

Evolution of demographic parameters and population stability

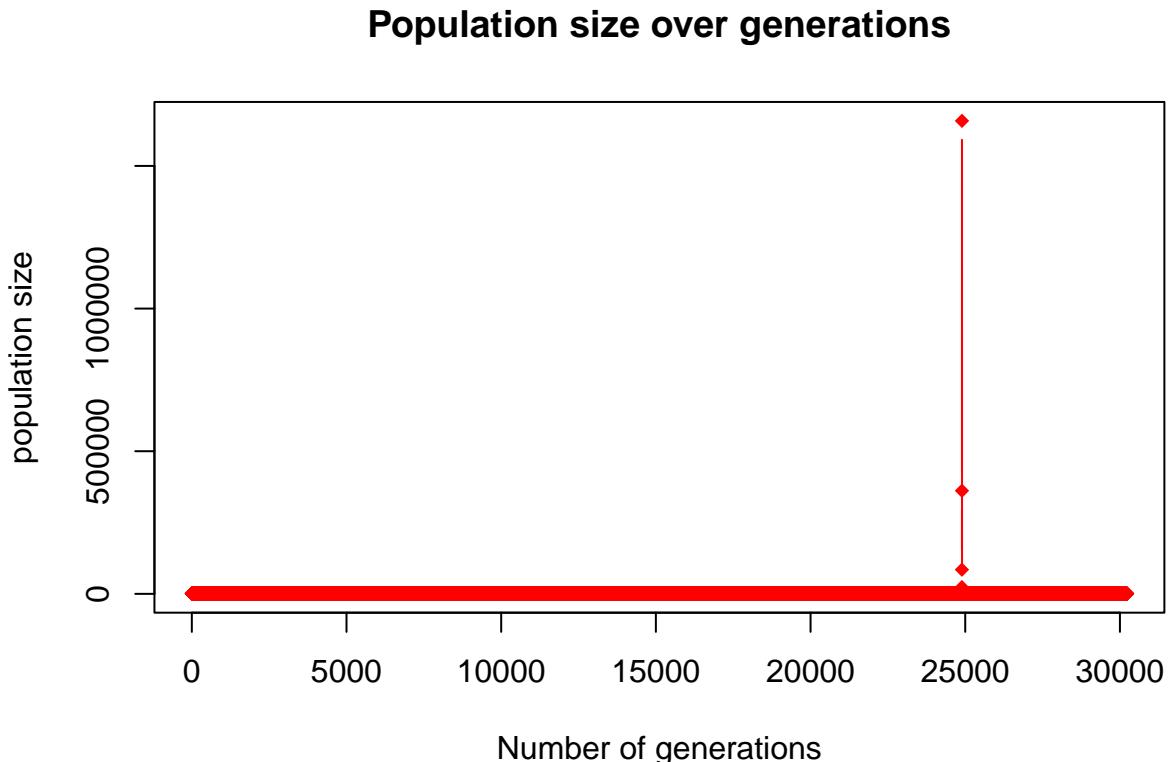
Computational biology project by Bianca BOI and Anne STAFF

Some plots:

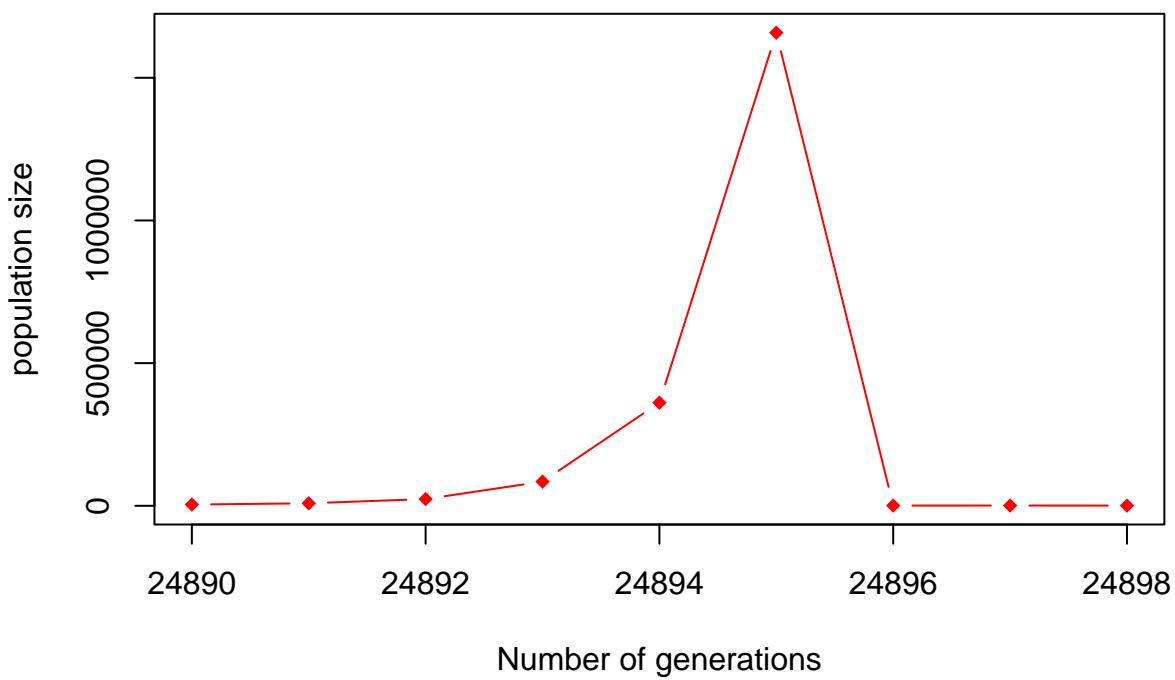
We left an endless loop running in a background process over night saving the resulting values to a textfile in order to retrieve it after we kill the process manually. This way we managed to get as many as over 30.000 generations!

