

Evolution of demographic parameters and population stability

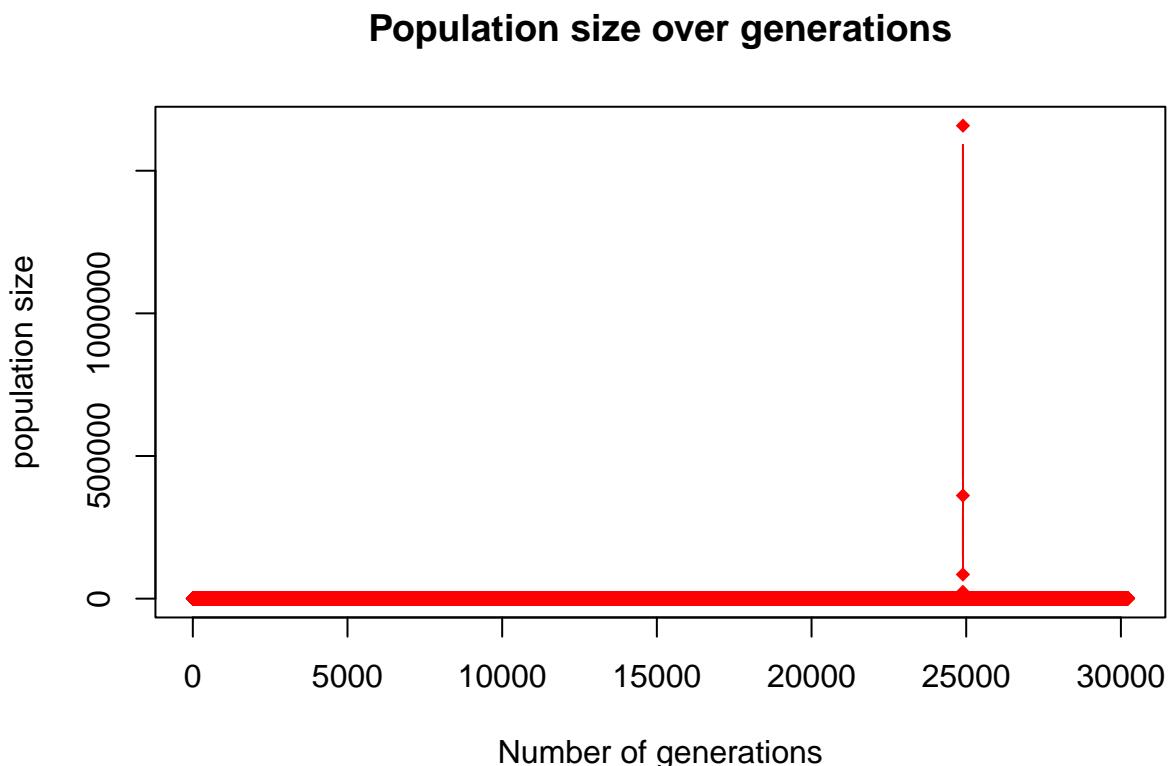
Computational biology project by Bianca BOI and Anne STAFF

Some plots:

We left an endless loop running in a background process over night saving the resulting values to a textfile in order to retrieve it after we kill the process manually. This way we managed to get more than 30.000 generations!

To reproduce this, simply run “over-night-code.R” (it is initialised with a seed of 420) for approx. 8h.

```
plot(1:x,
  gen$N,
  type="b",
  pch=18,
  col="red",
  xlab="Number of generations",
  ylab="population size",
  main="Population size over generations")
```



We display the size of the population through generations. We can see that there is a big peak around the

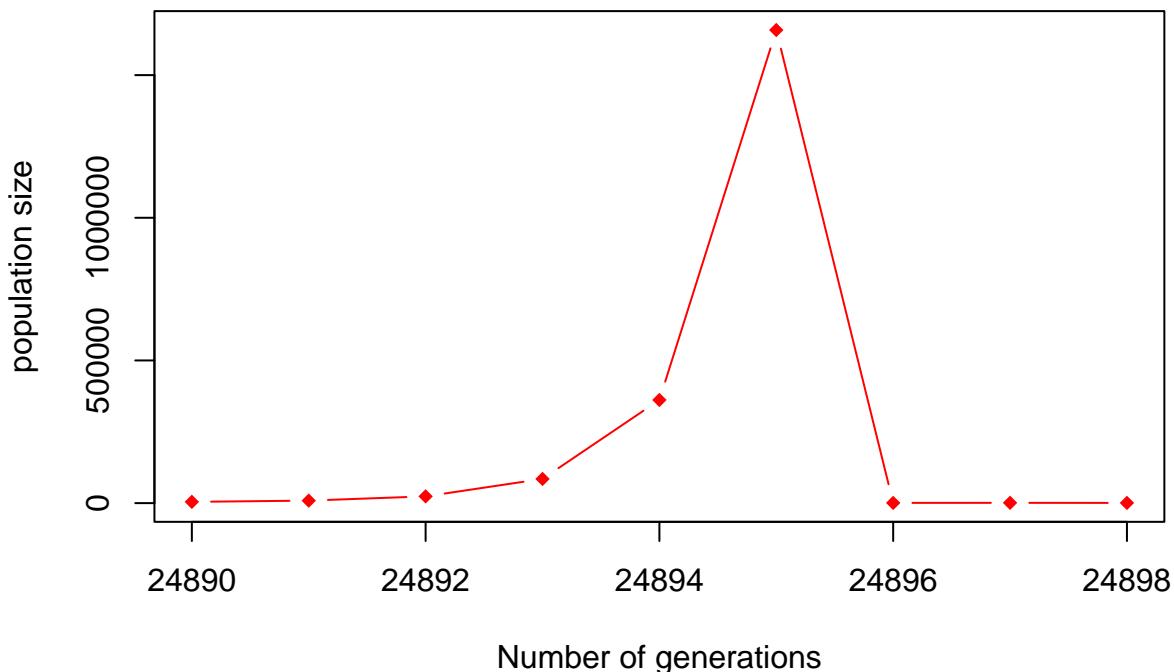
25000th generation. This peak is a bit strange and we will try to explain it thanks to other graphs.

```

plot(24890:24898,
     gen$N[24890:24898] ,
     type="b",
     pch=18,
     col="red",
     xlab="Number of generations",
     ylab="population size",
     main="Population size (zoom on the weird peak)")

