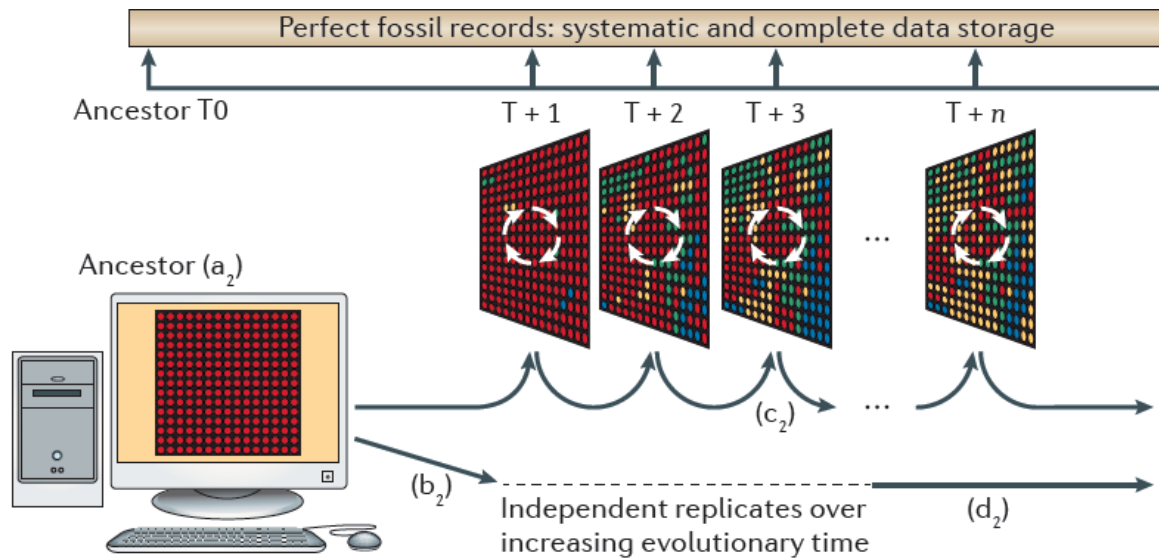


In silico experimental evolution: a tool to test evolutionary scenarios



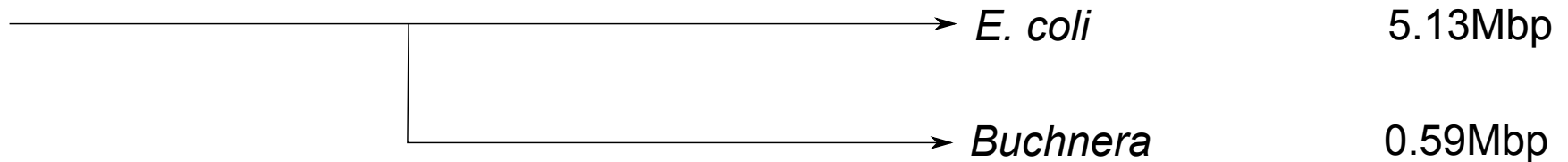
Adaptation from [Hindr  et al 2012]

B r nice Batut, D. P. Parsons, S. Fischer, G. Beslon, C. Knibbe

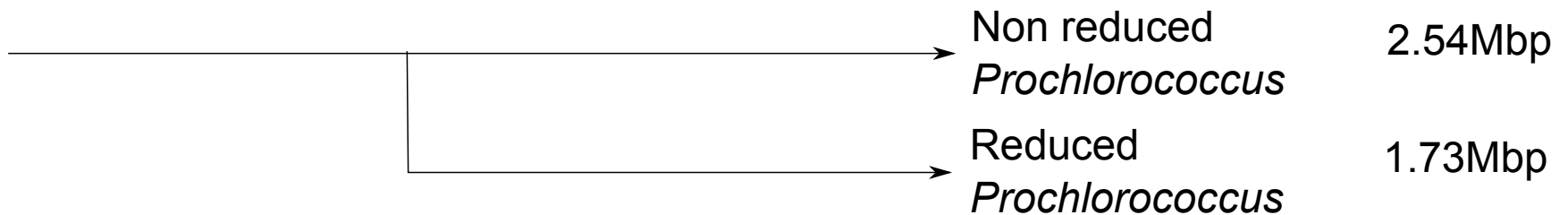
Elaboration of hypothetical evolutionary scenarios with comparative genomics

Genome size

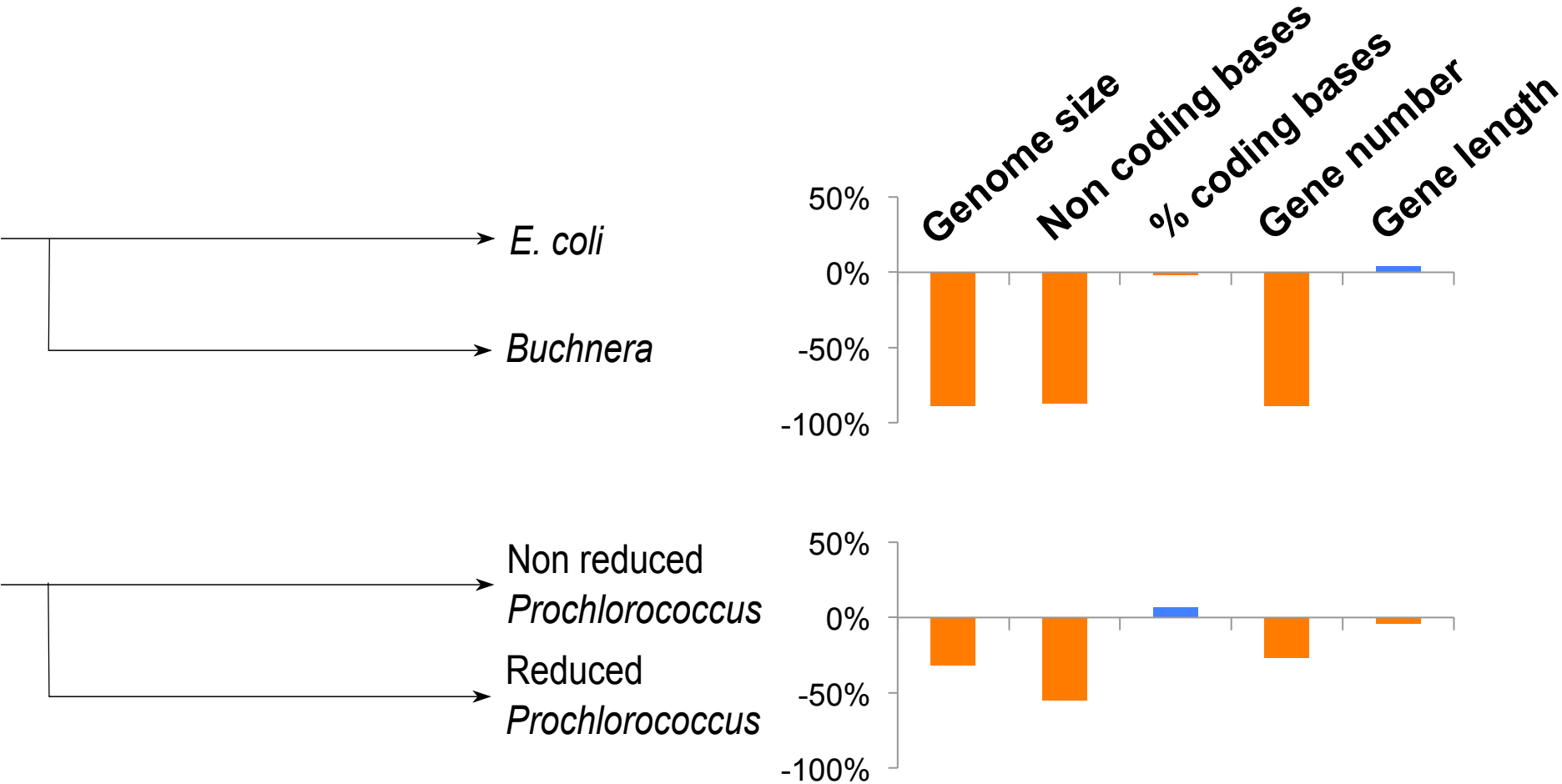
Free-living vs Endosymbionts



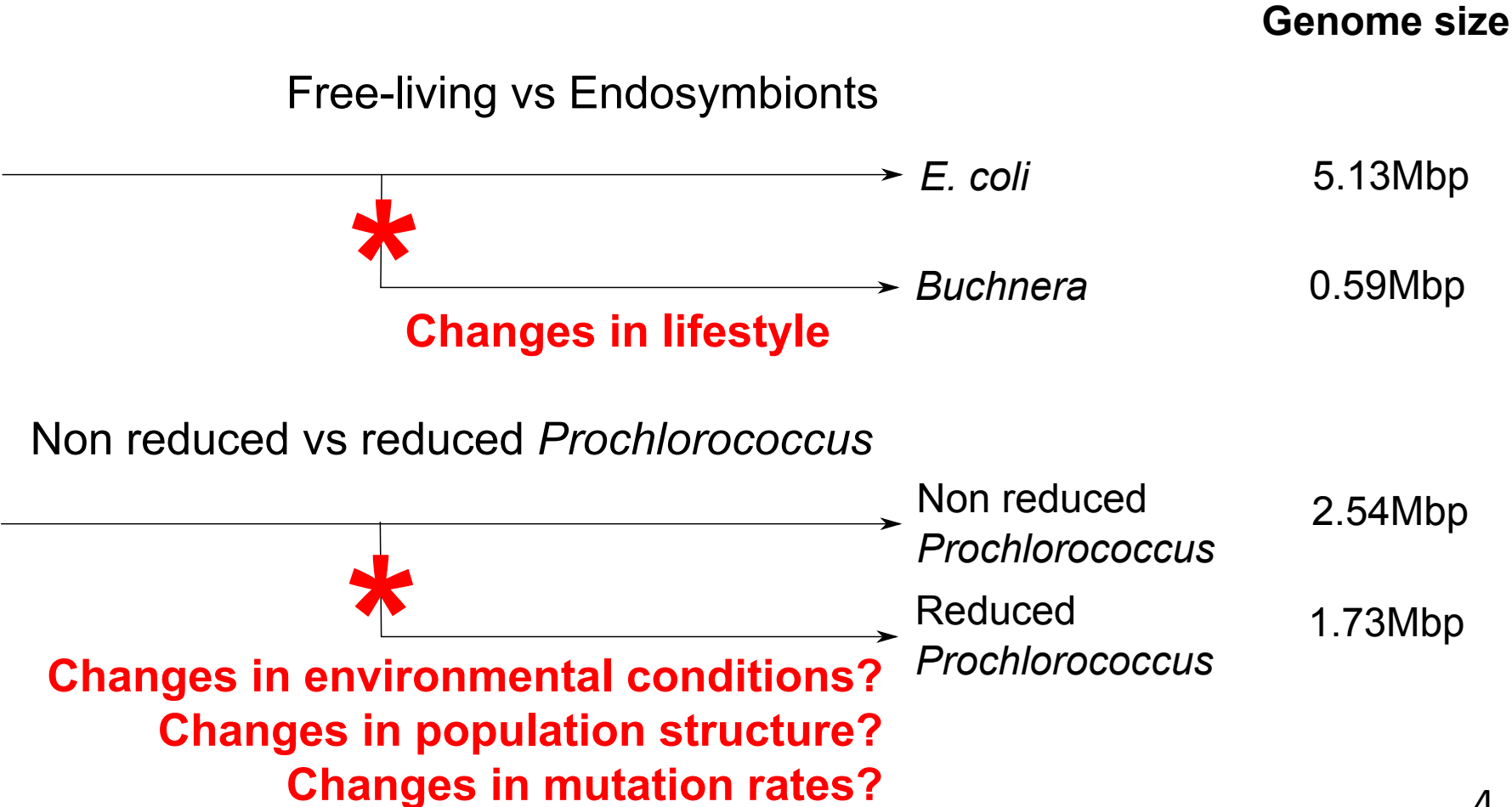
Non reduced vs reduced *Prochlorococcus*



Elaboration of hypothetical evolutionary scenarios with comparative genomics

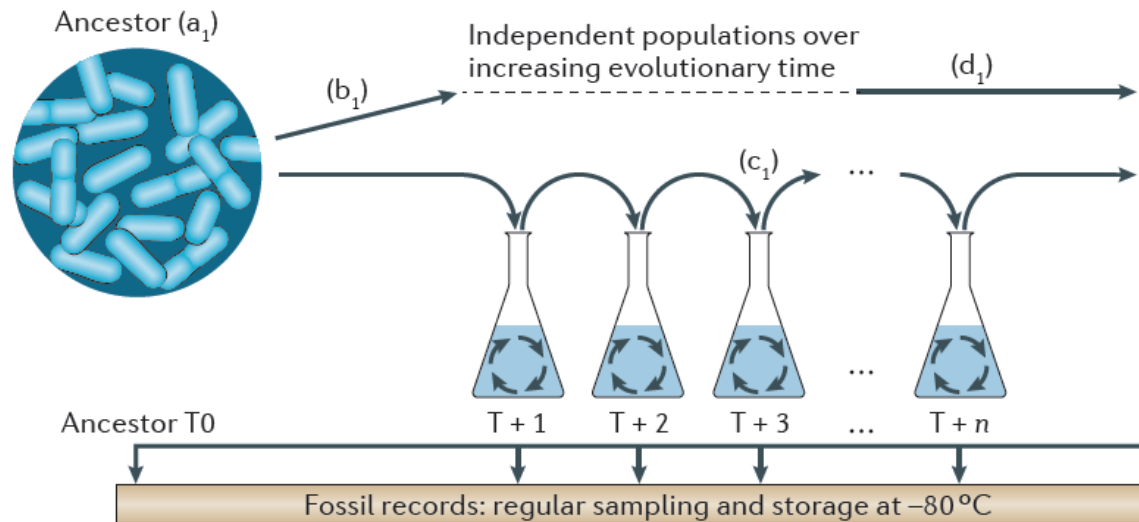


Elaboration of hypothetical evolutionary scenarios with comparative genomics



Experimental evolution to test evolutionary scenarios coming from comparative genomics

