

# Influence of the Rearrangement Rates on the Organization of Genome Transcription

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INSTITUT NATIONAL  
DE RECHERCHE  
EN INFORMATIQUE  
ET EN AUTOMATIQUE

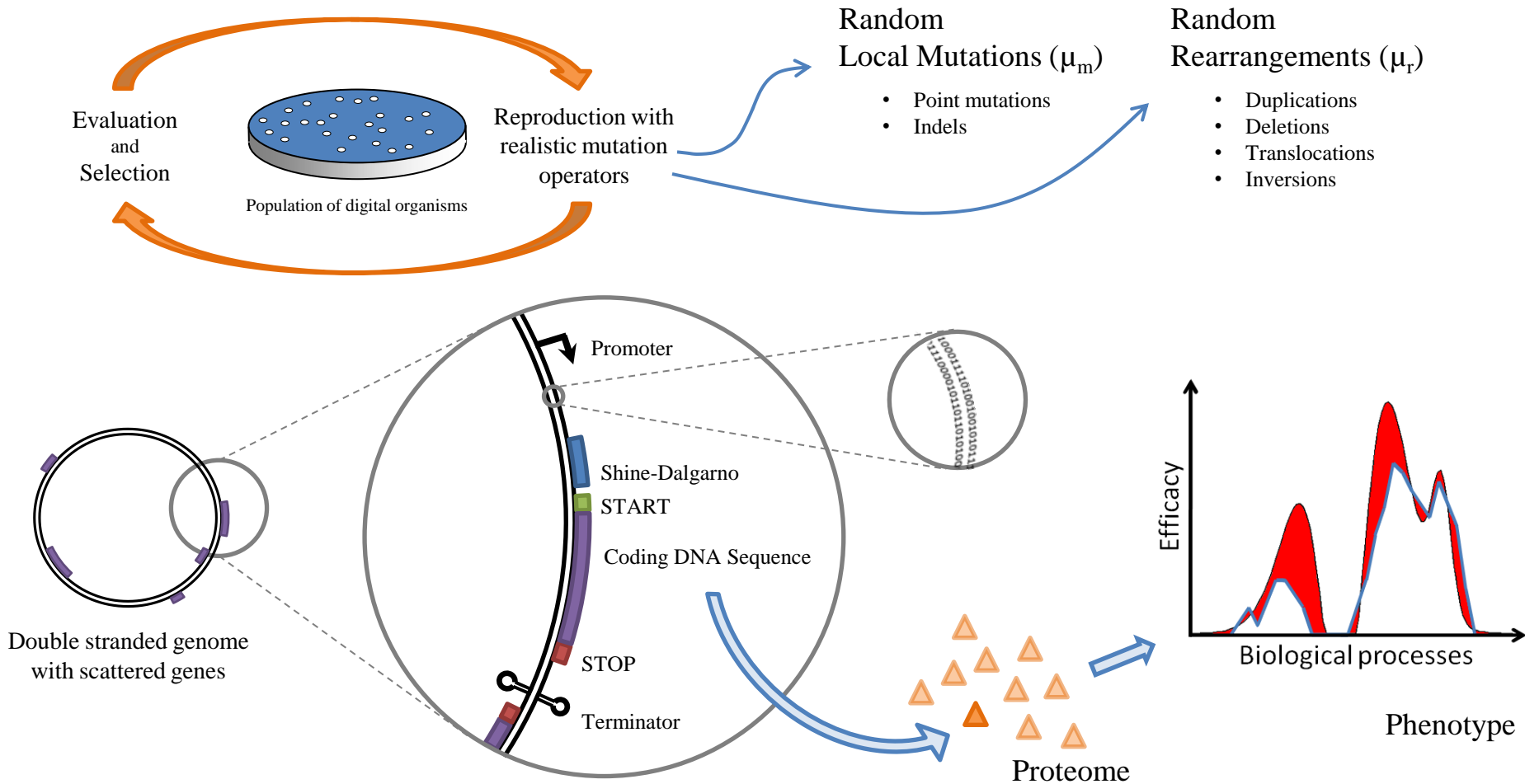


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**GRENOBLE - RHÔNE-ALPES**

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COMBINING

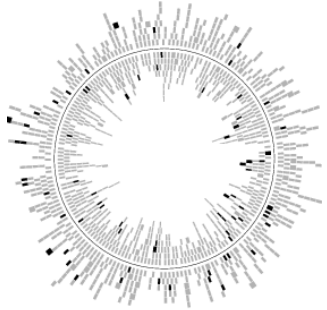
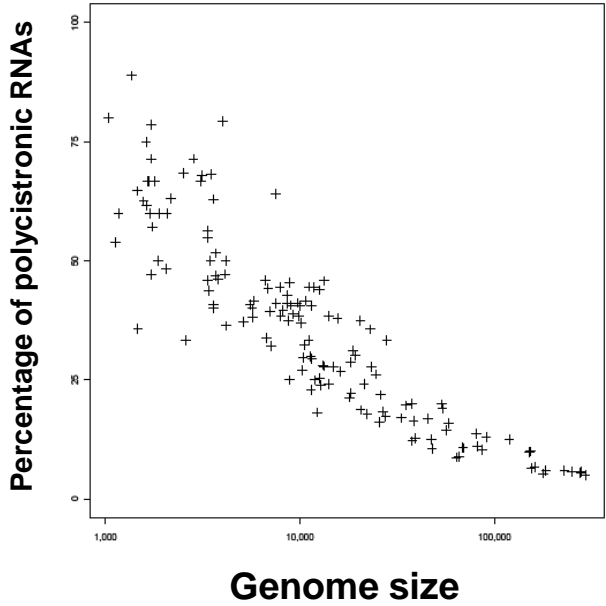
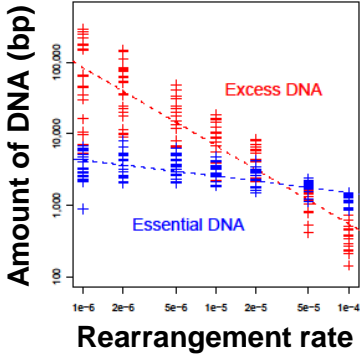


# Aevol: Simulating the Evolution of Digital Organisms



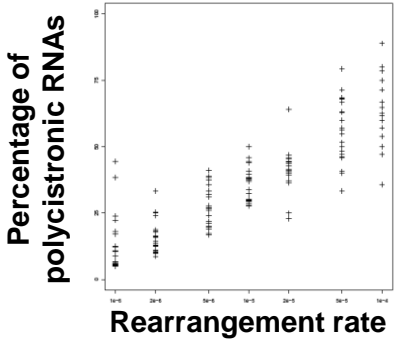
# Experimental Setup and Results

- 147 populations of 1,000 individuals each
- 20,000 generations
- Identical steady environments
- A combination of 7 values of mutation and rearrangement rates ranging from  $1 \cdot 10^{-6}$  to  $1 \cdot 10^{-4}$



Genome size : 249,557 bp  
 Excess DNA : 98%  
 Genes : 73  
 RNAs : 1236  
 Coding RNAs : 71  
 Operons : 2  
 RNA size (av) : 87 bp

**Low rate of spontaneous rearrangements**



Genome size : 1,131 bp  
 Excess DNA : 19%  
 Genes : 15  
 RNAs : 13  
 Coding RNAs : 7  
 Operons : 6  
 RNA size (av) : 202 bp

**High rate of spontaneous rearrangements**

# Conclusion

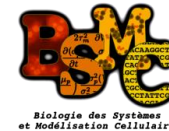
**Aevol allows to reproduce  
a great range of the genetic diversity of real organisms**

**In our experiments :**

- **Low rearrangement rate → Large genomes with many ncRNAs**
- **High rearrangement rate → Genome compaction → RNA lengthening**
- **Operons can arise without regulation nor horizontal transfer.**



Poster  
n°18



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