To reproduce this, simply run “CopyOfmain.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")
```



```
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)")
```



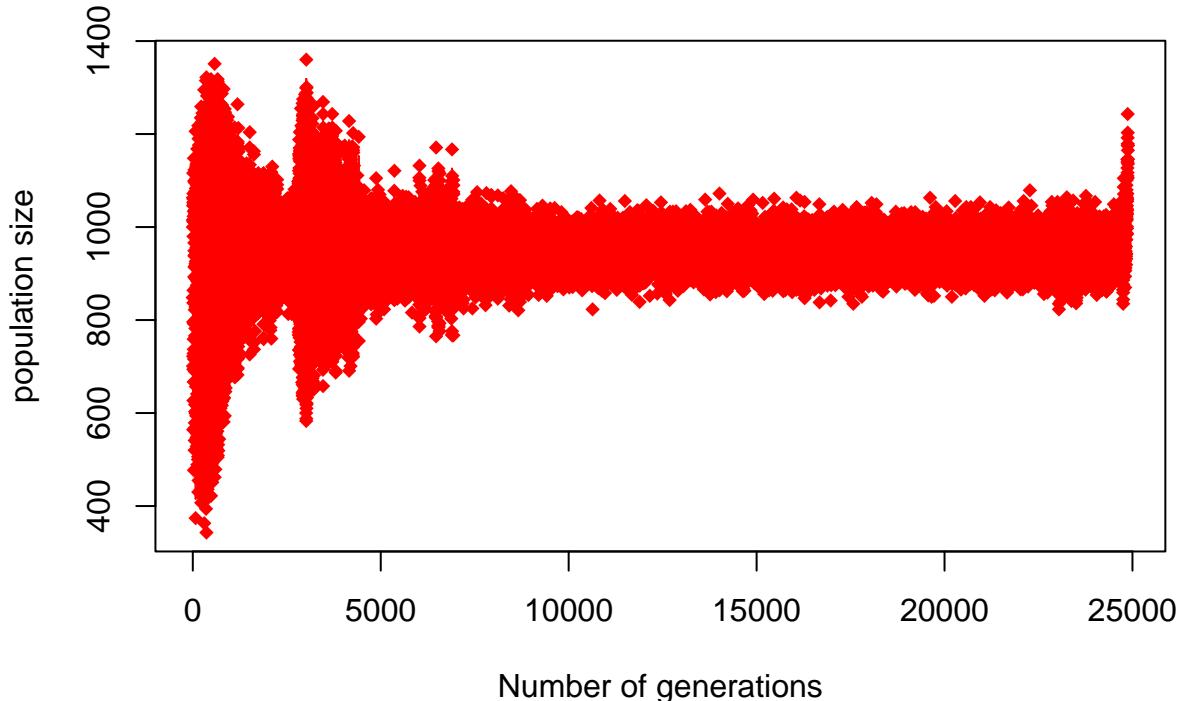
Some numbers for clarity (or confusion, that's up to the viewer to judge):