In vitro



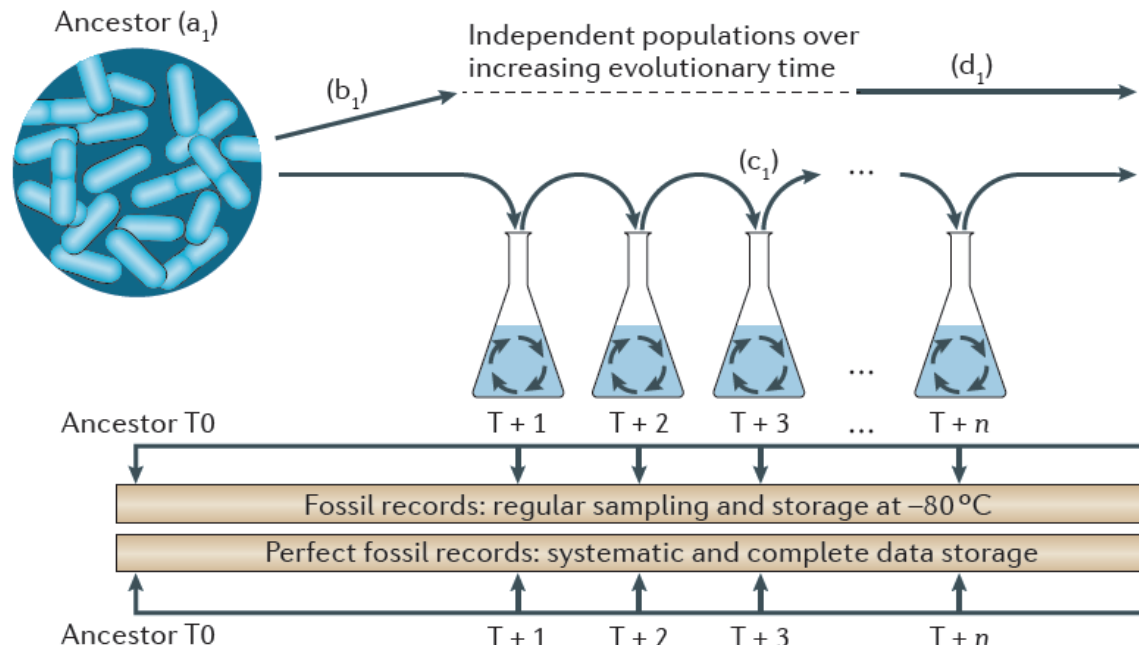
Adaptation from [Hindré et al 2012]

Weaknesses

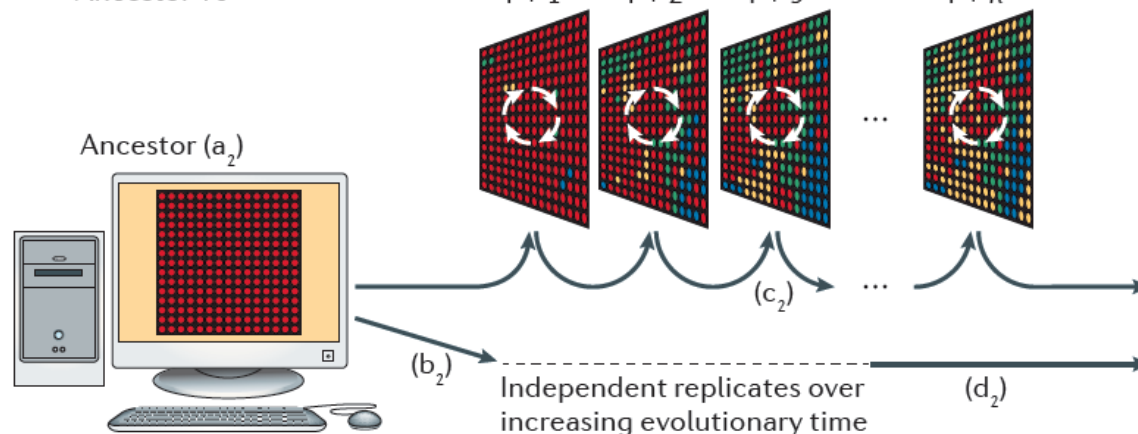
- Long-term experiments
- Difficulty to interpret the events
- Difficulty to reproduce any real environmental conditions and their variations

Experimental evolution to test evolutionary scenarios coming from comparative genomics

In vitro

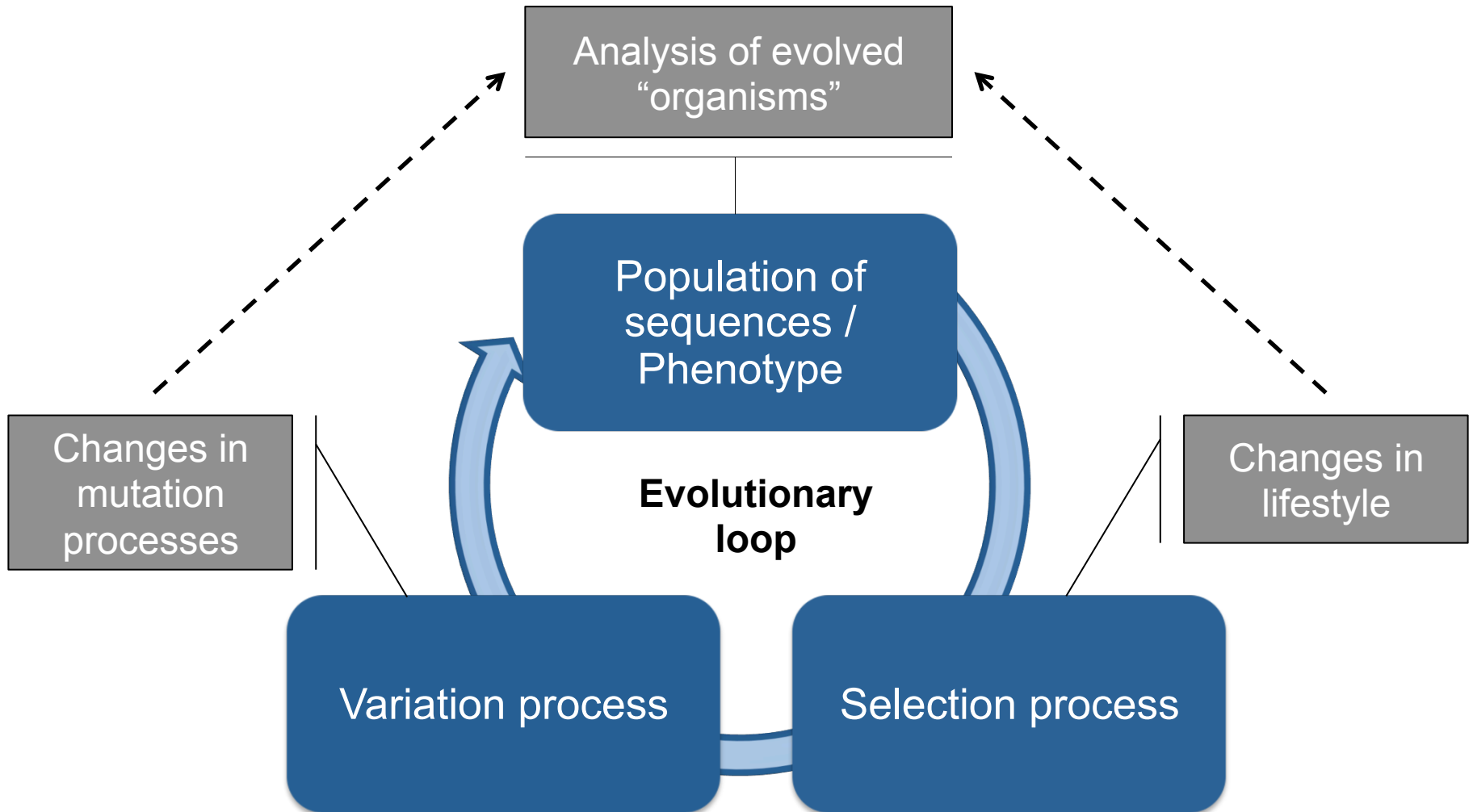


In silico

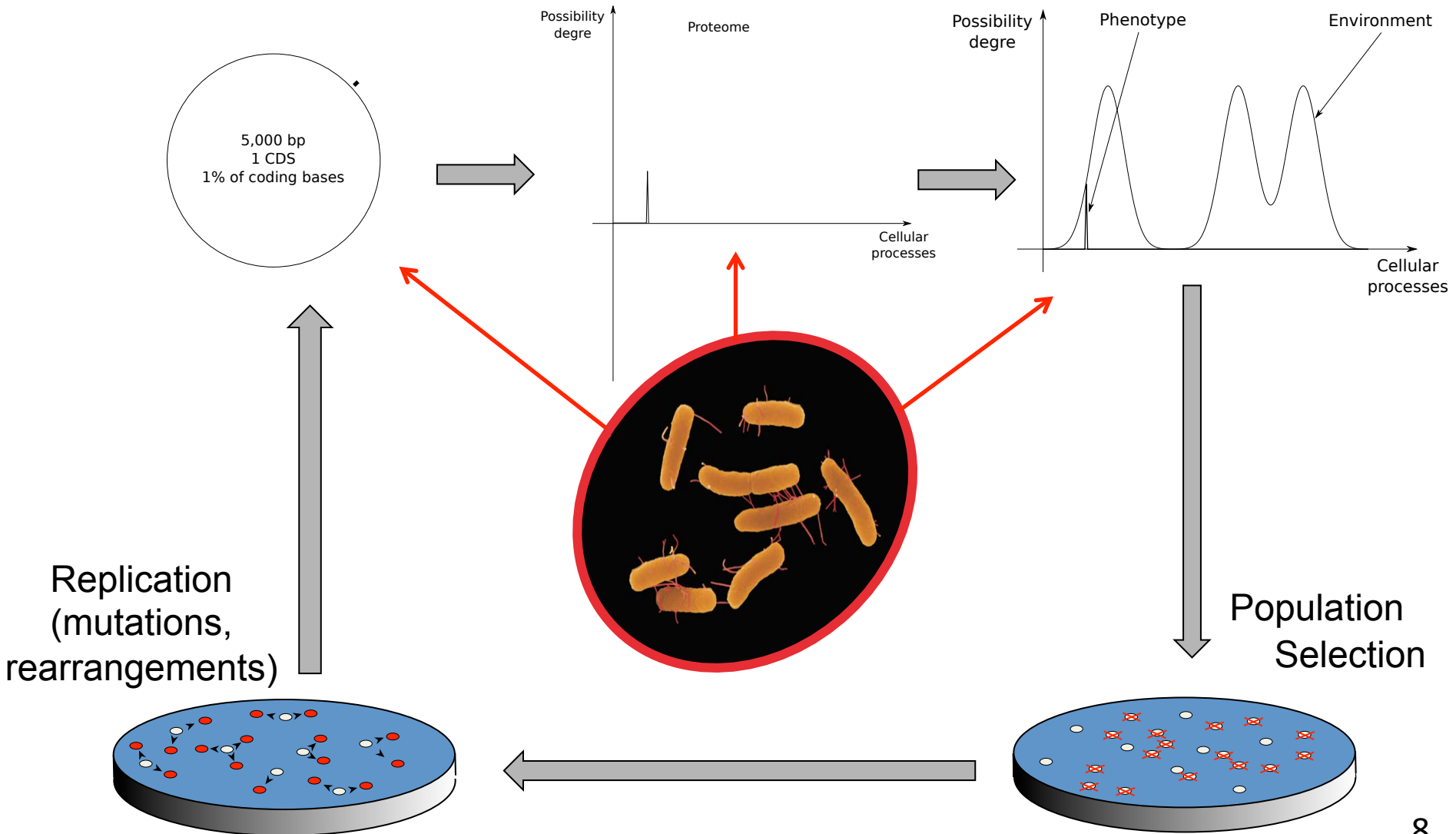
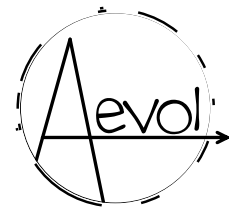


[Hindr  et al 2012]