```

Population size (zoom on the weird peak)



Some numbers for clarity (or confusion, that's up to the viewer to judge):

```
gen[24890:24898,]
```

```

##          N   K_means      K_sd lambda_means  lambda_sd    c_means
## 24890  4433 950.0514  0.060322402    4.576651 0.24444125  1.482215
## 24891  8760 950.0540  0.048046974    4.634170 0.21372629  1.556921
## 24892 23697 950.0545  0.035395564    4.687163 0.16768733  1.621690
## 24893 84798 950.0544  0.026806192    4.718118 0.12680991  1.661082
## 24894 361512 950.0535  0.023274423    4.733562 0.09955824  1.678128
## 24895 1657970 950.0530  0.021785928    4.739432 0.08554585  1.685728
## 24896   801 950.0005  0.004539574    1.499320 0.00576356 -2.000869
## 24897  1051 950.0002  0.005003638    1.498036 0.01418426 -2.000277
## 24898   724 950.0002  0.004666904    1.499646 0.01890517 -1.998070
##          c_sd fitness_means  fitness_sd           r
## 24890 0.274408802    1.9637766  0.572223950    4.6660635
## 24891 0.236612076    2.6651119  0.737620565    9.2205290
## 24892 0.181627310    3.5772392  0.754209446   24.9427792

```

```

## 24893 0.130415915      4.2700505 0.569596143    89.2559413
## 24894 0.097755758      4.5837443 0.361578280    380.5175026
## 24895 0.081173533      4.6903928 0.226683100   1745.1341310
## 24896 0.007371190      1.3539614 0.001829542     0.8431574
## 24897 0.008600425      0.6688268 0.002804792     1.1063155
## 24898 0.020186655      1.4371259 0.011544347     0.7621051

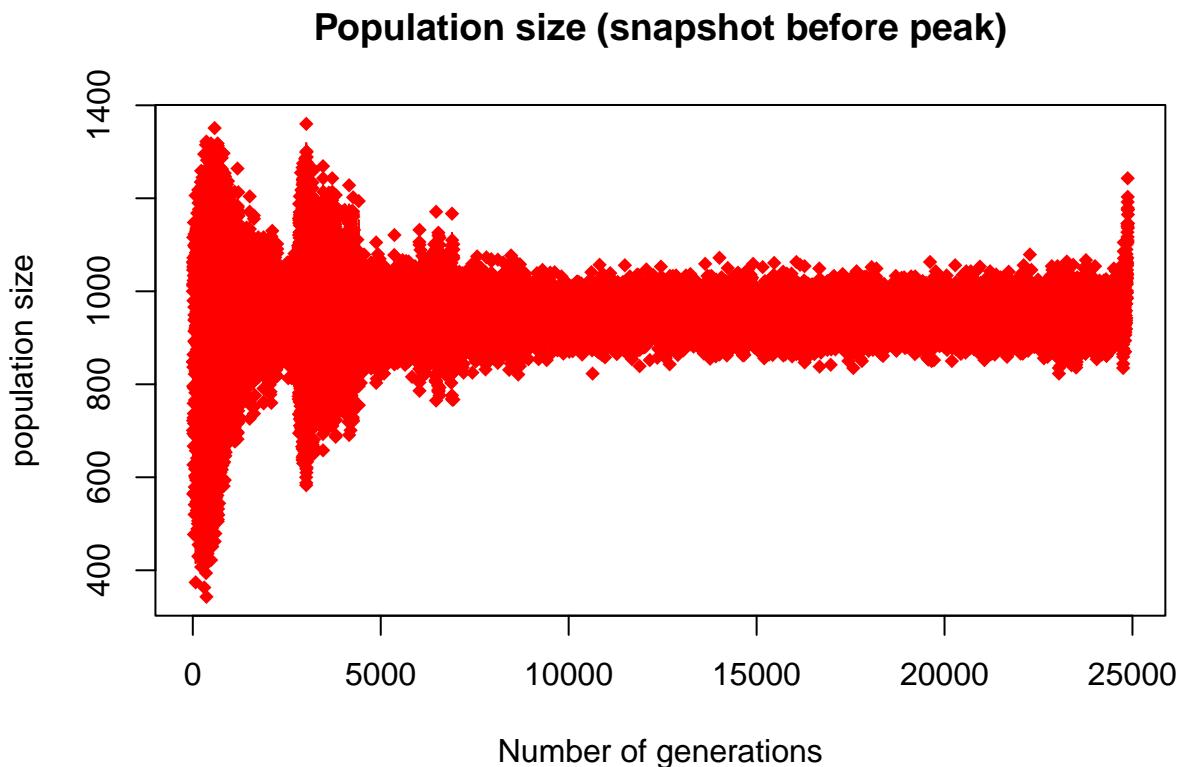
```

We see that the number of individuals is the highest at the 24895th generation, and right after it decrease abruptly. some values as K mean are not much evolving but, the C and the fitness are changing much we will see this later.

```

plot(1:24880,
      gen$N[1:24880],
      type="b",
      pch=18,
      col="red",
      xlab="Number of generations",
      ylab="population size",
      main="Population size (snapshot before peak)")