```
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
```

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

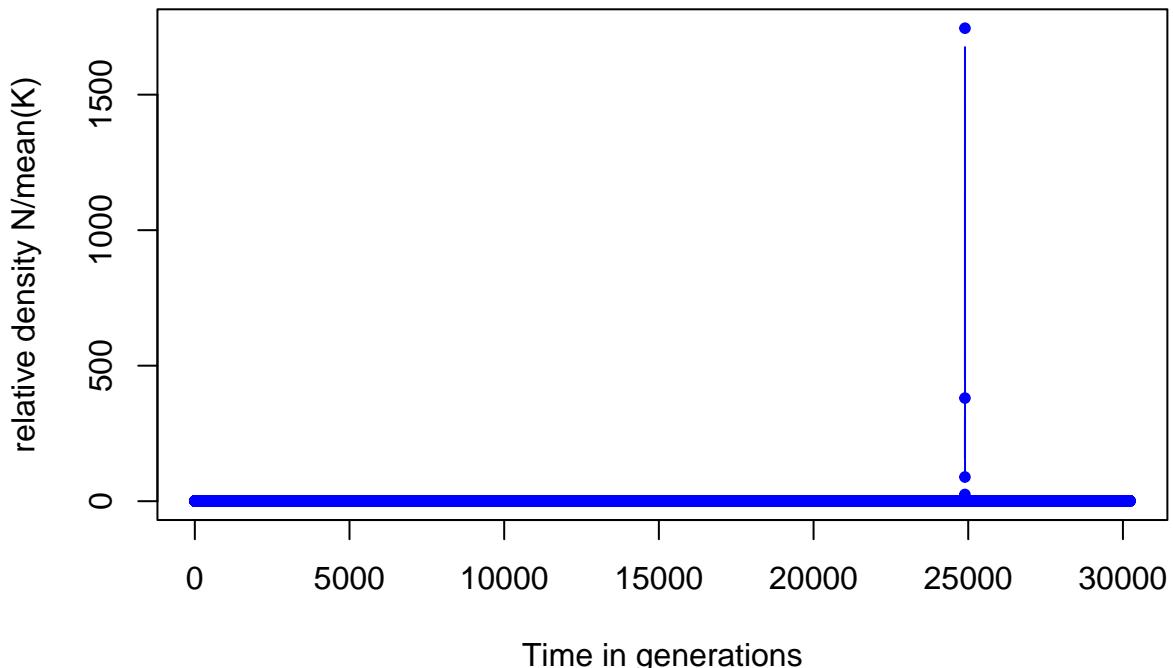
Population size (snapshot before peak)



```
# 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")
```

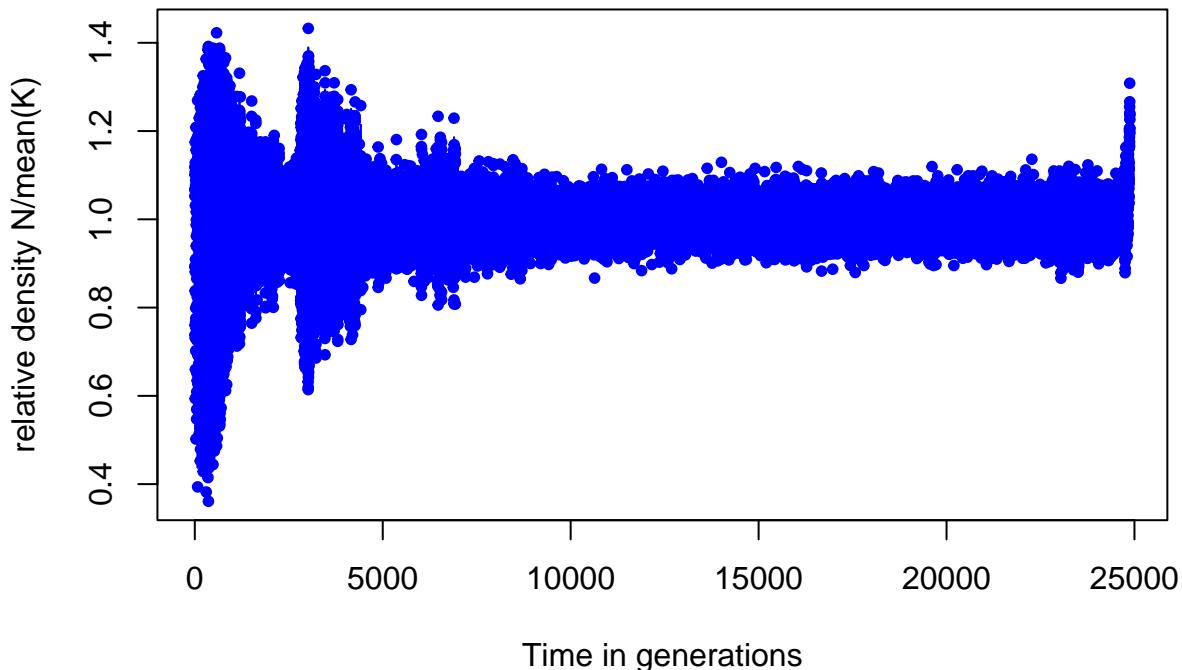
Evolution of the relative density over generations