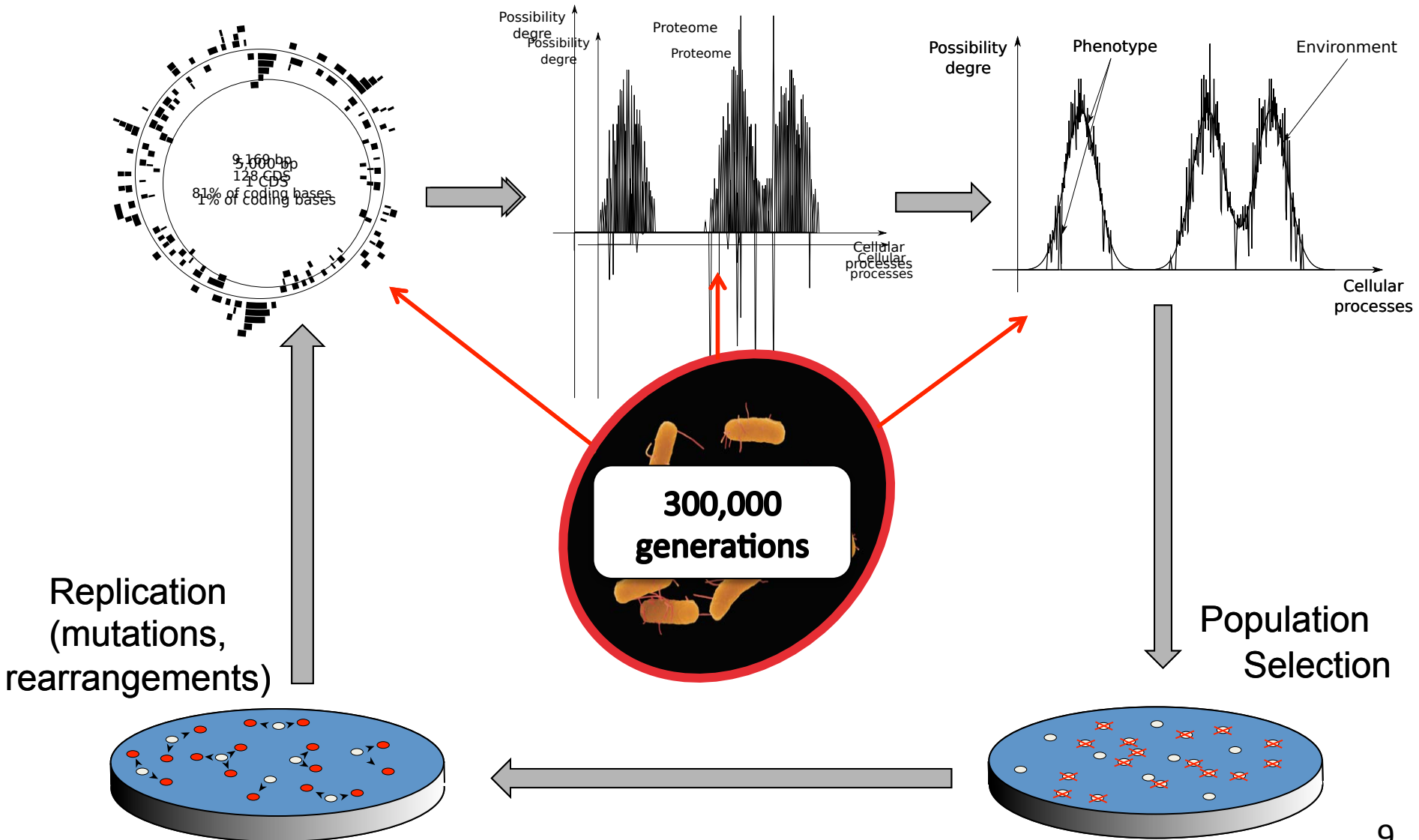
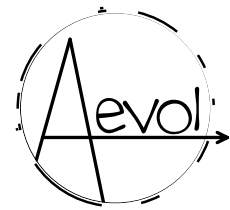
In silico experimental evolution



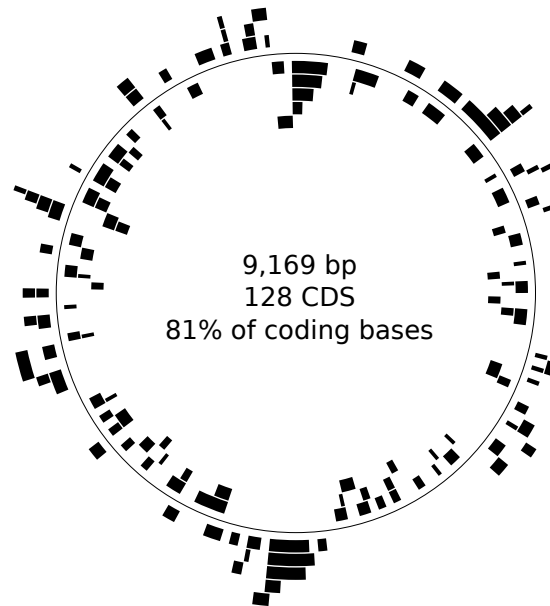
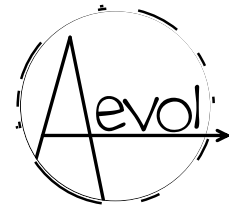
Aevol: an *in silico* experimental evolution platform - www.aevol.fr



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Aevol: an *in silico* experimental evolution platform - www.aevol.fr



An organism => a structured genome with

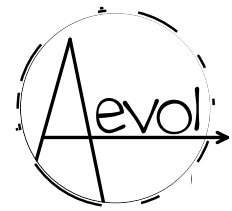
a variable number of genes in a variable order

a variable amount of non coding sequences

a variable number of operons

...

Using aevol to test evolutionary scenarios

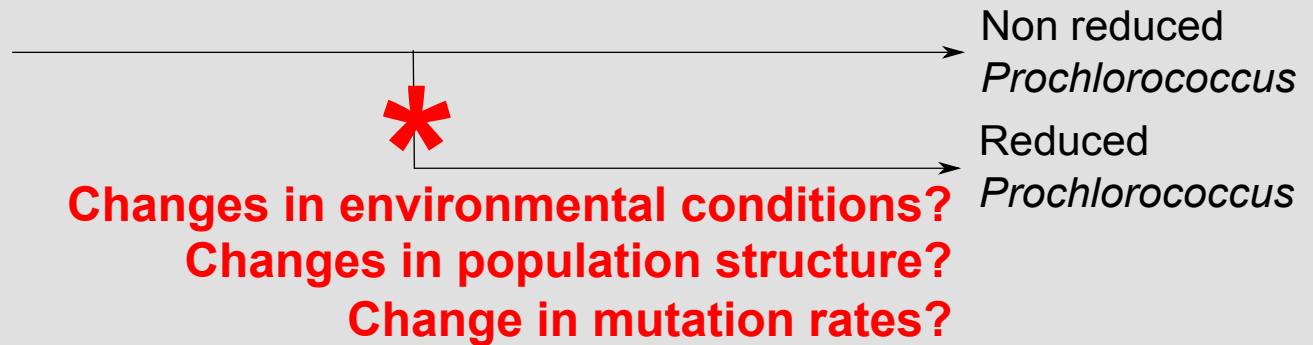


Comparative
genomics

Free-living vs Endosymbionts

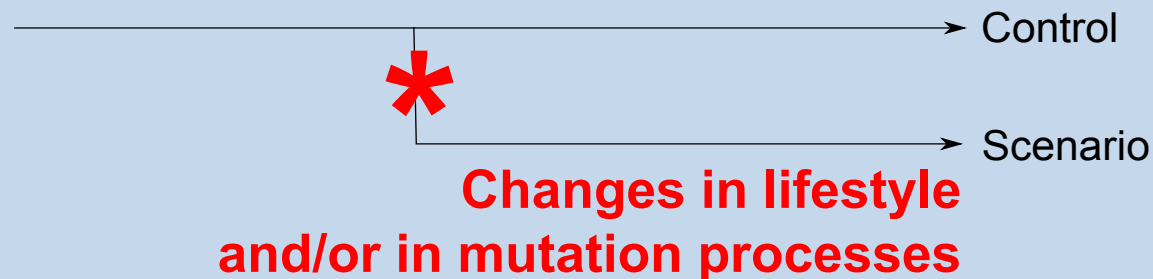


Non reduced vs reduced *Prochlorococcus*

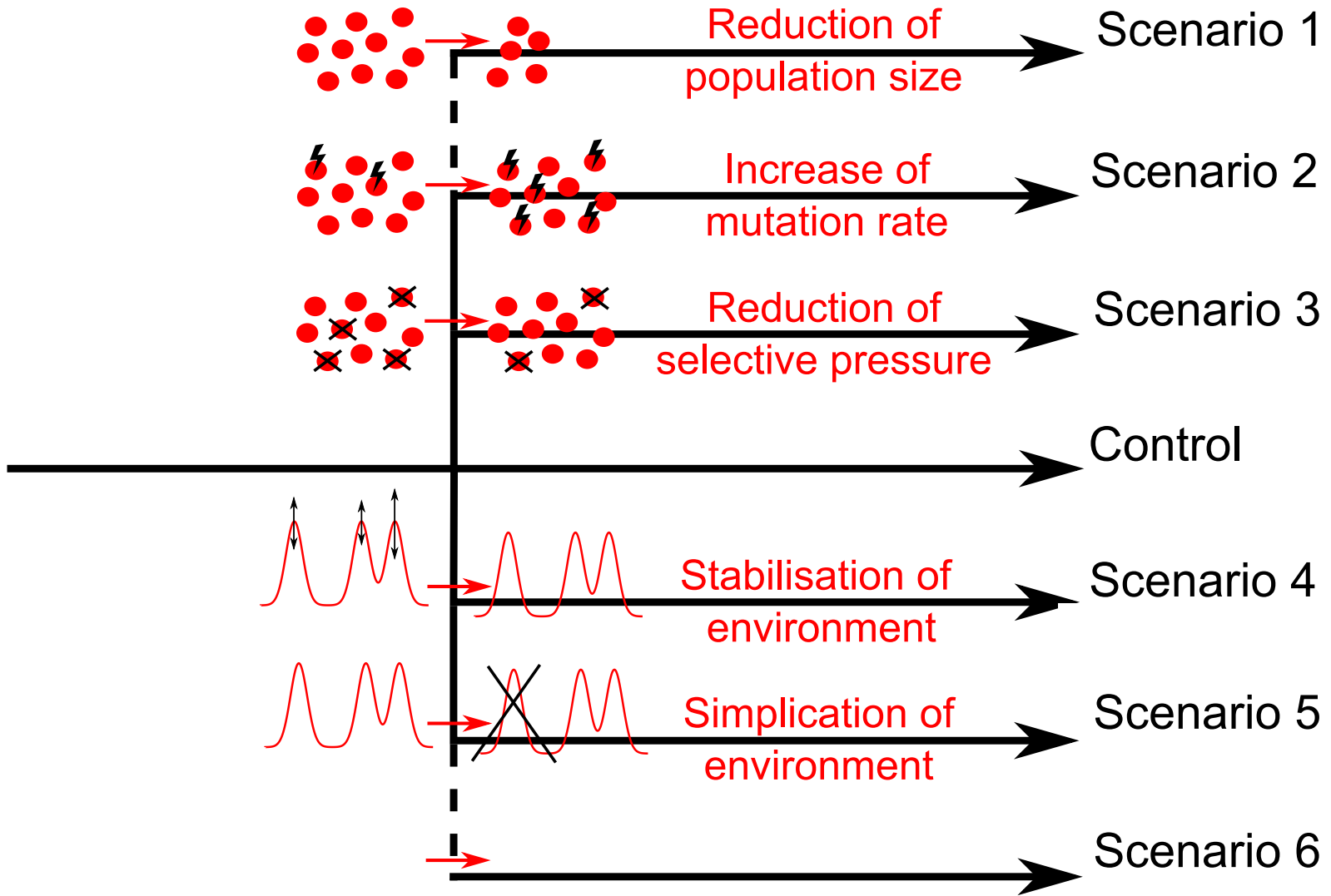
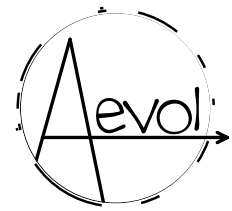