```



Before the big peak the population tend to stabilize around 1000 individuals.

```

# plot the relative density of population with mutation
plot(1:x,
      gen$r,
      type="b",
      pch=20,
      col="blue",

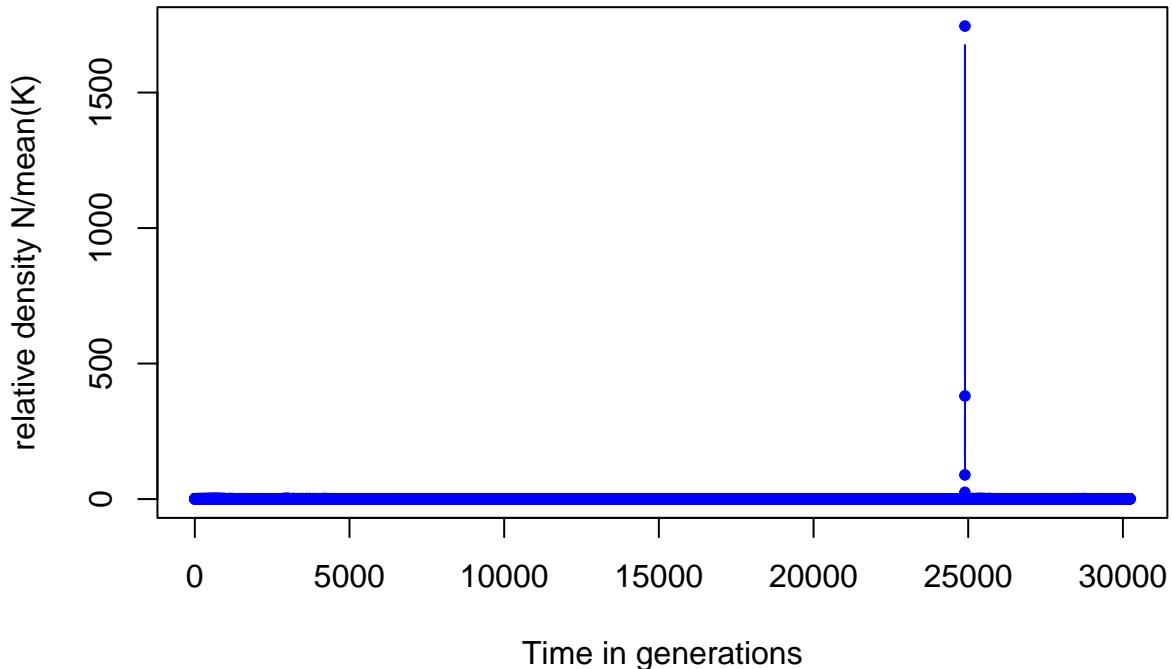
```

```

xlab="Time in generations",
ylab="relative density N/mean(K)",
main="Evolution of the relative density over generations")

```

Evolution of the relative density over generations



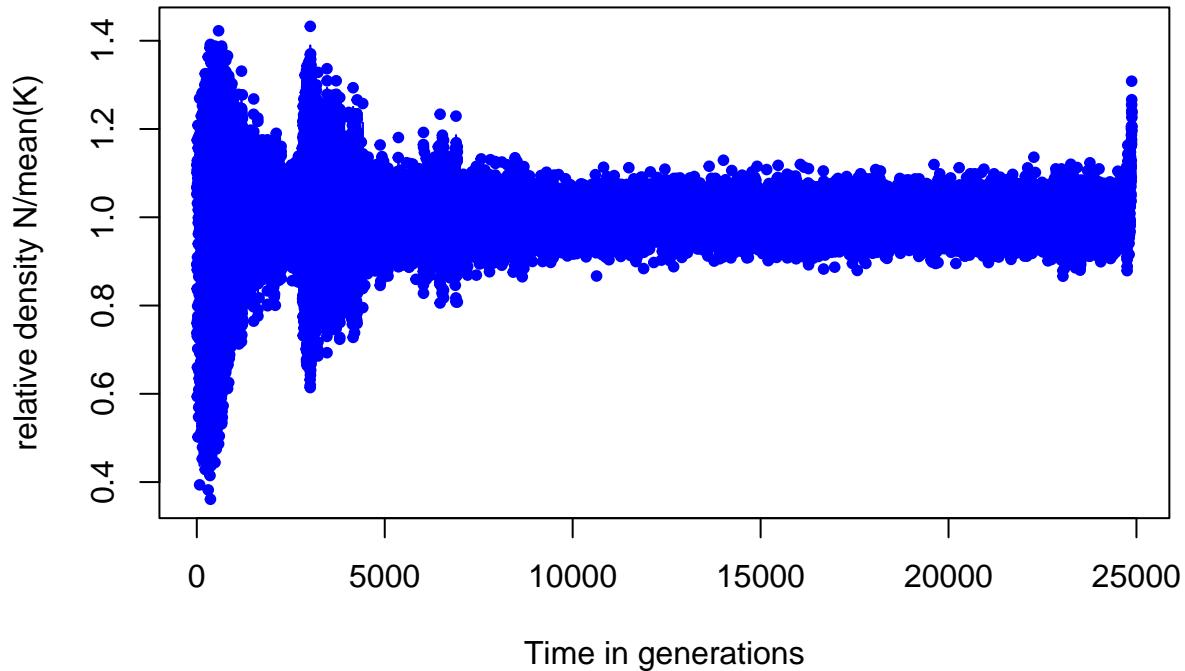
The relative density follow the same problem, there is a big peak around the 25000th generation. the rest tend to stabilize around a very low value.

```

# plot the relative density of population with mutation
plot(1:24880,
      gen$r[1:24880],
      type="b",
      pch=20,
      col="blue",
      xlab="Time in generations",
      ylab="relative density N/mean(K)",
      main="Evolution of the relative density (snapshot before peak)")

```

Evolution of the relative density (snapshot before peak)



As in the paper, the relative density starts out pretty chaotically but then stabilize around 1.

