



towards mimicking wet experiments

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Simulating evolutionary scenarios (like the adaptation to a new environment, the lab)

1. Create one (or several) « wild type » to be used as the ancestor

```
cd wildtype
# Prepare a text file called param.in with a fluctuating
# environment
aevol_create
aevol_run -n 10000
```

2. Prepare replicate lines with aevol_propagate

```
cd ..
mydirnameA="line01 line02 line03 line04 line05"
mydirnameB="line06 line07 line08 line09 line10"
for mydir in $mydirnameA $mydirnameB
do
    echo $mydir
    aevol_propagate -g 10000 -i wildtype -o $mydir -S $RANDOM
done
```

- ➔ Statistical power
- ➔ Distinguish between necessity and contingency in evolutionary trajectories

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3. For each group, create a text file with the parameters to change

newparam-groupA.in

```
# New environment
ENV_GAUSSIAN 0.5 0.2 0.05
ENV_GAUSSIAN 0.5 0.4 0.05
ENV_GAUSSIAN 0.5 0.8 0.05
ENV_VARIATION none
```

newparam-groupB.in (mutators)

```
# New environment
ENV_GAUSSIAN 0.5 0.2 0.05
ENV_GAUSSIAN 0.5 0.4 0.05
ENV_GAUSSIAN 0.5 0.8 0.05
ENV_VARIATION none
```

```
# New rearrangement rates
DUPLICATION_RATE      1e-5
DELETION_RATE          1e-5
TRANSLOCATION_RATE      1e-5
INVERSION_RATE         1e-5
```

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4. Apply the modifications with aevol_modify

```
for mydir in $mydirnamesA
do
    cd $mydir
    echo $mydir
    aevol_modify --gener 0 --file ../newparam-groupA.in
    cd ..
done

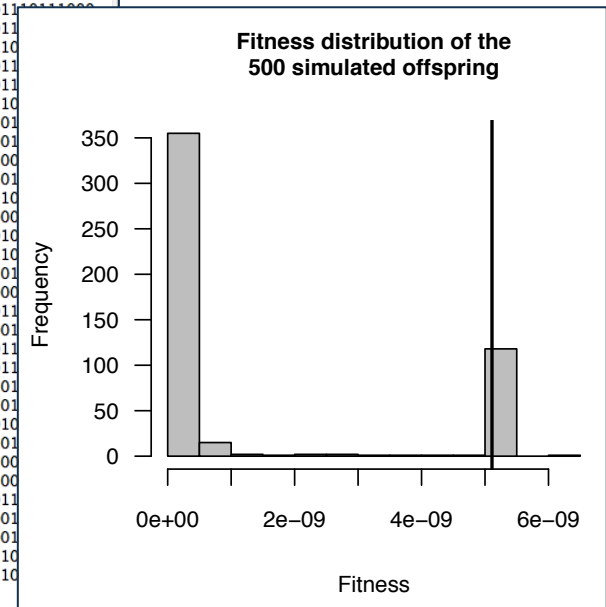
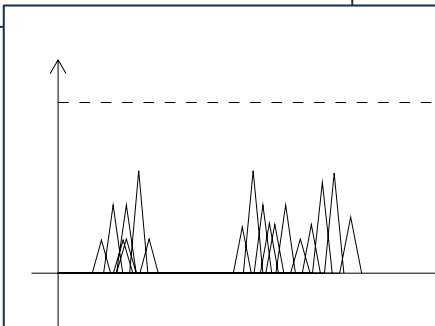
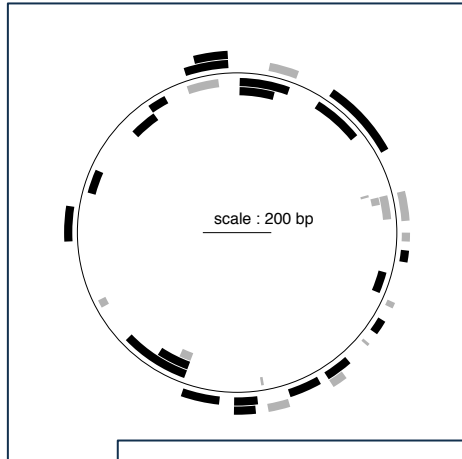
for mydir in $mydirnamesB
do
    cd $mydir
    echo $mydir
    aevol_modify --gener 0 --file ../newparam-groupB.in
    cd ..
done
```

5. Ready to run!

```
for mydir in $mydirnamesA $mydirnamesB
do
    cd mydir
    aevol_run -n 2000
    cd ..
done
```

Analyzing the evolved bacteria

```
aevol_misc_view_generation -g 2000  
  
aevol_misc_create_eps -g 2000  
  
aevol_misc_extract -r 2000 -b -s best-sequence.txt -t best-proteins.txt  
  
aevol_misc_robustness -g 2000 -n 500  
  
aevol_misc_mutagenesis -g 2000 -m 0
```