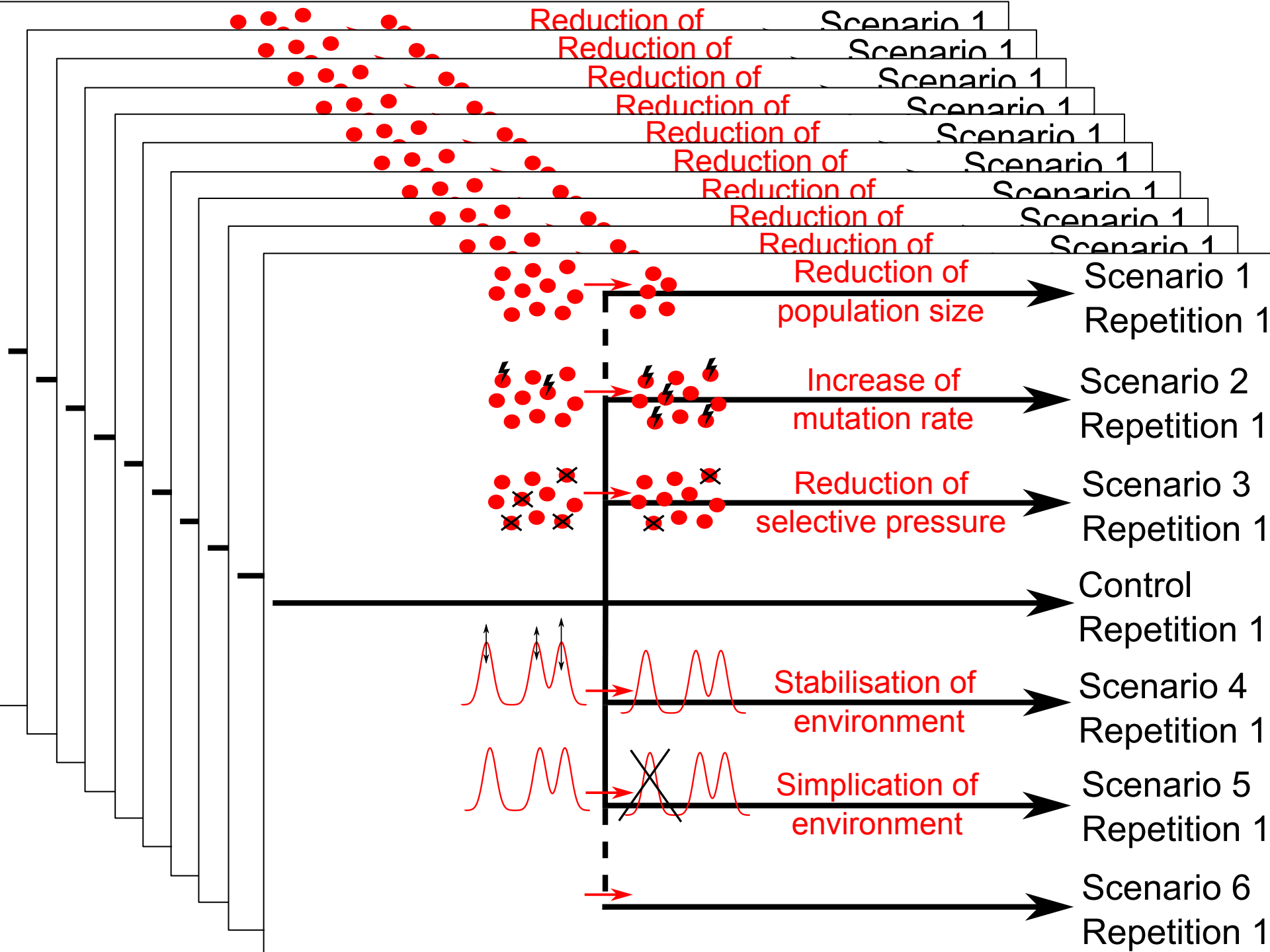
In silico
experimental
evolution

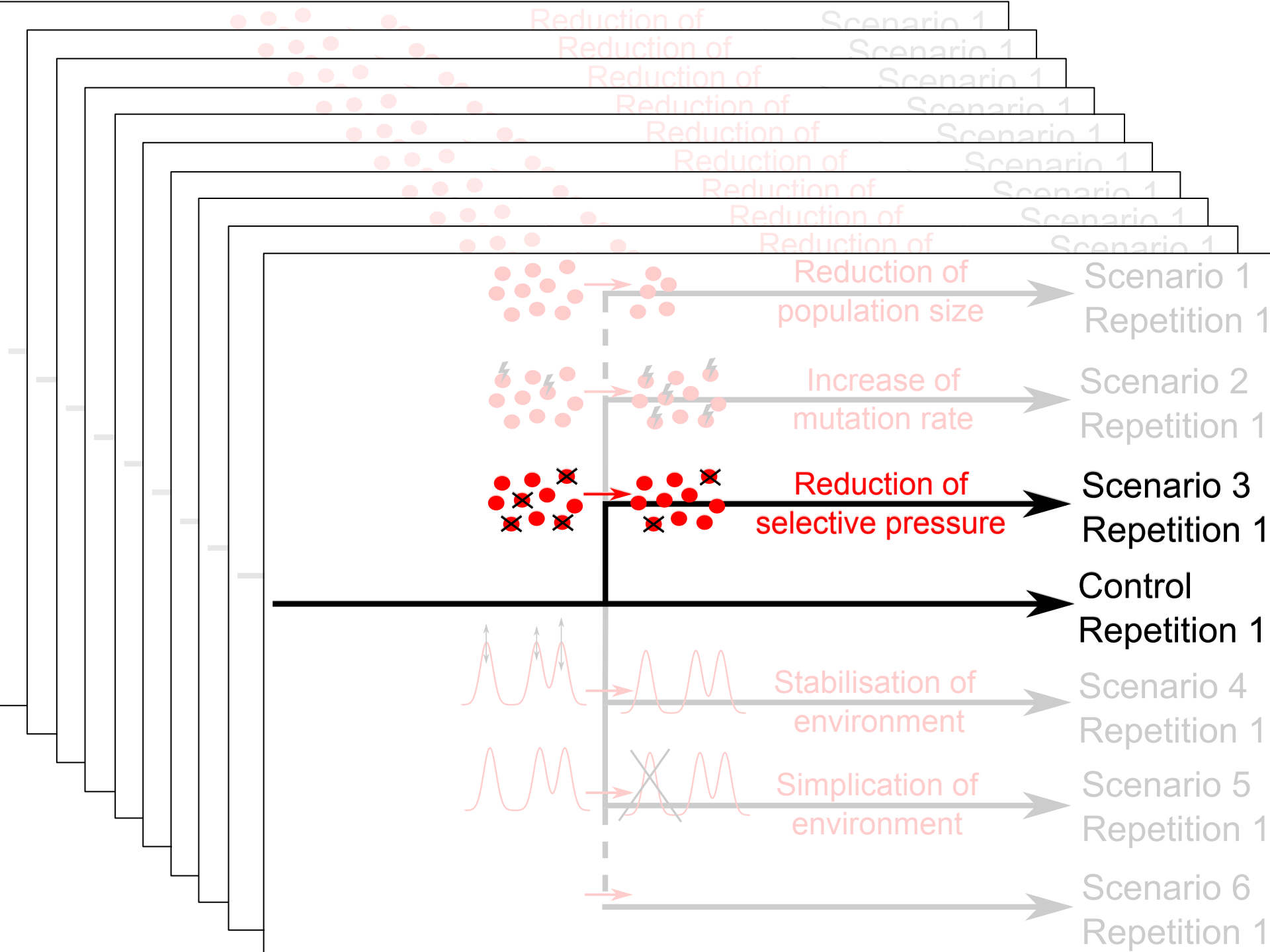
Experimental evolution



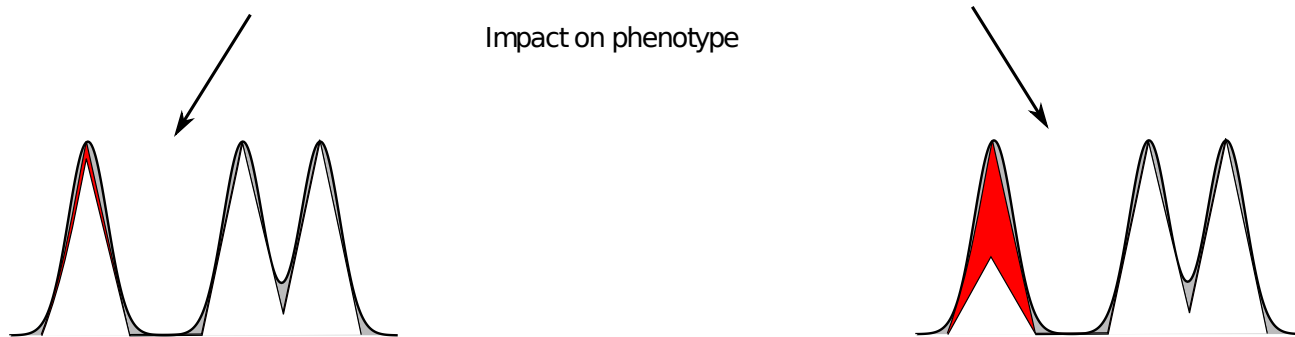
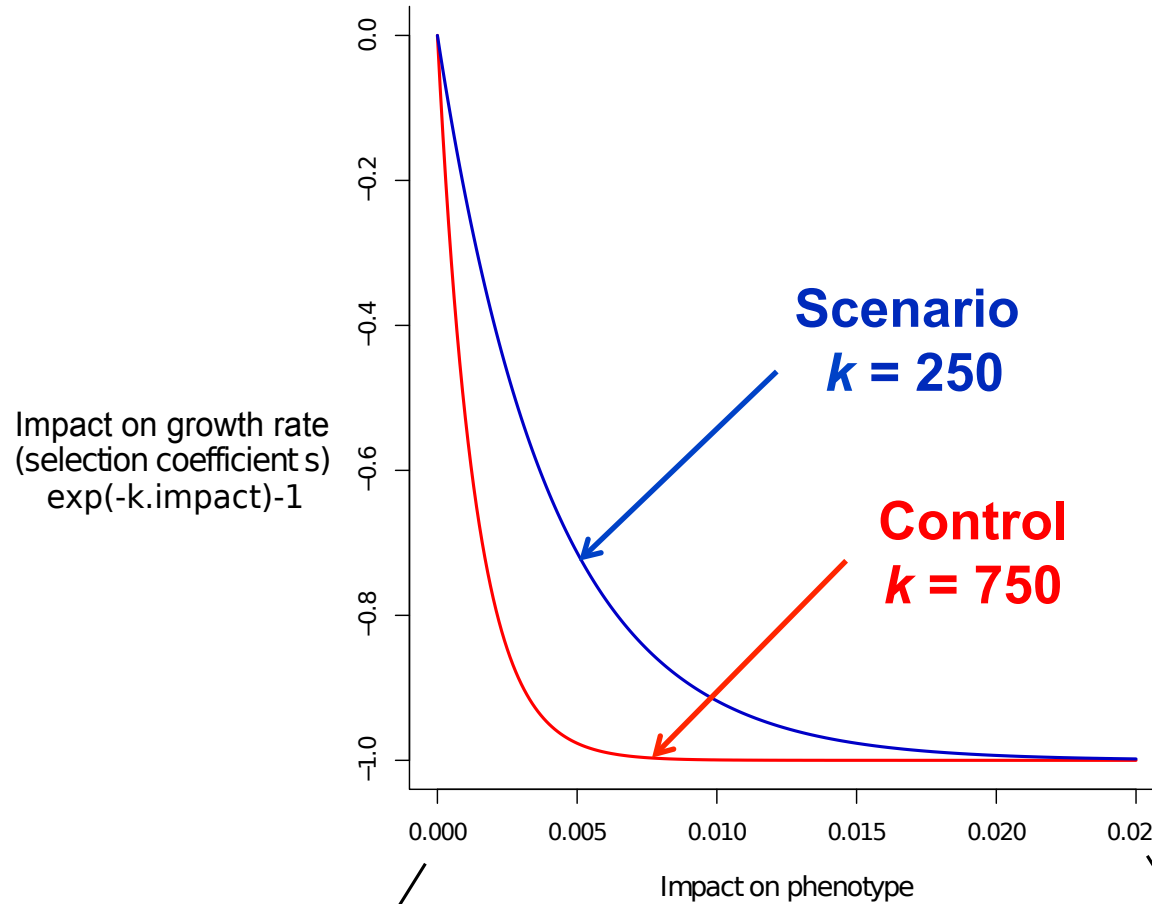
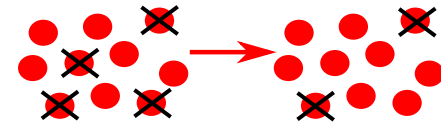
Using aevol to test evolutionary scenarios



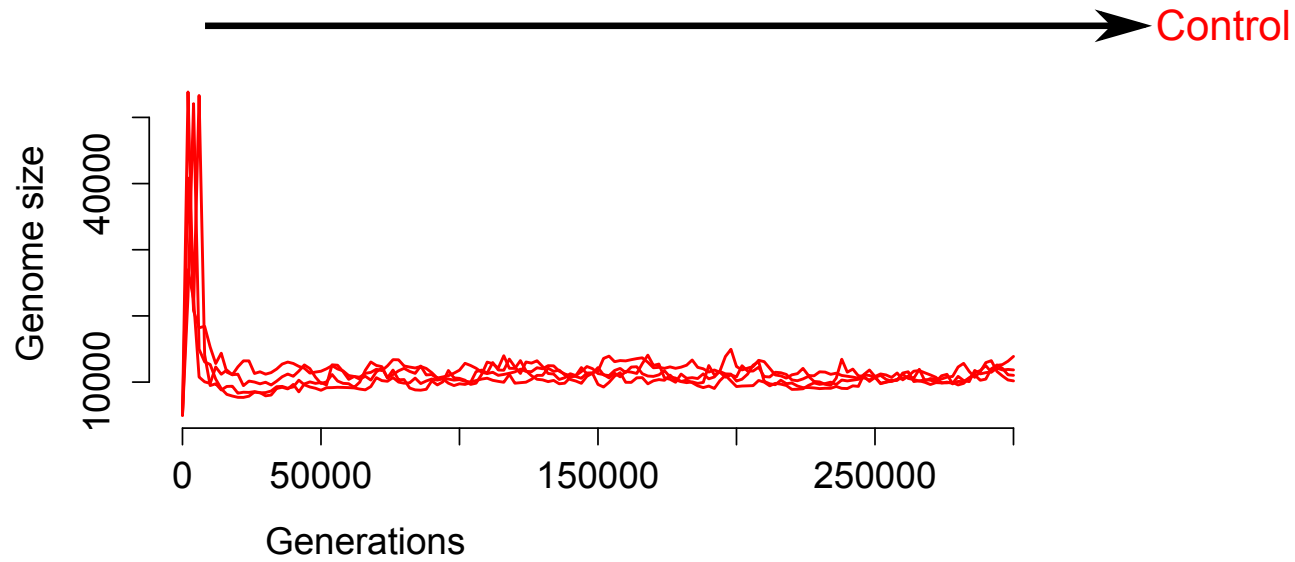
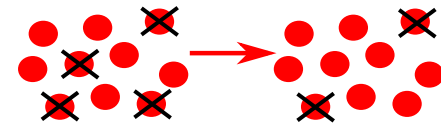