This function plots the mean values of the traits we monitored along with their corresponding standard deviation:

```
plot_mean_with_sd <- function(means,
                                sd,
                                interval=NULL,
                                xlab="Time in generations",
                                ylab=NULL,
                                main=NULL)
{
  if (is.null(interval)) {
    interval <- 1:length(means)
  }
  plot(interval,
        means[interval],
        type = 'l',
        col="blue",
        ylim=c(min(means-sd), max(means+sd)),
        xlab=xlab,
        ylab=ylab,
        main=main)

  polygon(c(rev(interval), interval),
          c(rev(means[interval]-sd[interval]),
            means[interval]+sd[interval])),
          col = 'grey80', border = NA)

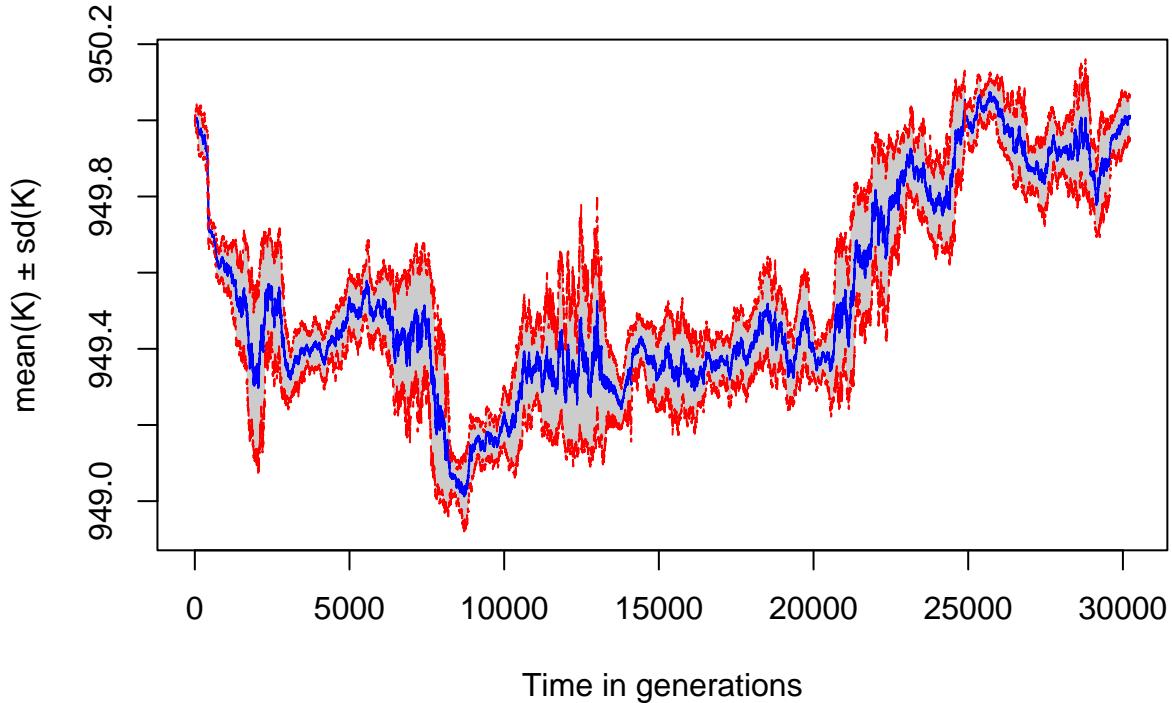
  lines(interval, means[interval], col="blue")
  lines(interval, means[interval]-sd[interval], lty = 'dashed', col = 'red')
  lines(interval, means[interval]+sd[interval], lty = 'dashed', col = 'red')
}
```

```

plot_mean_with_sd(gen$K_means,
                  gen$K_sd,
                  ylab="mean(K) \u00B1 sd(K)",
                  main="Mean equilibrium density per generation and their standard deviation")

```

Mean equilibrium density per generation and their standard deviation



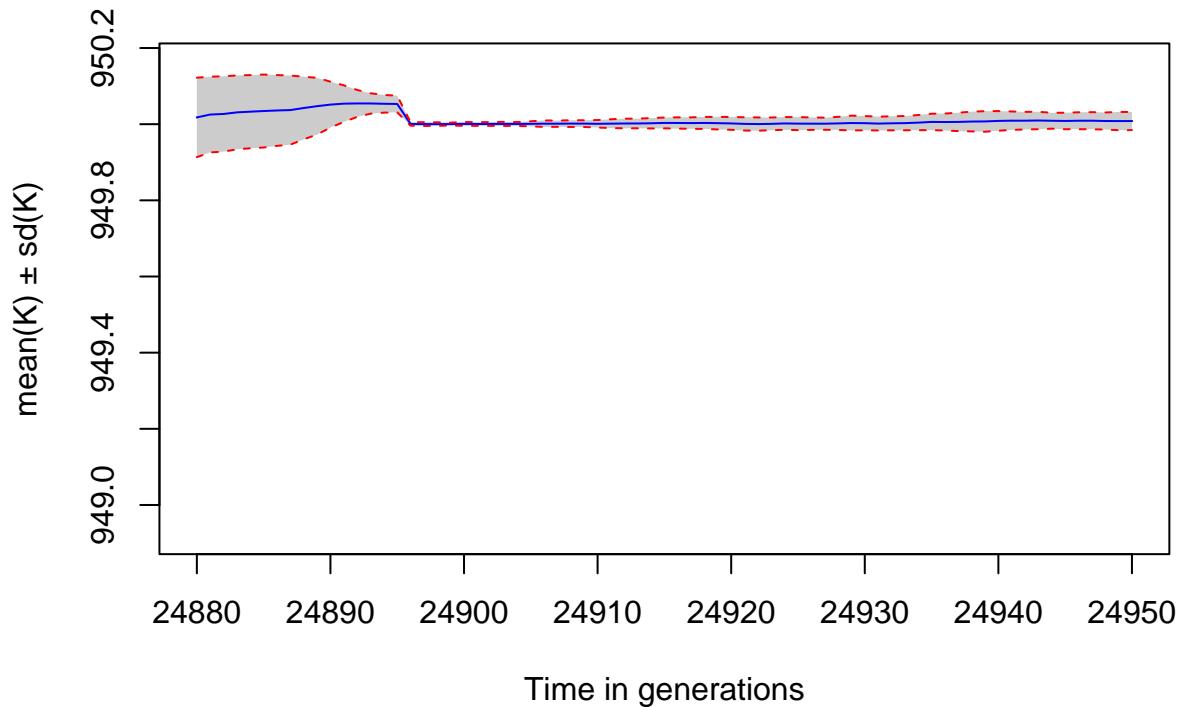
The mean equilibrium density (K) are always between 949 and 950 as we have seen in the tabs, its value is not evolving that much. The standard deviation of K is pretty close to the mean value.

```

plot_mean_with_sd(gen$K_means,
                  gen$K_sd,
                  interval = 24880:24950,
                  ylab="mean(K) \u00B1 sd(K)",
                  main="Equilibrium density (zoom around peak)")