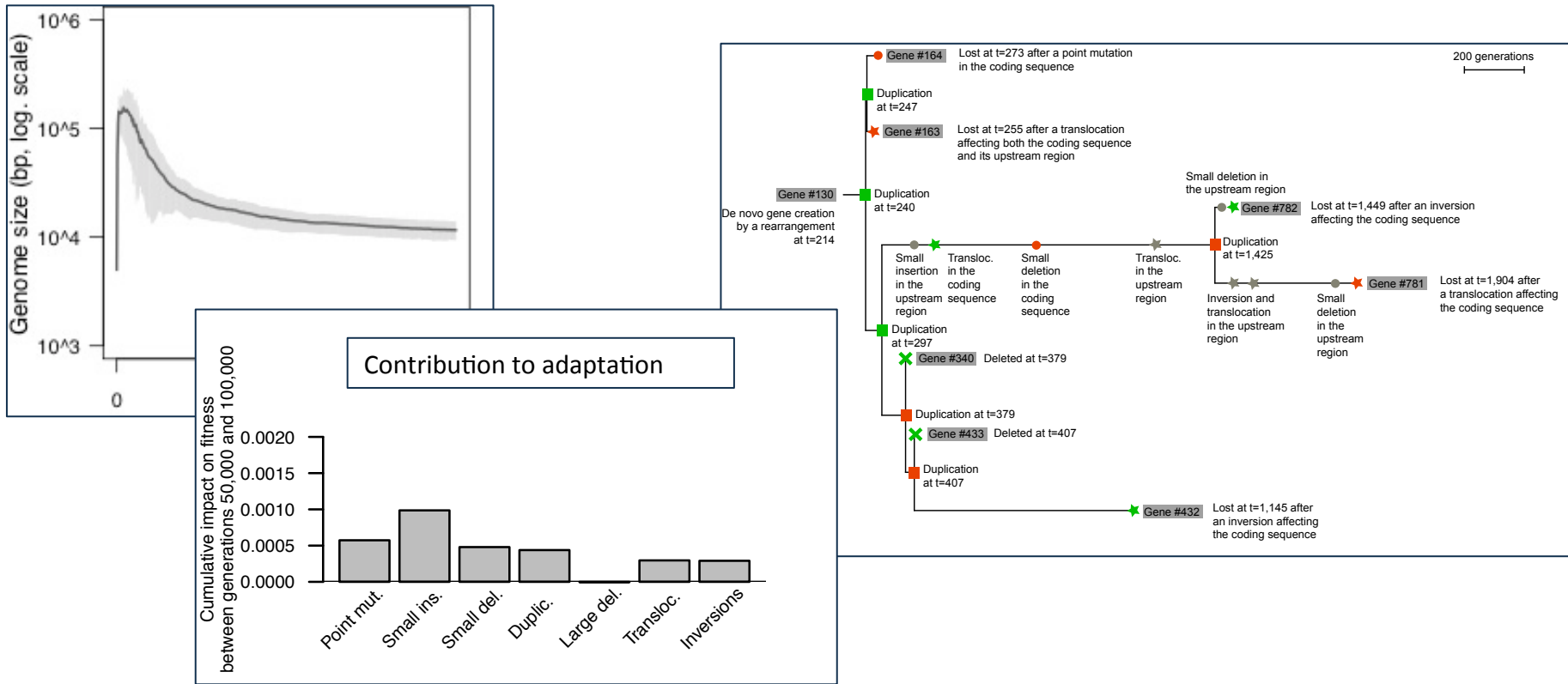
Analyzing the evolutionary trajectories

```
aevol_misc_lineage -b 0 -e 2000
```

```
aevol_misc_ancstats -f lineage-b000000-e002000-i628-r1000.ae
```

```
aevol_misc_fixed_mutations -f lineage-b000000-e002000-i628-r1000.ae
```

```
aevol_misc_gene_families -f lineage-b000000-e002000-i628-r1000.ae
```



To do

- Improve the gene_families tool to follow the fate of pseudogenes
- Allow for user-defined, gene-targeted mutations in the mutagenesis tool?
- R-aevol : resurrect the “knockout” tool
- Write an “epistasis” tool (double mutants)
- Write a “competition” tool
- Write a “fitness landscape” tool -- possible?

And in the other models of the project?

- Tracking the fate of genes: in principle easier in POAS-like models
- Knockout, mutagenesis.....: how to measure the effect of mutations when there is no explicit fitness measure? ==> invasion experiments?