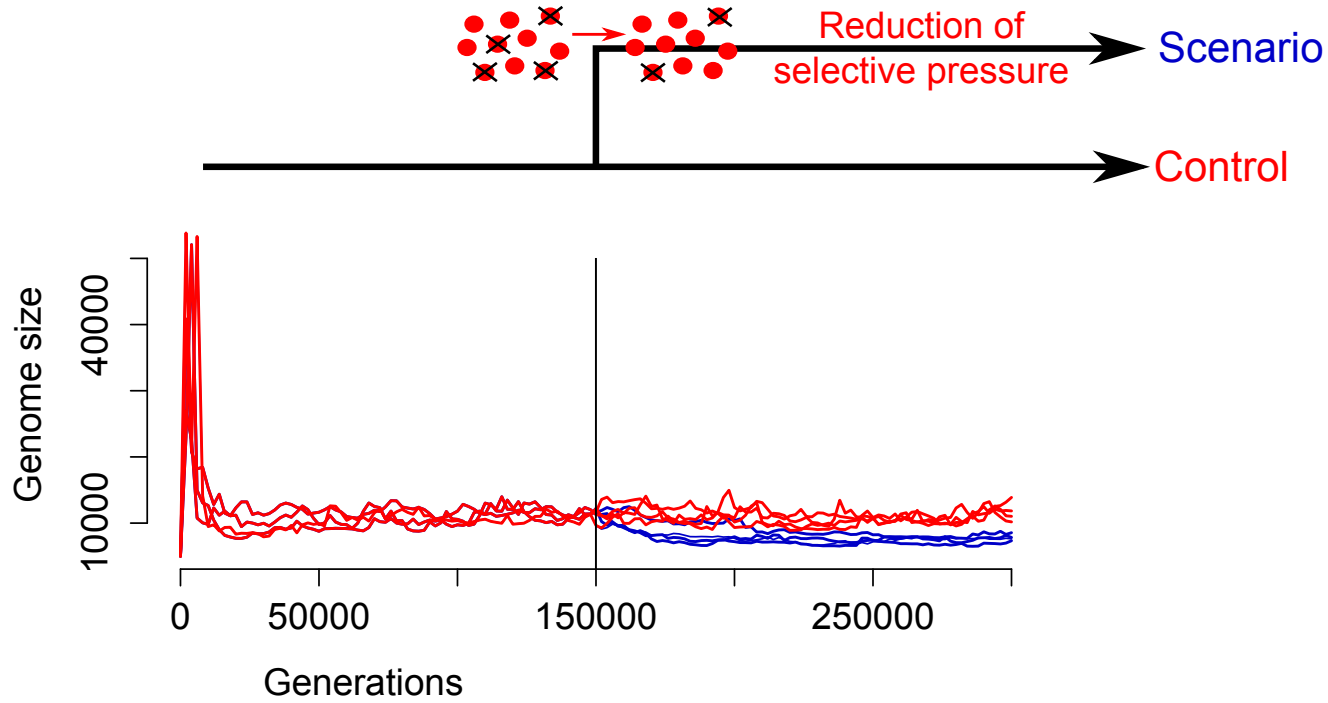
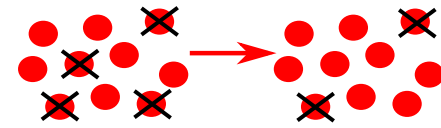
Smotherer distribution of growth rates



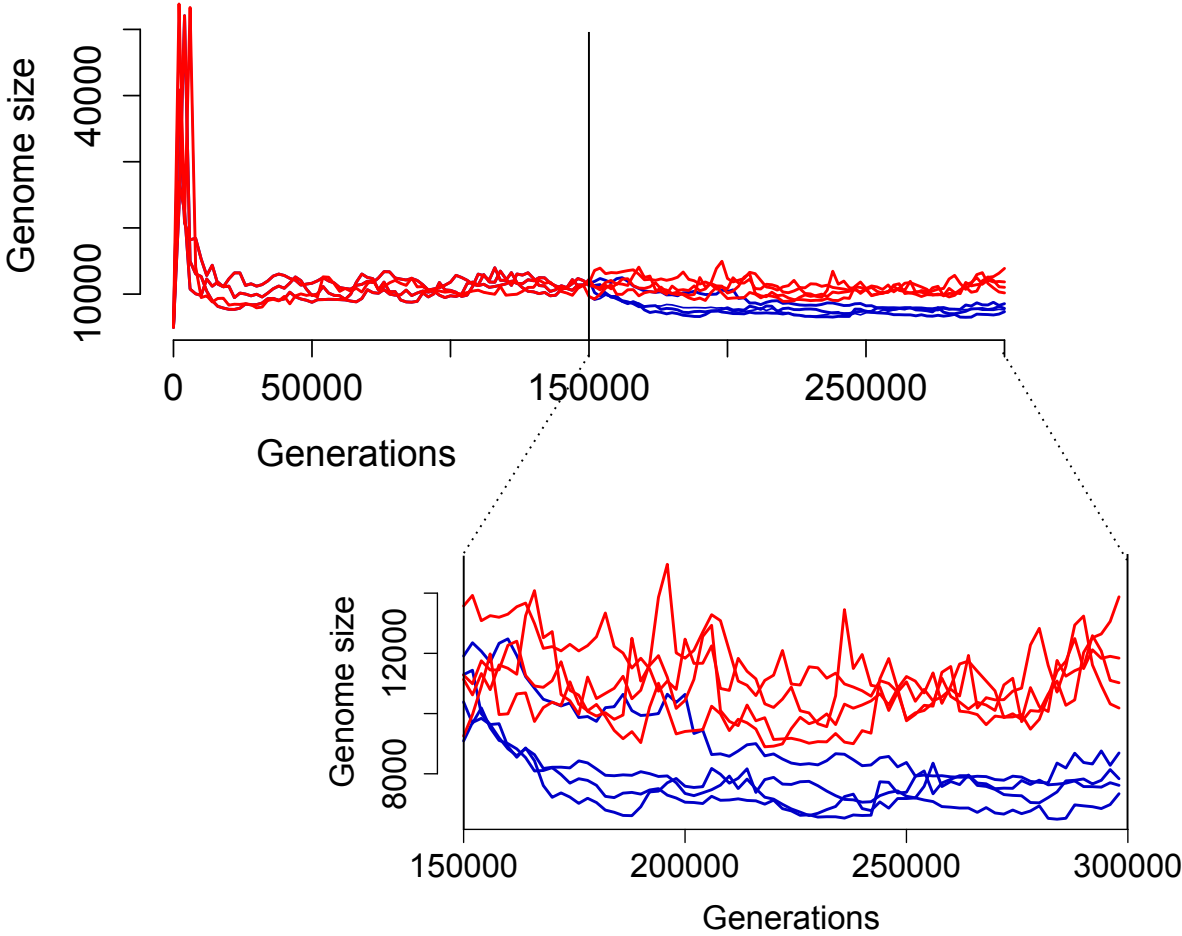
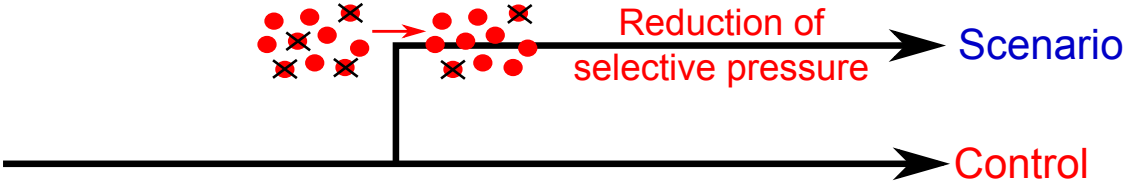
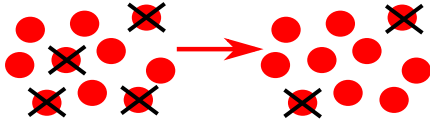
Genome shrinkage under relaxed selection



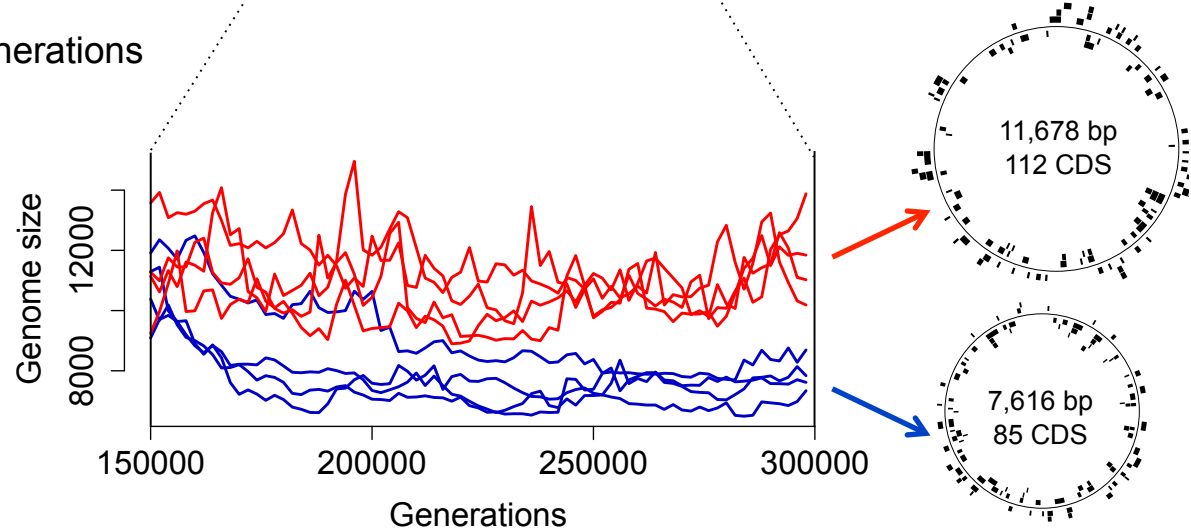
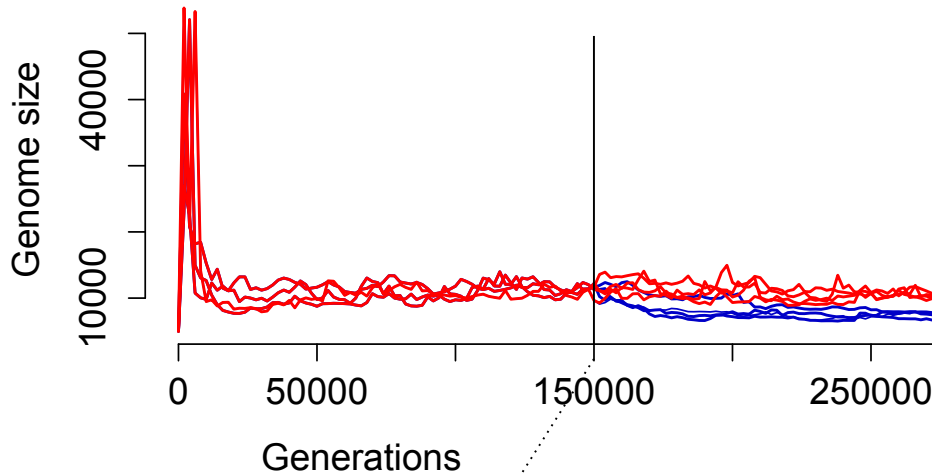
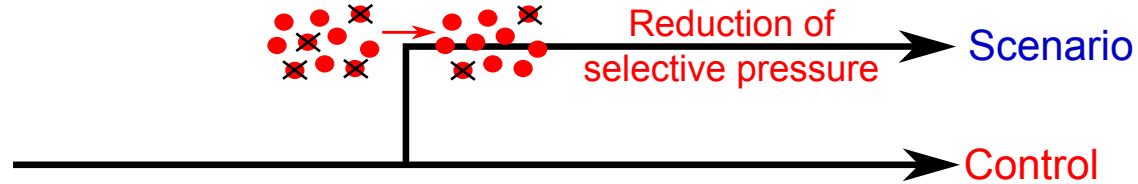
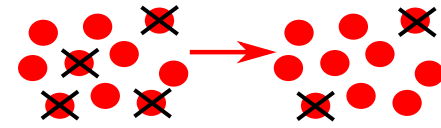
Genome shrinkage under relaxed selection