```

Equilibrium density (zoom around peak)



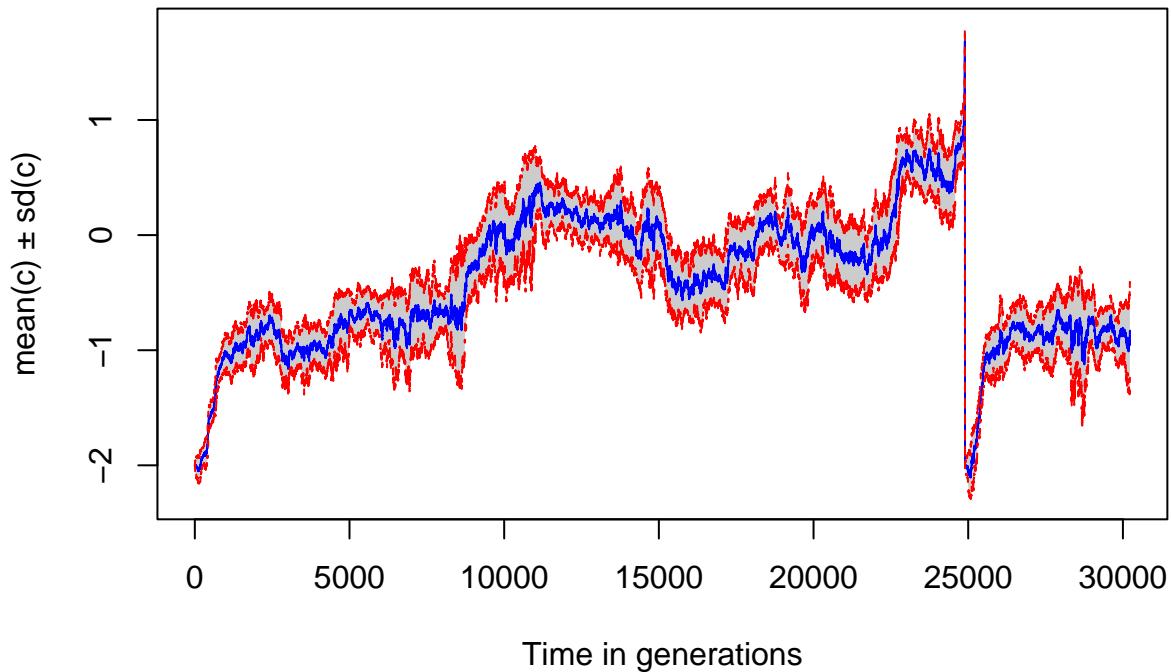
The equilibrium density has a little decrease around the peak value, and we can see that the standard derivation become closer to the mean value at the peak.

```

plot_mean_with_sd(gen$c_means,
                  gen$c_sd,
                  ylab="mean(c) \u00B1 sd(c)",
                  main="Mean complexity per generation and their standard deviation")

```

Mean complexity per generation and their standard deviation



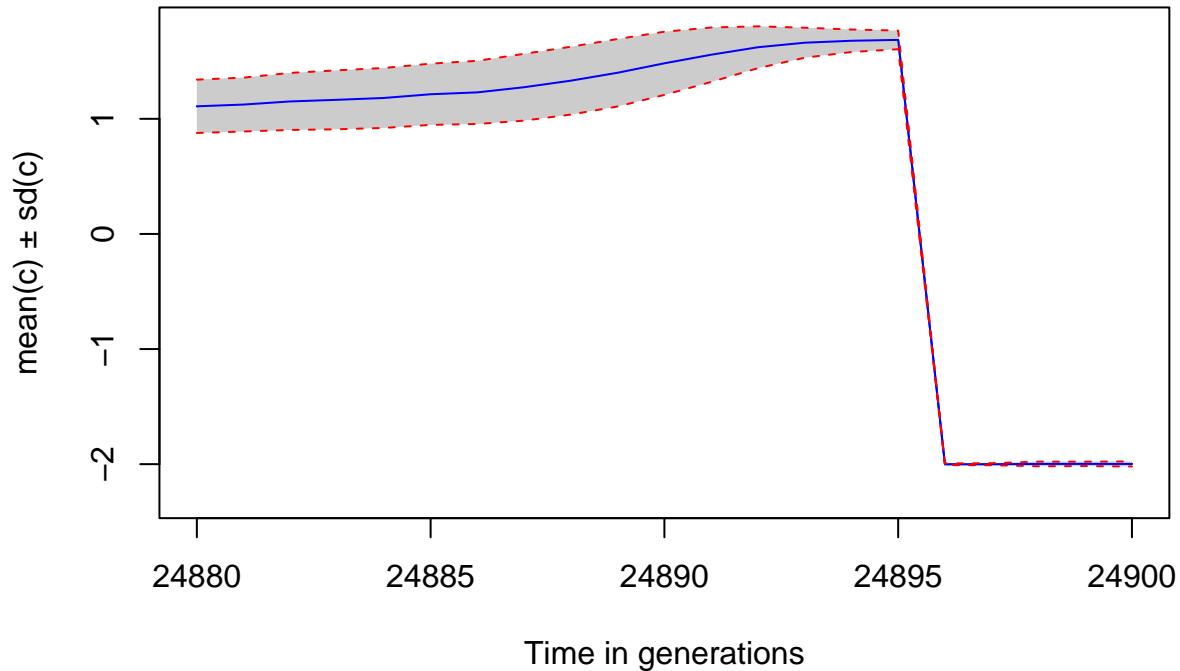
The mean complexity per generation is most of the time between -1 and 1 but has a big decrease around the 25000th generation. the value pass from 1 to -2 which is a huge gap.

```

plot_mean_with_sd(gen$c_means,
                  gen$c_sd,
                  interval=24880:24900,
                  ylab="mean(c) \u00B1 sd(c)",
                  main="Complexity (zoom around peak)")