```
# 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")
```

Evolution of the relative density (snapshot before peak)



As in the paper, the relative density starts out pretty chaotically but then stabilises 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)

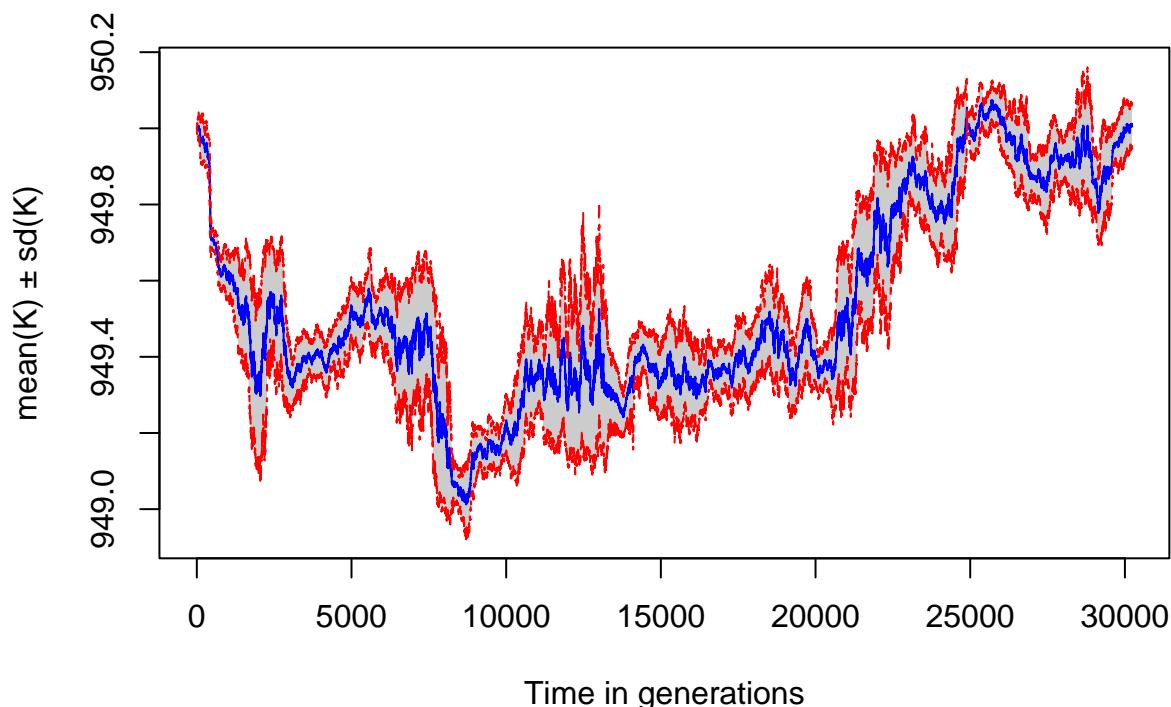
  lines(interval, means[interval], col="blue")
  lines(interval, means[interval]-sd[interval], lty = 'dashed', col = 'red')
  lines(interval, means[interval]+sd[interval], lty = 'dashed', col = 'red')
}
```

```

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

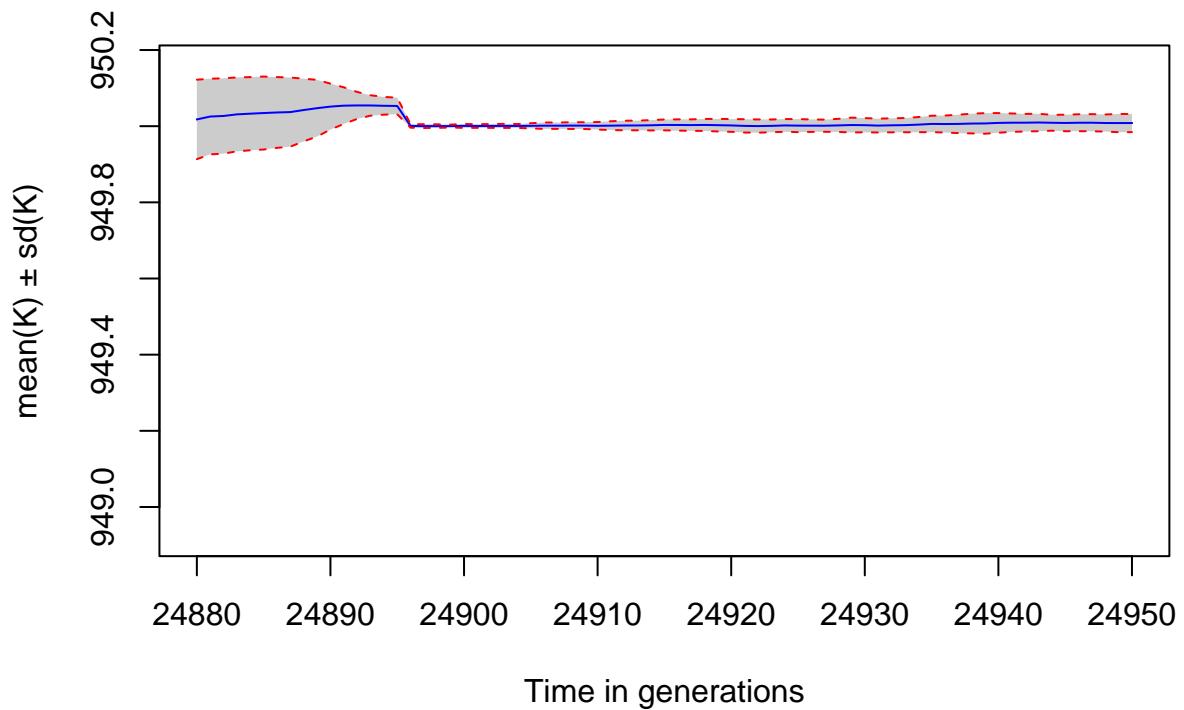