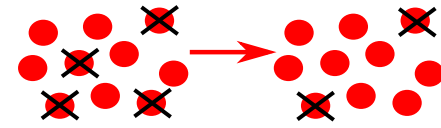
Genome shrinkage under relaxed selection



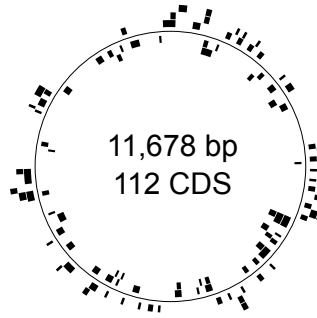
Genome shrinkage under relaxed selection



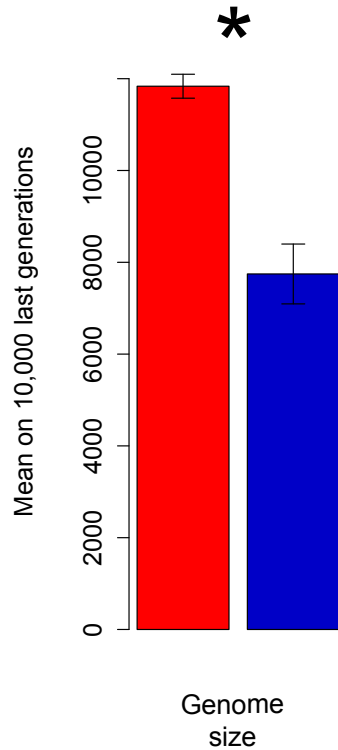
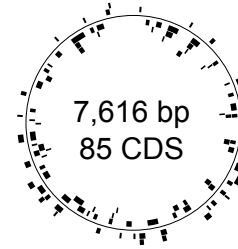
Smaller and more compact genomes



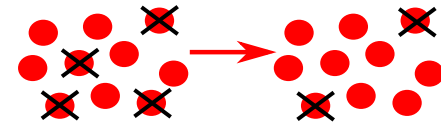
Control



Scenario

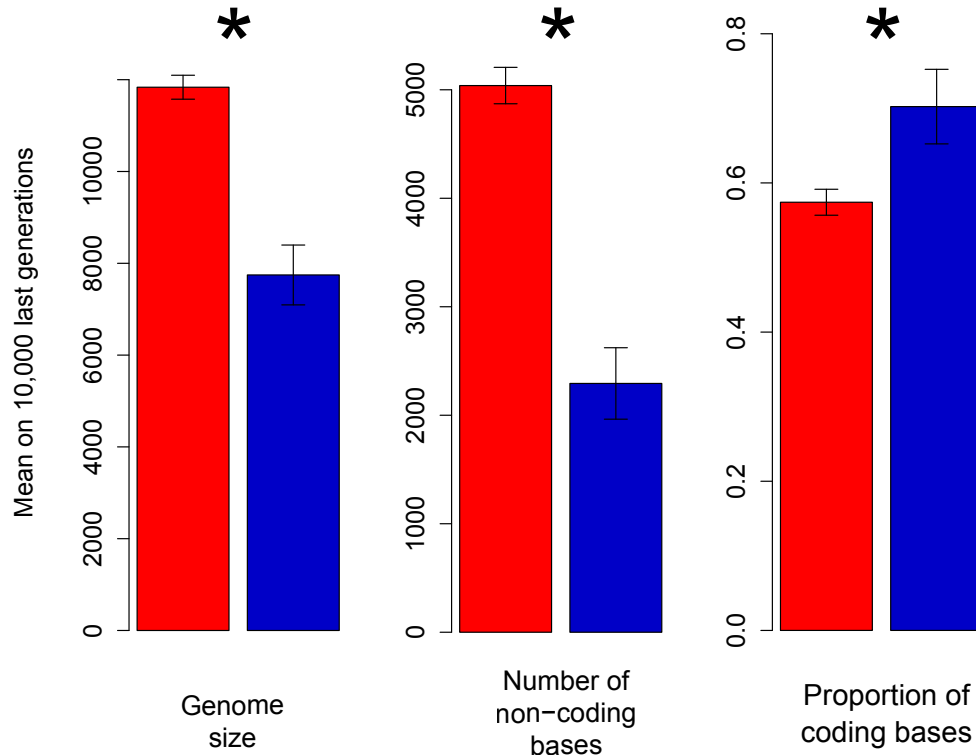
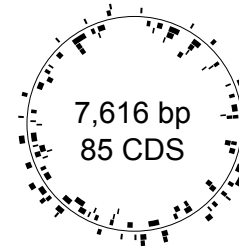
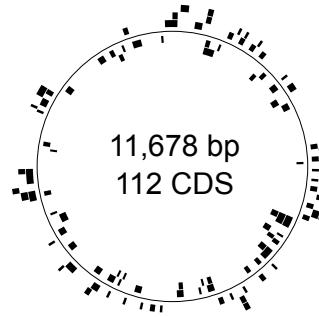


Smaller and more compact genomes

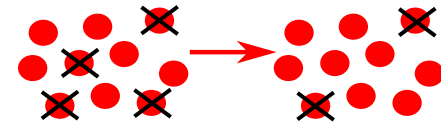


Control

Scenario

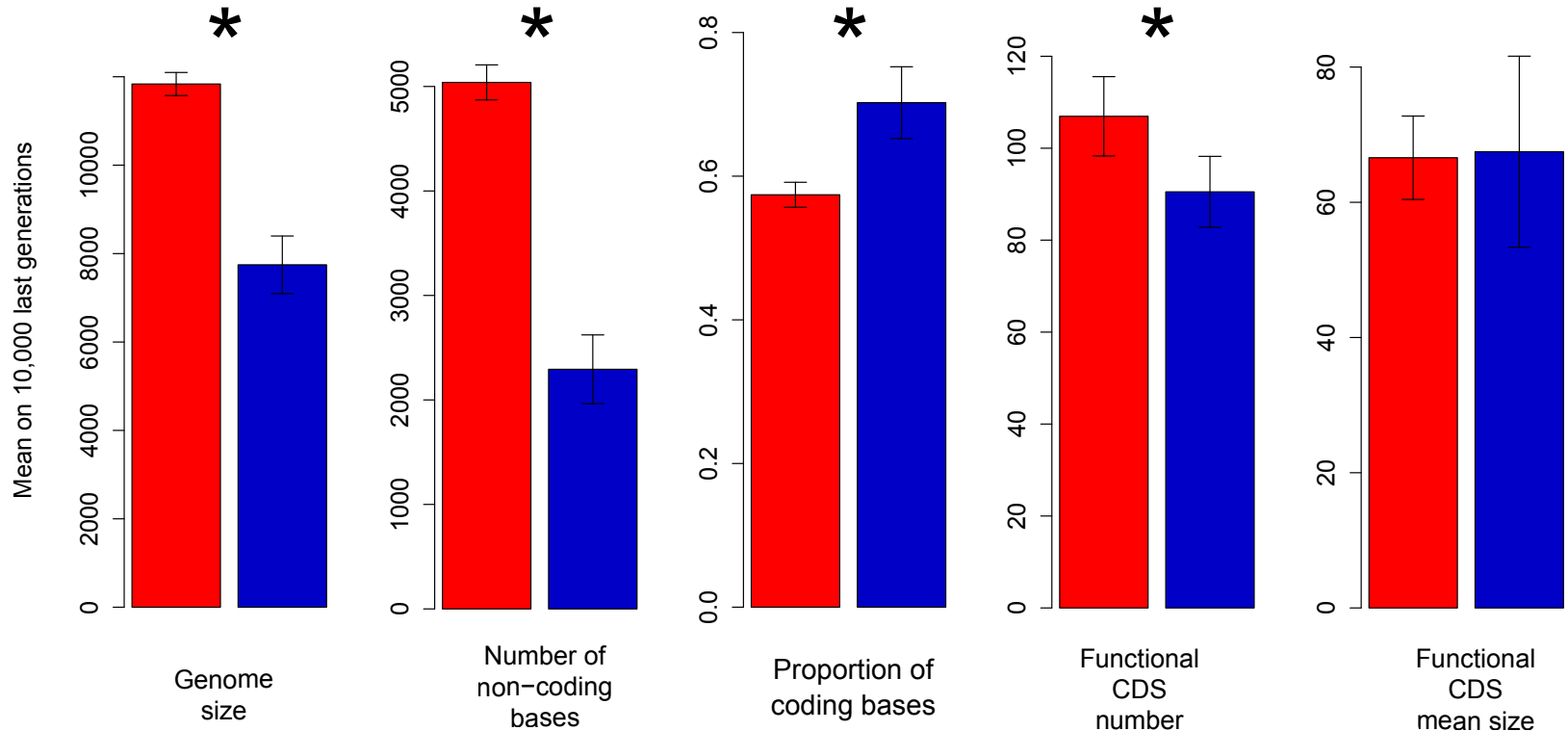
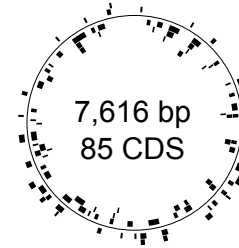
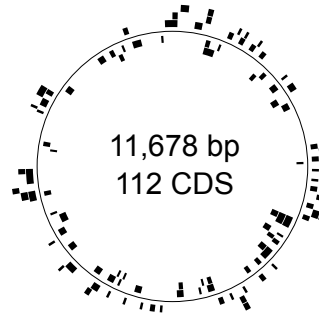