```

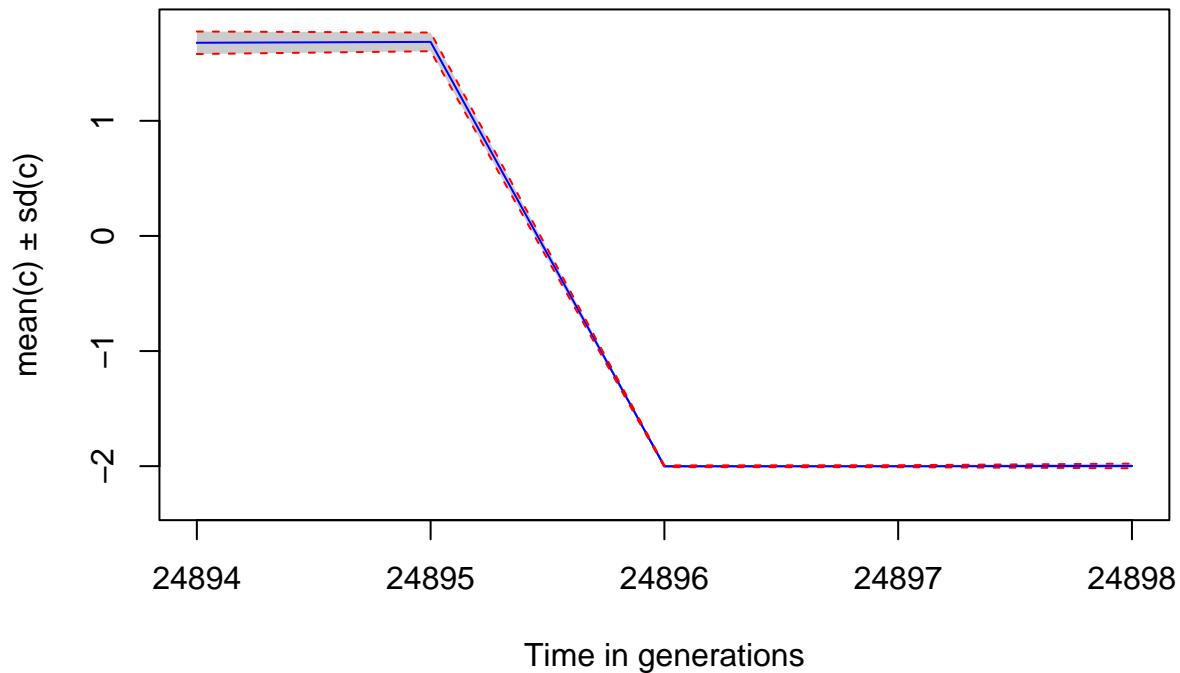
Complexity (zoom around peak)



To see it more in details we've done a zoom on the big decrease. The value seems constant before the 24895th generation then the standard deviation become closer and closer from the mean value and there is a big decrease. The value falls to -2 abruptly.

```
plot_mean_with_sd(gen$c_means,
                   gen$c_sd,
                   interval=24894:24898,
                   ylab="mean(c) \u00B1 sd(c)",
                   main="Complexity (closer zoom around peak)")
```

Complexity (closer zoom around peak)

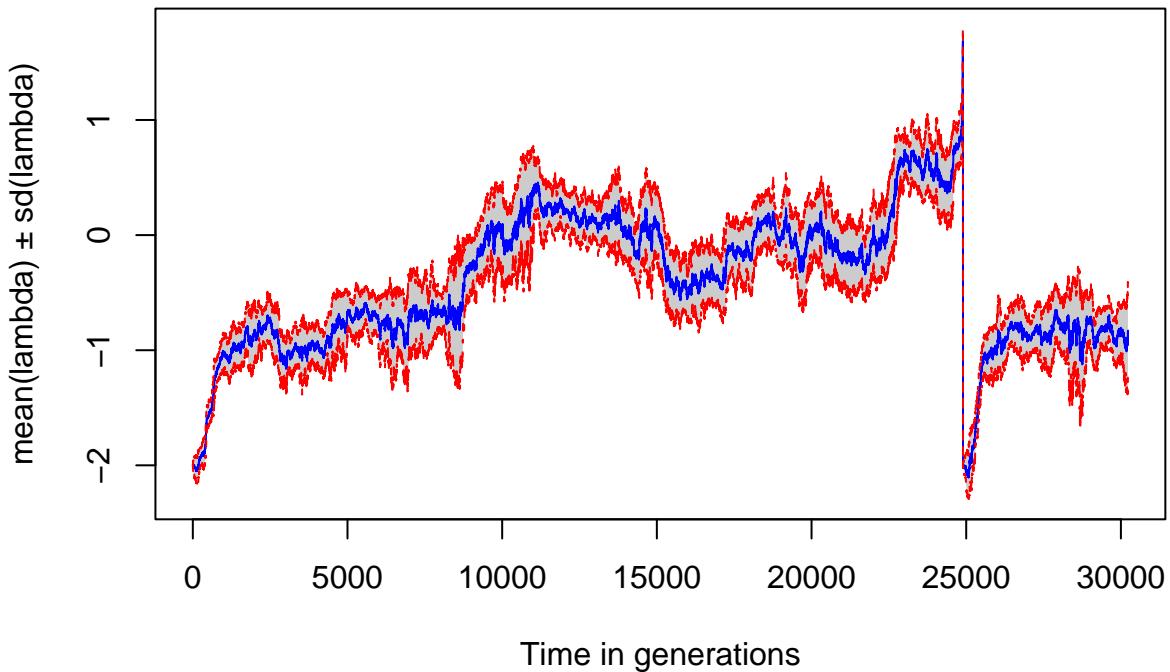


```

plot_mean_with_sd(gen$c_means,
                  gen$c_sd,
                  ylab="mean(lambda) \u00B1 sd(lambda)",
                  main="Mean growth rate per generation and their standard deviation")