```

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)

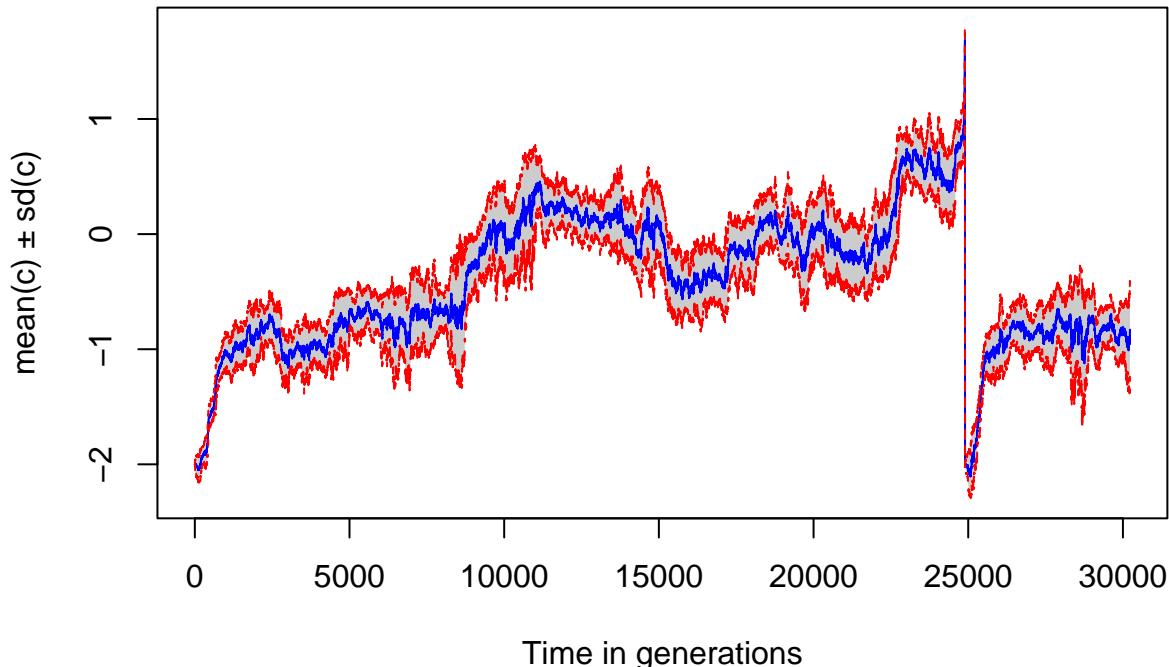


```

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

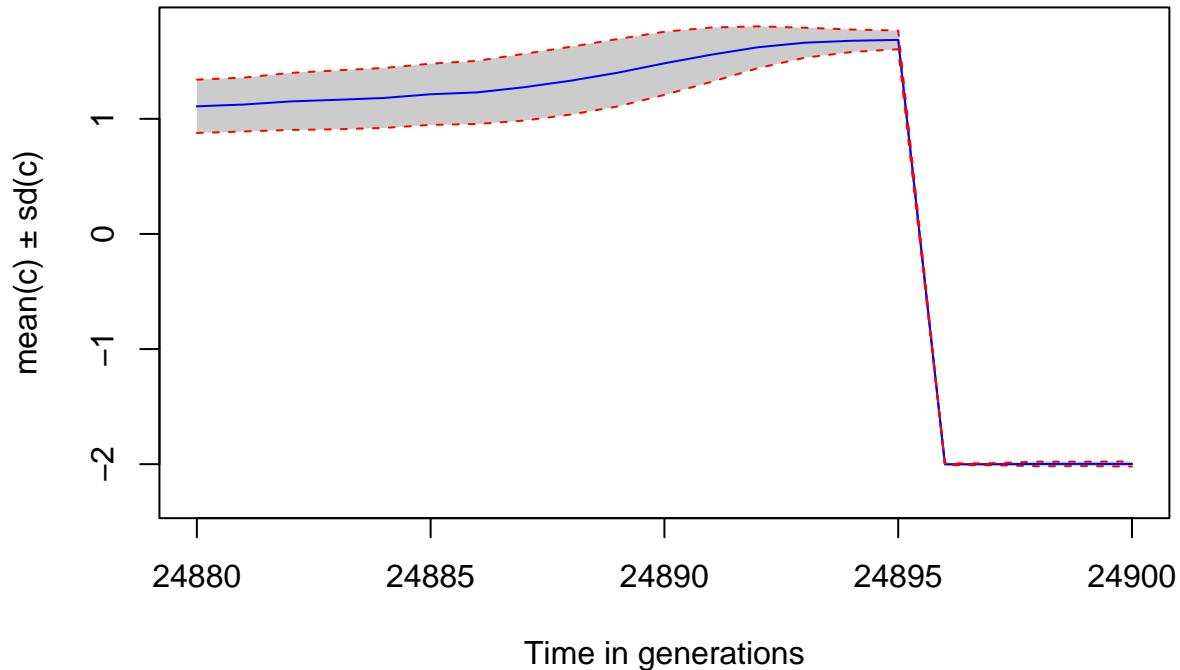