Smaller and more compact genomes

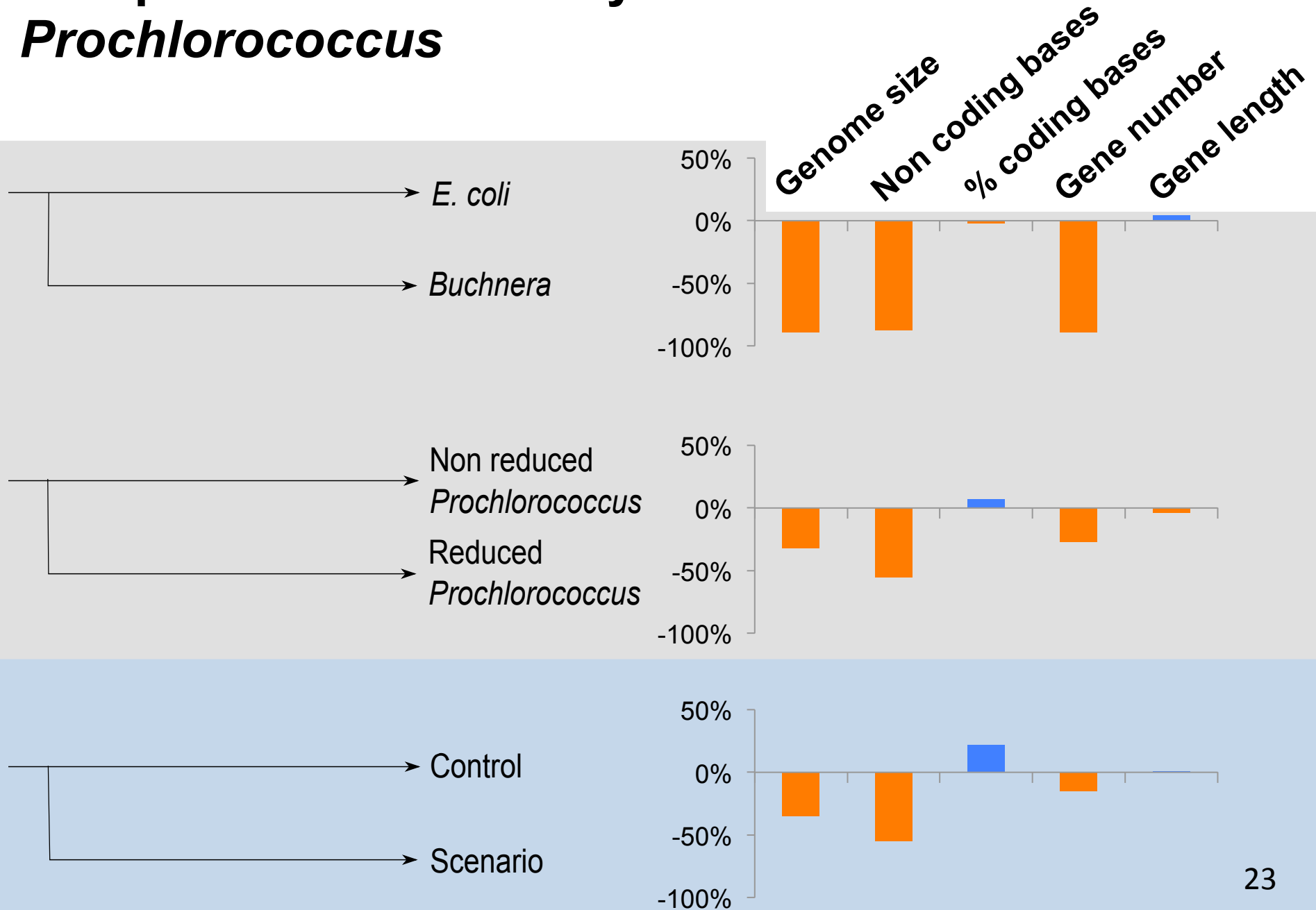


Control

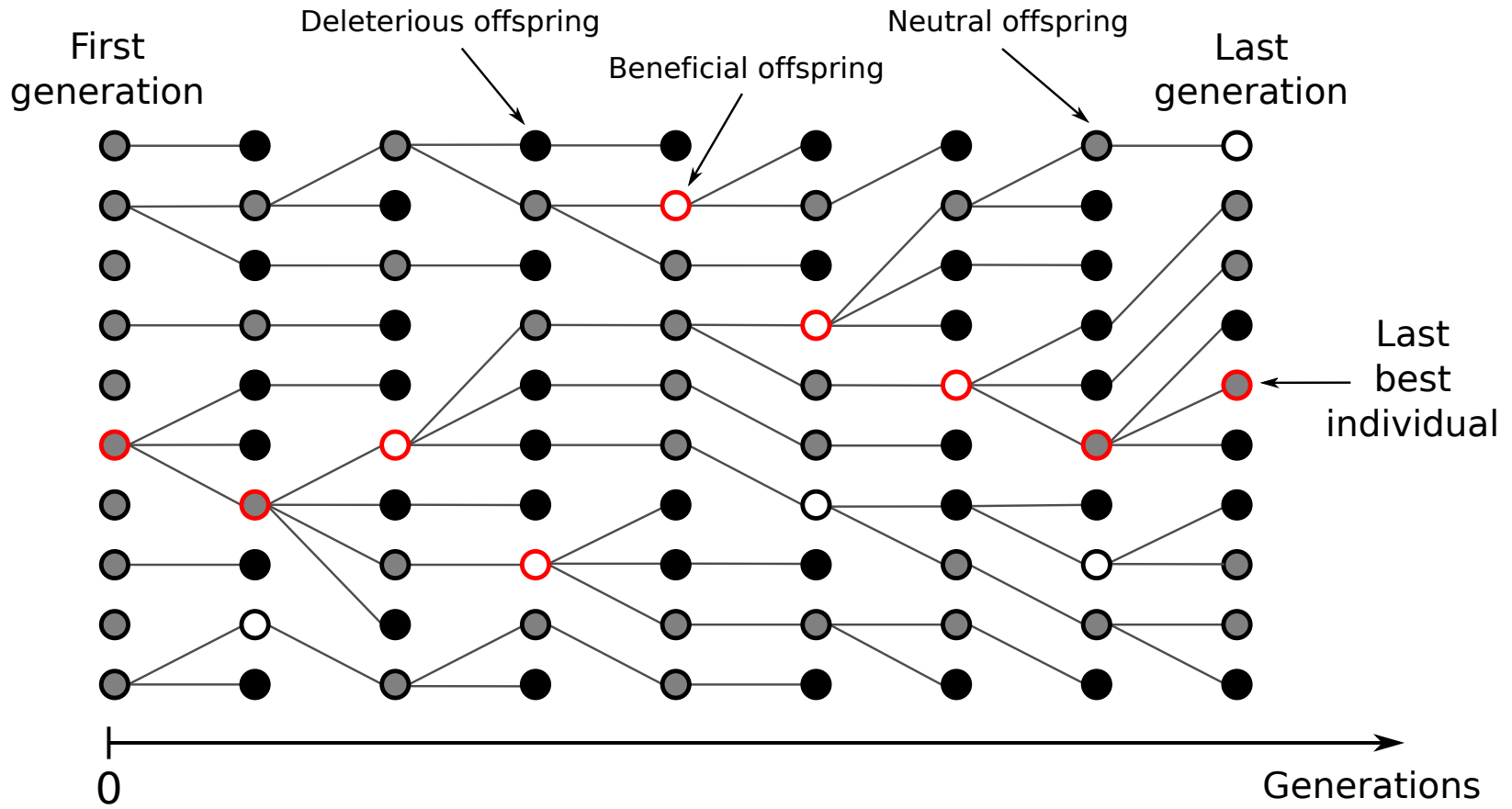
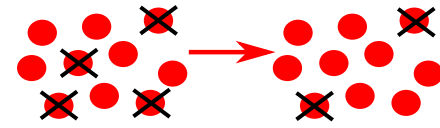
Scenario



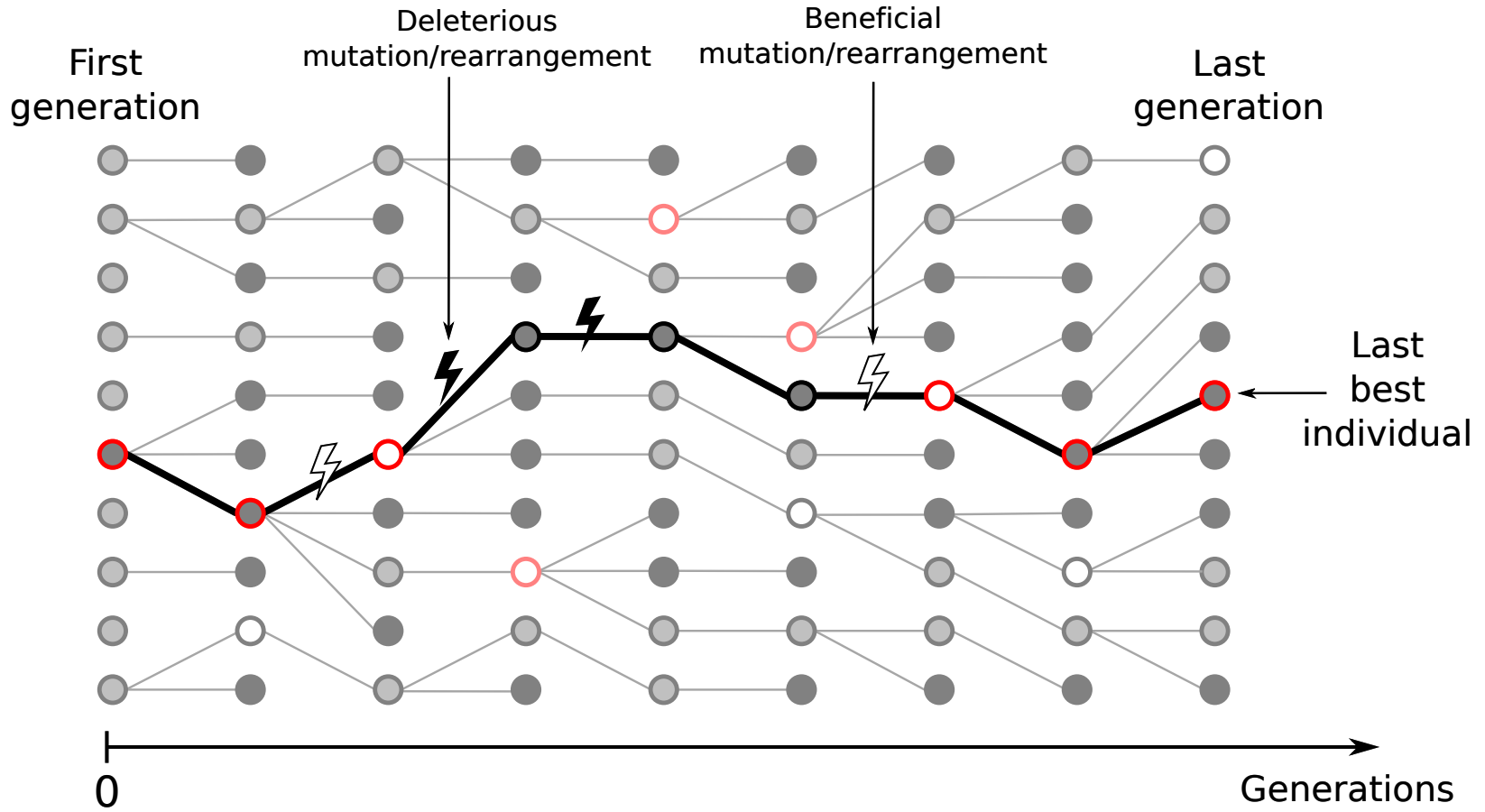
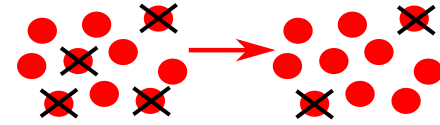
Comparison with endosymbionts and *Prochlorococcus*



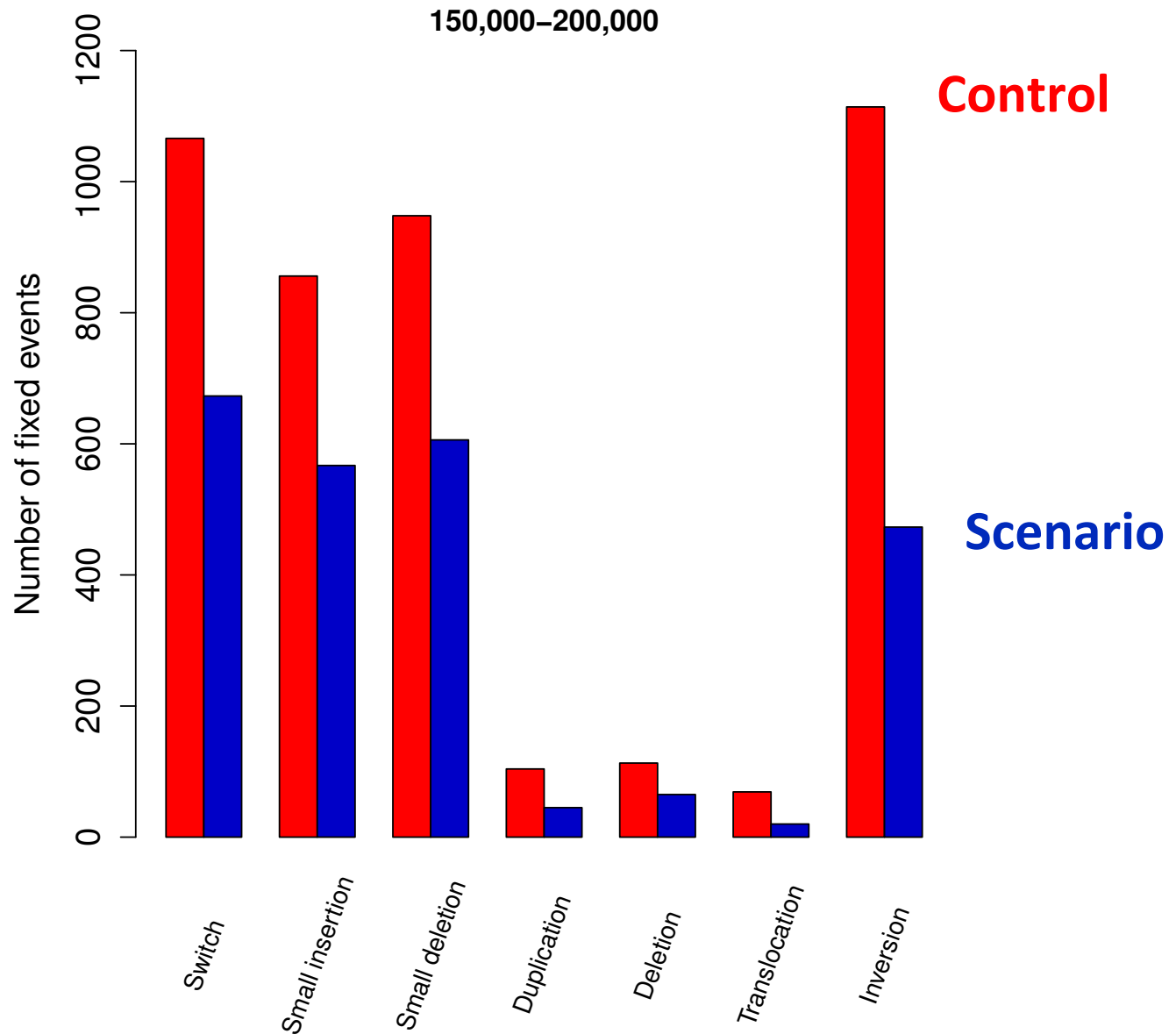
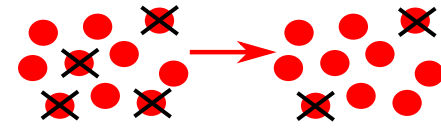
An exact “fossil record” is saved during each run