```

Mean growth rate per generation and their standard deviation



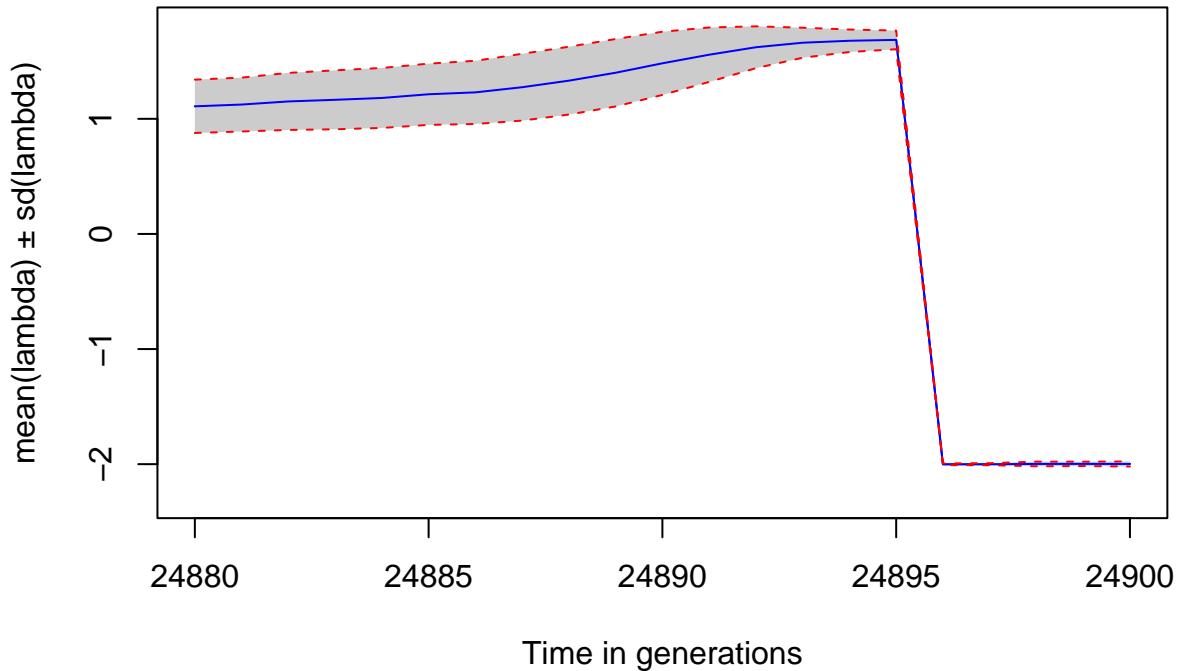
As for the mean complexity per generation, the mean growth rate per generation knows also a big decrease around the 25000th generation. The curve looks approximately the same as the previous one.

```

plot_mean_with_sd(gen$c_means,
                  gen$c_sd,
                  interval = 24880:24900,
                  ylab="mean(lambda) \u00B1 sd(lambda)",
                  main="Growth rate (zoom around peak)")

```

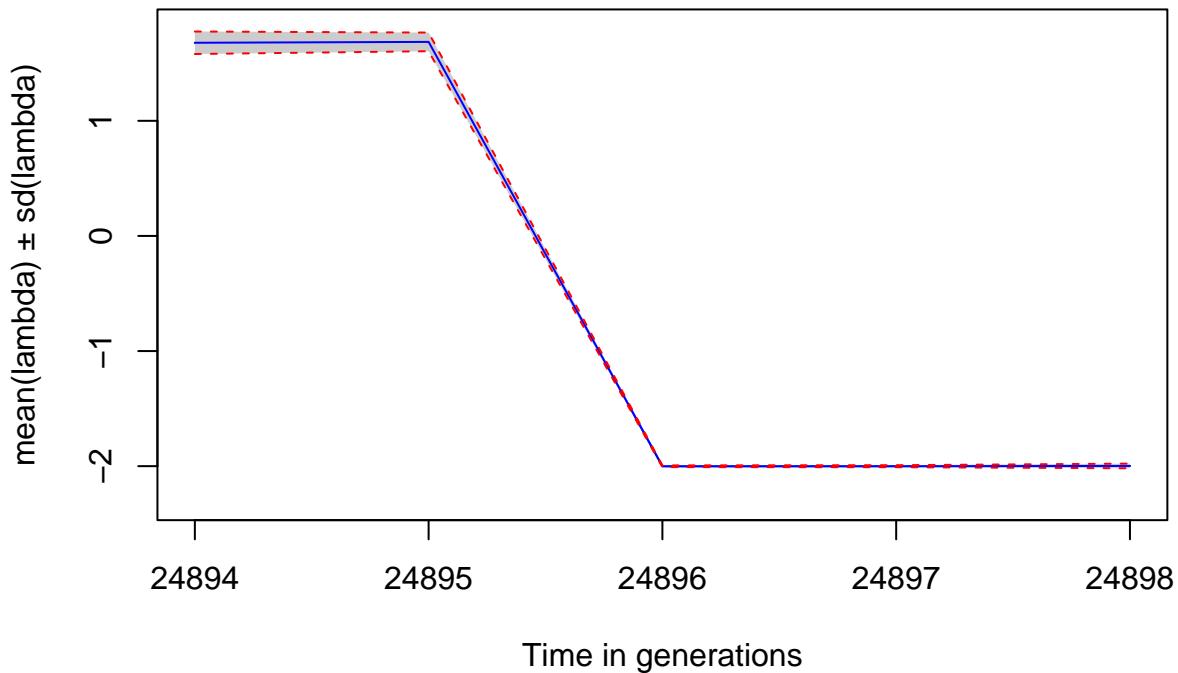
Growth rate (zoom around peak)



The values go from 1 to -2 and the standard derivation is also becoming closer and closer to the mean value when we are closer from the big decrease.

```
plot_mean_with_sd(gen$c_means,
                   gen$c_sd,
                   interval = 24894:24898,
                   ylab="mean(lambda) \u00B1 sd(lambda)",
                   main="Growth rate (closer zoom around peak)")
```

Growth rate (closer zoom around peak)

