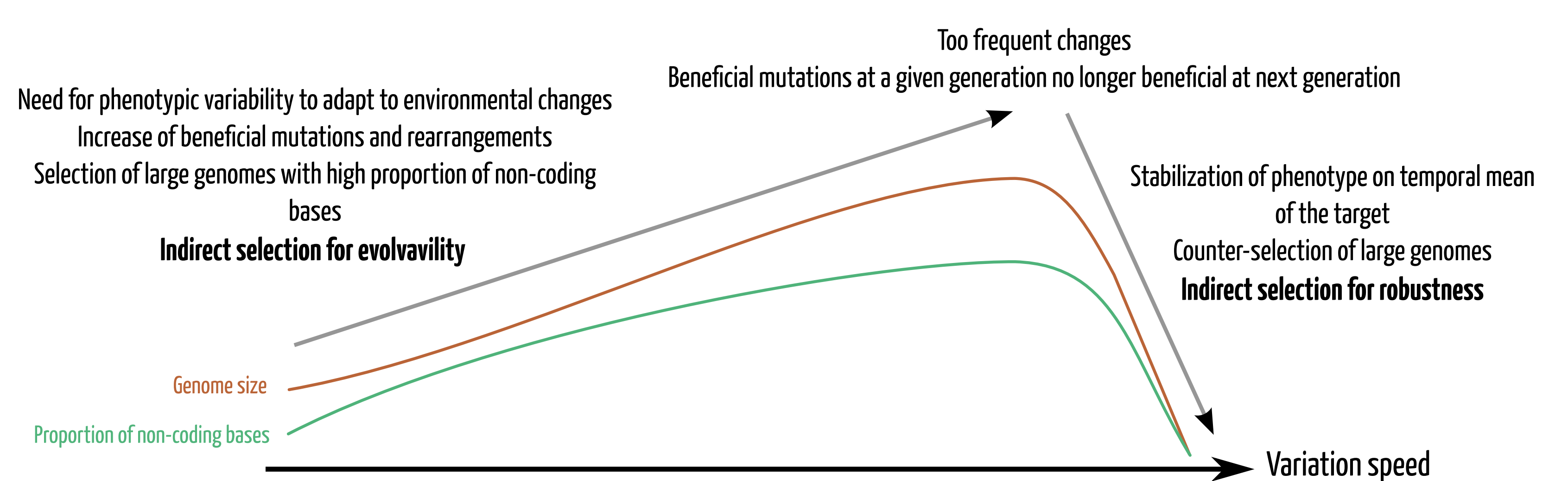
To estimate the impact of environmental variation on genome organization, simulations were run the 5 different σ values and 21 different τ values during 300,00 generations. Each (σ, τ) couple was tested with 5 independent populations.

Results

For all σ values, variation speed (inverse of τ) has a non-linear impact on genome structure:



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



Conclusion

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

As environments varying at mild speeds require more phenotypic variability, they promote indirect selection of variability and the genome inflation through the accumulation of non-coding sequences. Indeed, 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 and 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

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