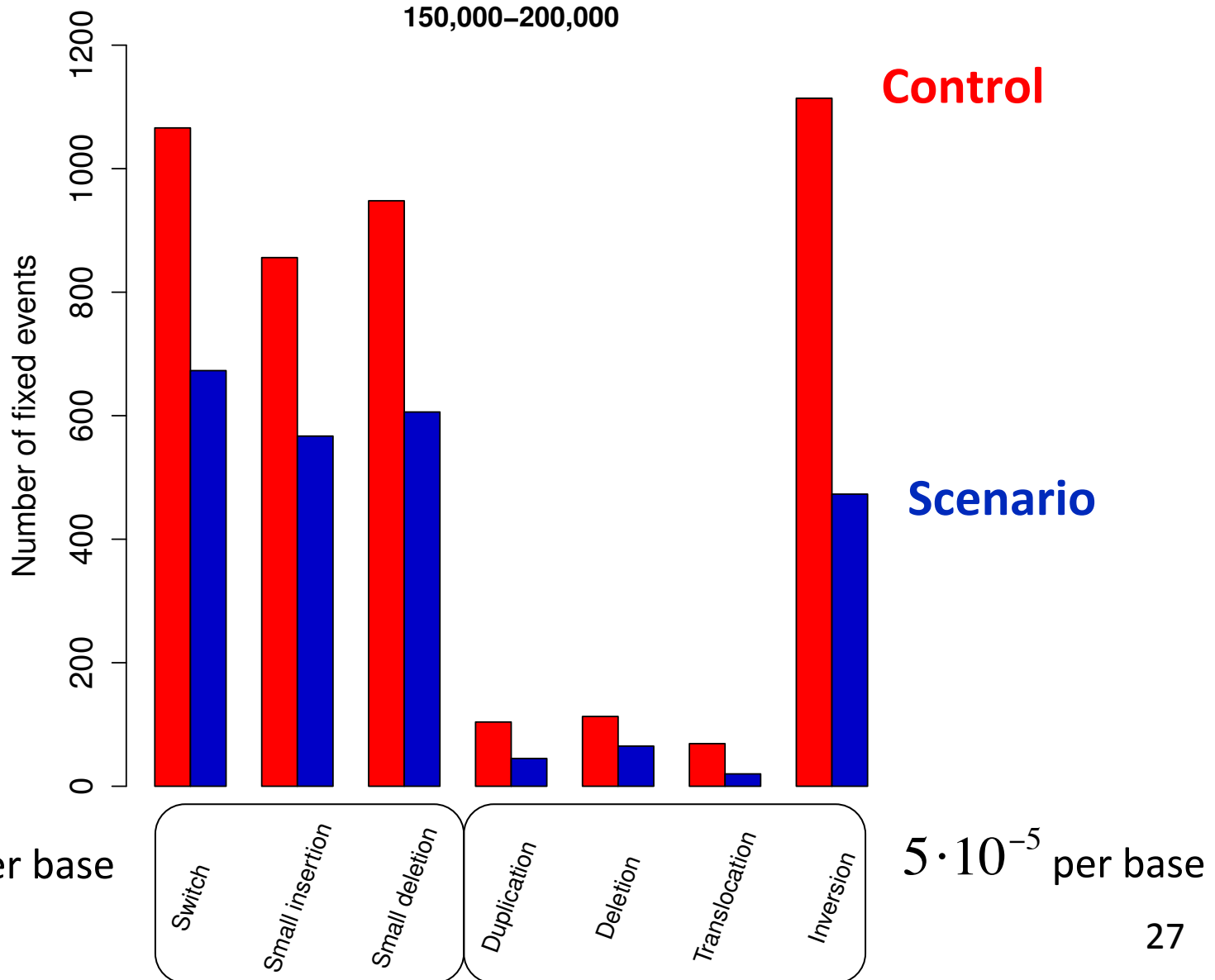
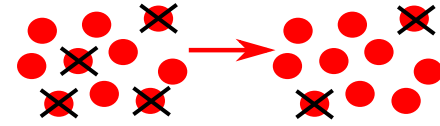
Mutational events on winning lineage



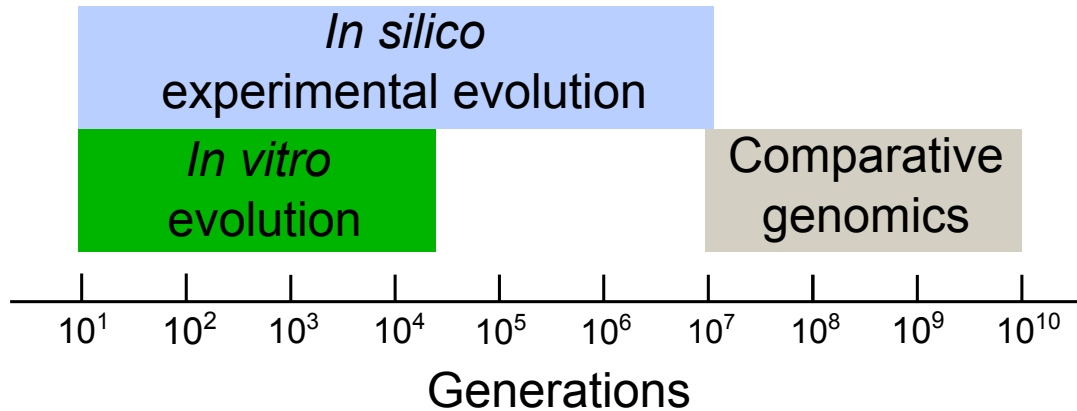
Mutational events on winning lineage



Mutational events on winning lineage

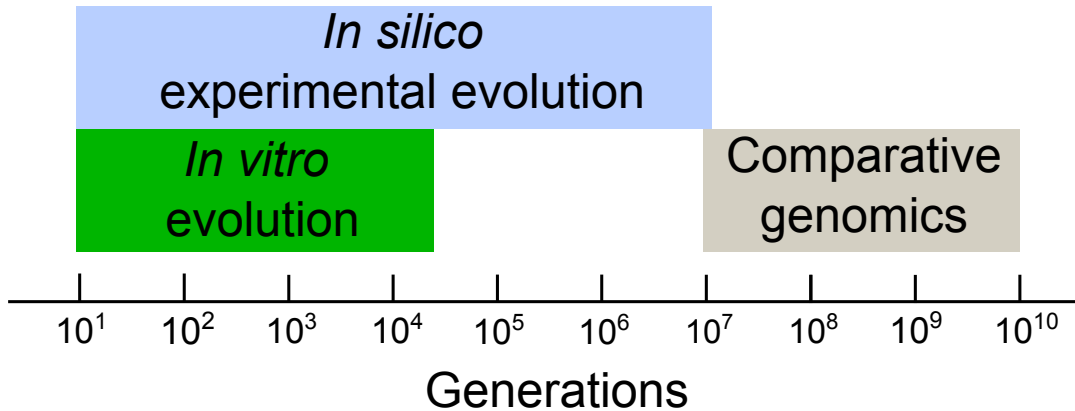


In silico experimental evolution: a tool to test evolutionary scenarios



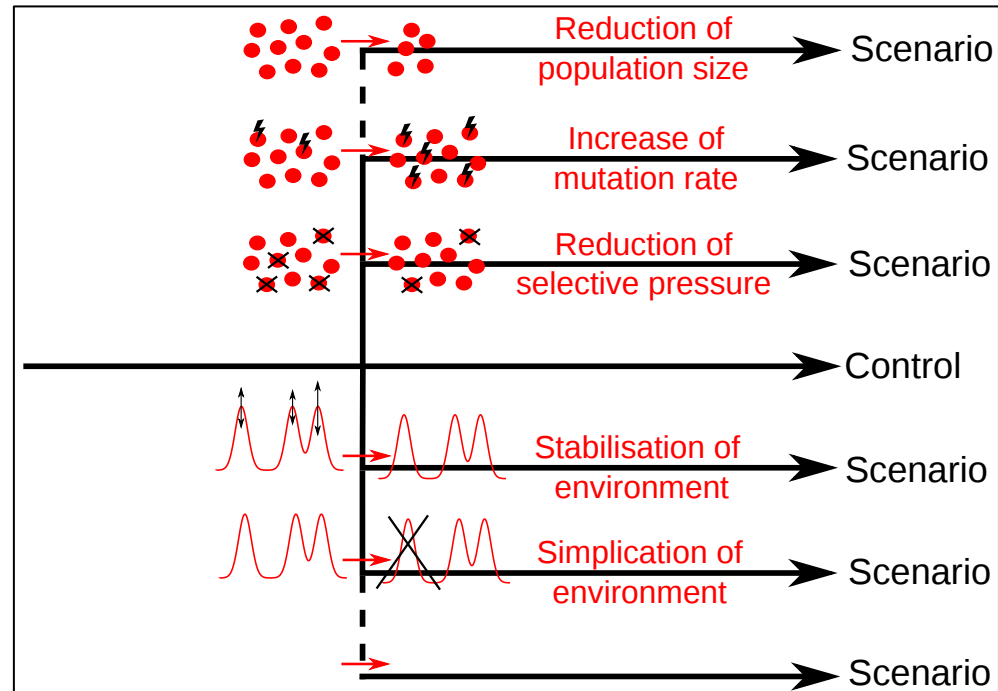
Adaptation from [Wagner 2009]

In silico experimental evolution: a tool to test evolutionary scenarios



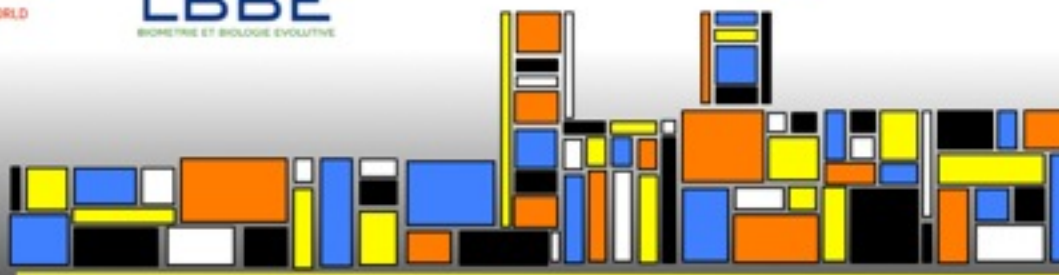
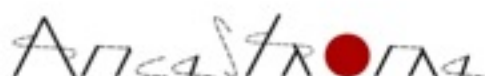
Adaptation from [Wagner 2009]

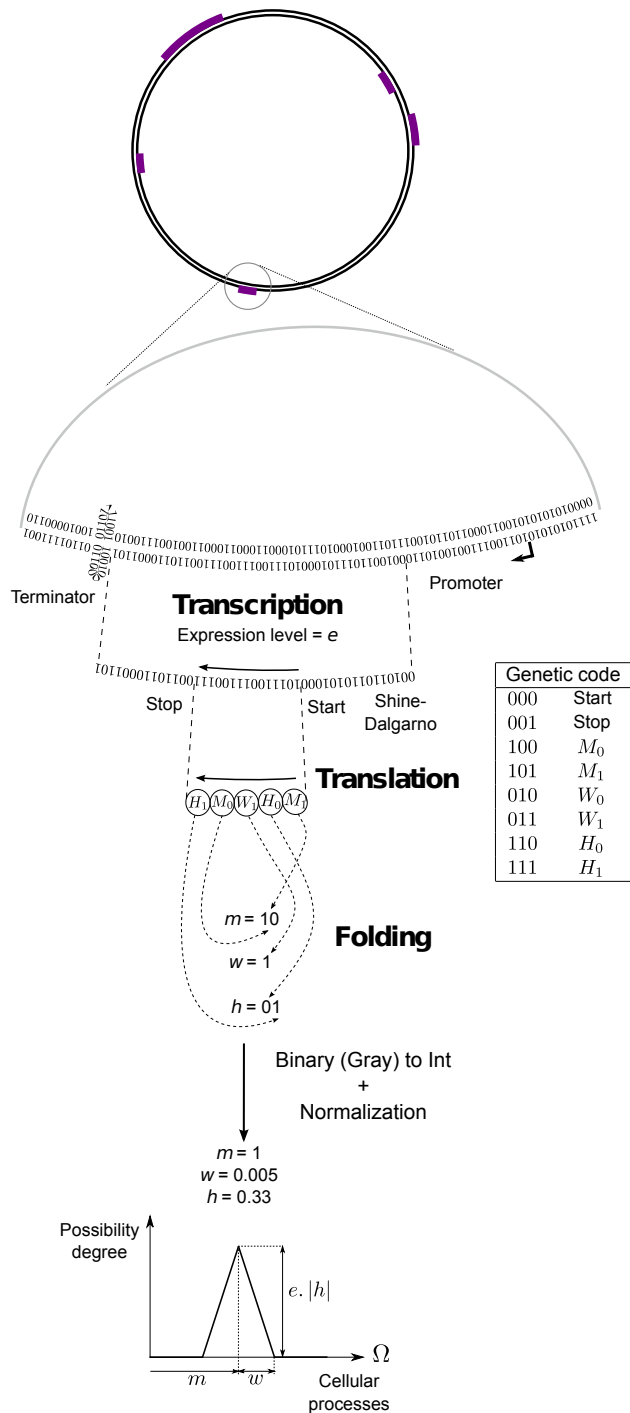
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11th RECOMB satellite meeting on Comparative Genomics

17 - 19 Oct. 2013 Lyon - Villeurbanne





```

foreach Generation do
  //Genome decoding and evaluation
  foreach Individual do
    Identify coding sequences
    foreach CodingSequence do
      Translation into abstract protein
    end
    Compute phenotype  $f_P$  by combining protein
    contributions
    Compute gap with target  $g$  by comparing the
    phenotype  $f_P$  to the environmental target  $f_E$ 
  end

  //Selection
  Compute the probabilities of reproduction based on
  gap with target  $g$ 

  //Reproduction with mutations and rearrangements
  foreach Individual do
    foreach Offspring do
      Create Offspring
      Do rearrangements
      Do local mutations
    end
  end

  Replace current population
end

```