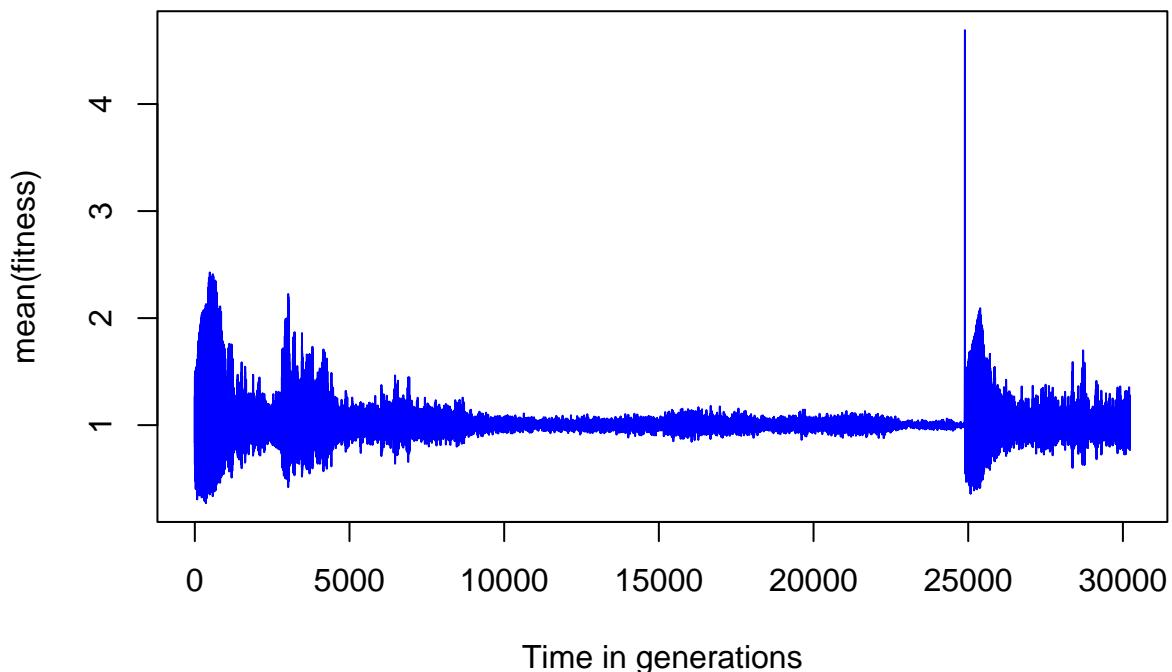


```

plot(1:x,
  gen$fitness_means,
  type = 'l',
  col="blue",
  xlab="Time in generations",
  ylab="mean(fitness)",
  main="Mean fitness per generation")

```

Mean fitness per generation



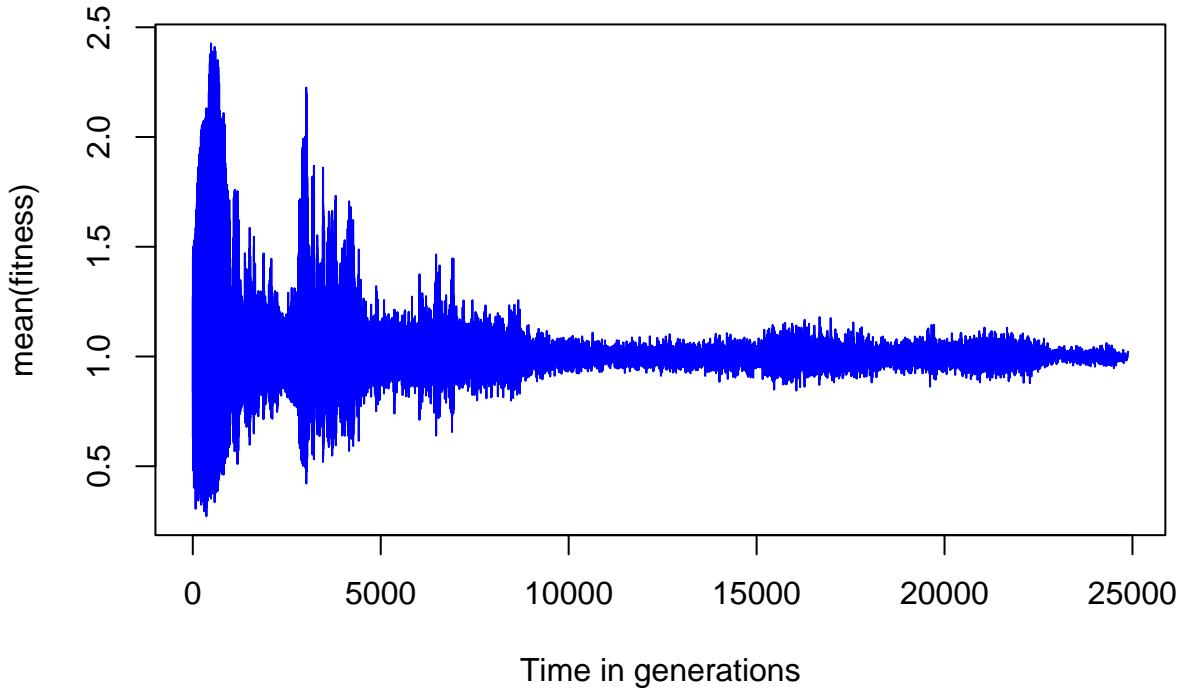
The mean fitness is at the beginning really heterogeneous then tend to stabilize around 1 but knows a big peak always at the same generation and the values are again heterogeneous (but will probably tend to stabilize back).

```

plot(1:24880,
  gen$fitness_means[1:24880],
  type = 'l',
  col="blue",
  xlab="Time in generations",
  ylab="mean(fitness)",
  main="Mean fitness per generation (snapshot before peak)")

```

Mean fitness per generation (snapshot before peak)



we see more in details the way that the fitness tend to stabilize around 1. This result is exactly the same than the one in the paper.

Moreover the big “peak” that we’ve meet in the experiment is probably linked to the way we’ve distributed the number of offspring per individuals. This is following a Poisson law and could absolutely take a high or low value, which could explain those results.