```

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

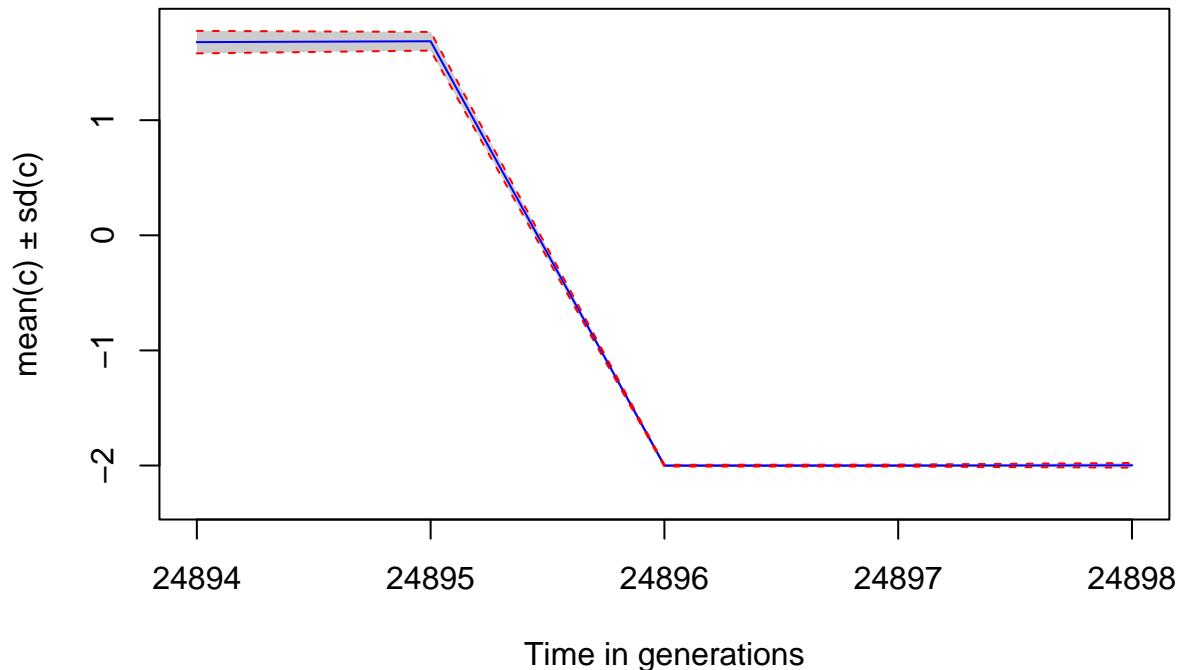
```

Complexity (zoom around peak)



```
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)

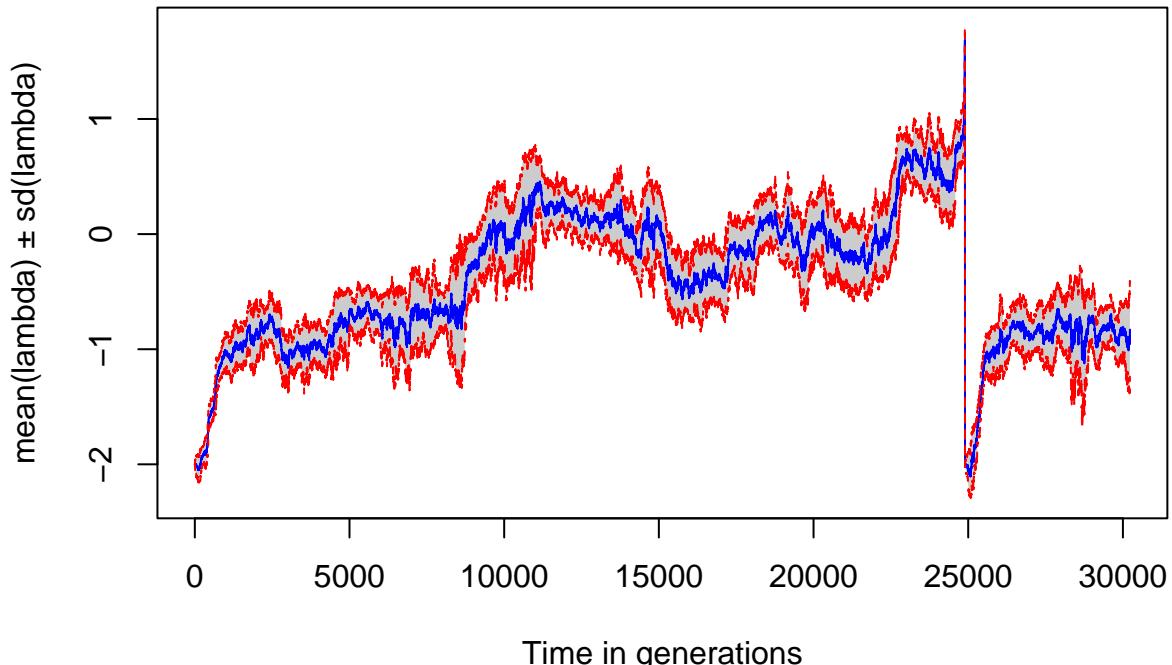


```

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

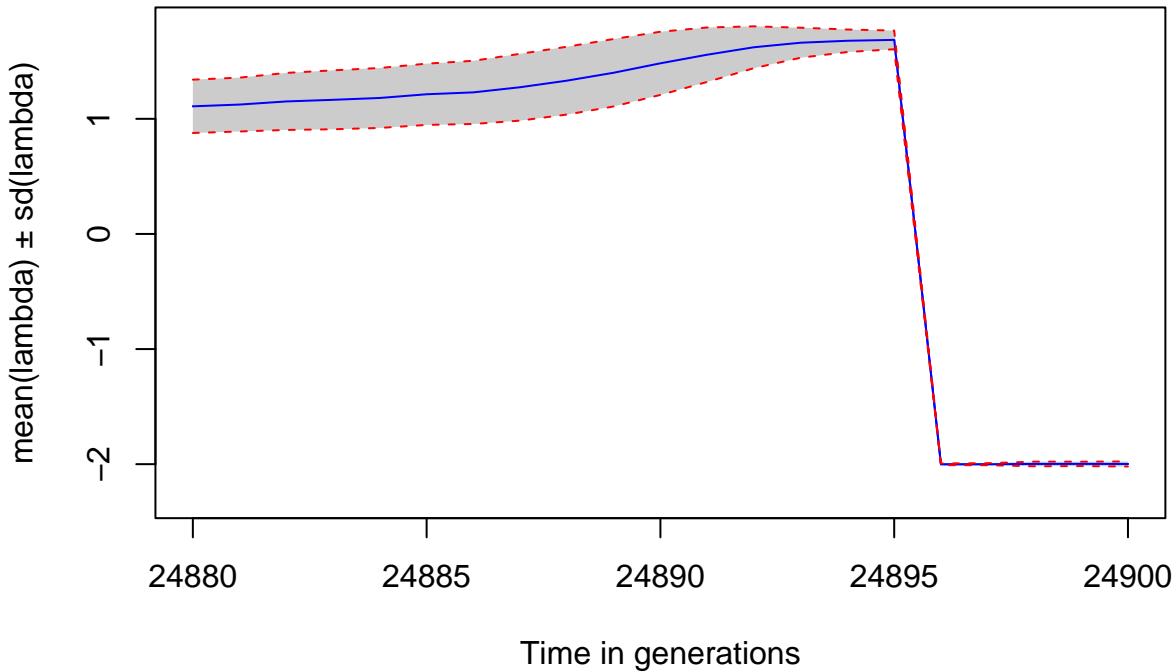


```

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)")

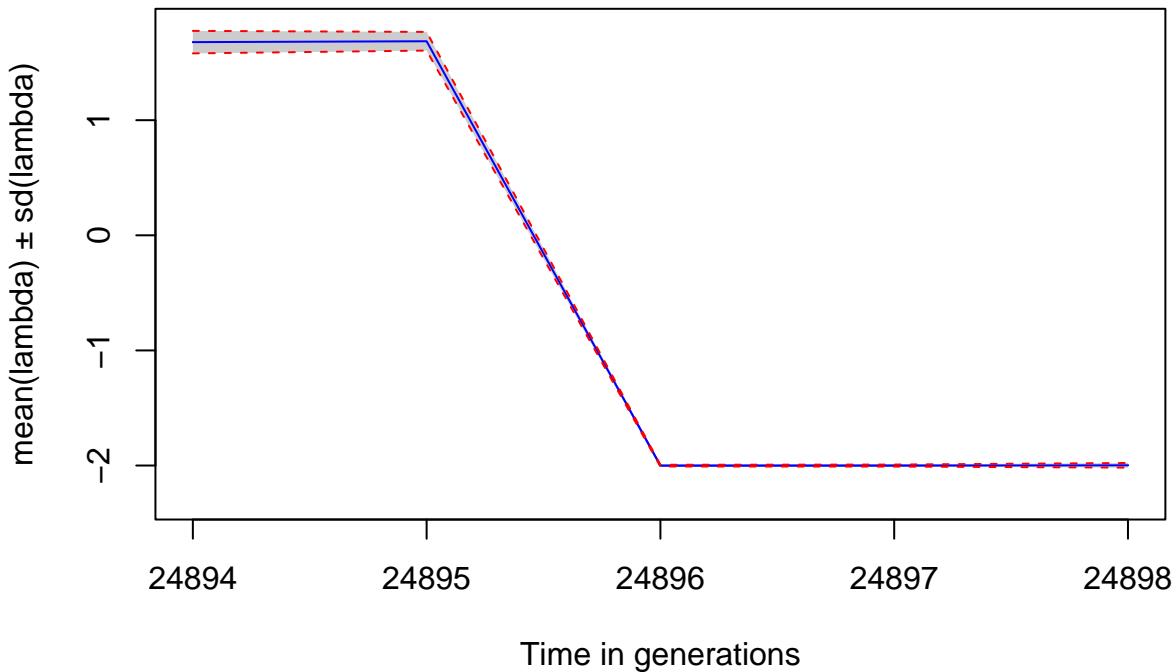
```

Growth rate (zoom around peak)



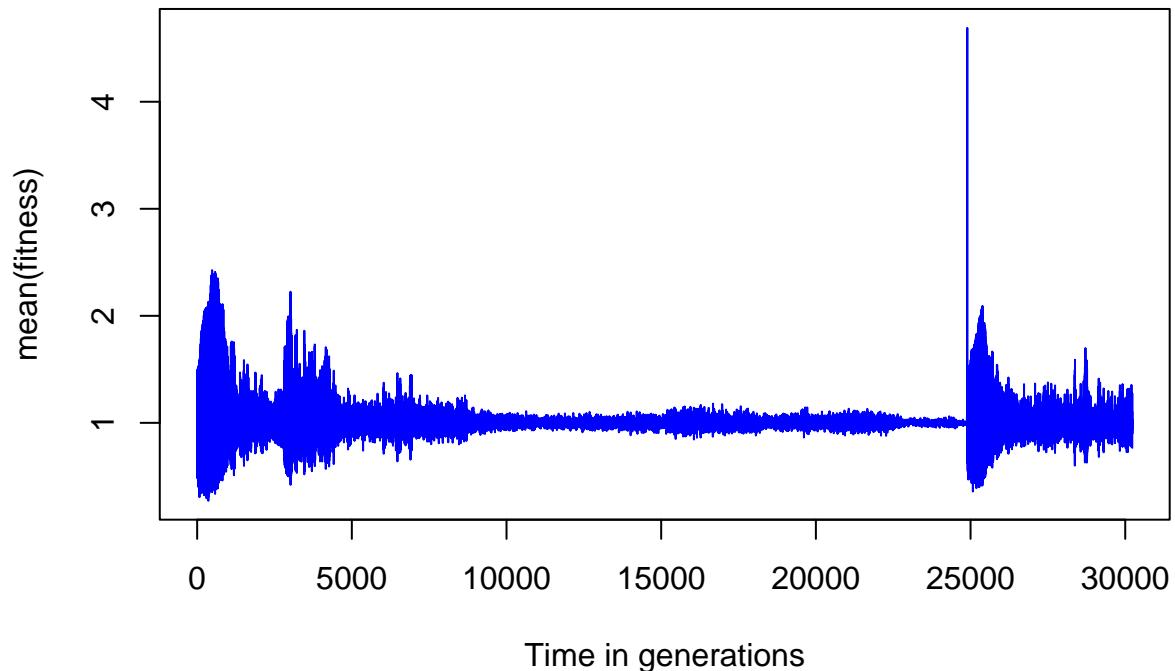
```
plot_mean_with_sd(gen$c_means,
                   gen$c_sd,
                   interval = 24894:24898,
                   ylab="mean(lambda) \u00B1 sd(lambda)",
                   main="Growth rate (closer zoom around peak)")
```

Growth rate (closer zoom around peak)



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

Mean fitness per generation



```
plot(1:24880, gen$fitness_means[1:24880], type = 'l', col="blue", xlab="Time in generations", ylab="mean(fitness)", ...)
```

Mean fitness per generation (snapshot before peak)

