

# Evolution of demographic parameters and population stability

Code ▾

Computational biology project by Bianca BOI and Anne STAFF

Hide

```
set.seed(42)
library(tidyverse)
```

## Our model

We initialise the model with the following values:

Hide

```
# initial values
K <- 950 # equilibrium density, we interpreted "relaitevly small" as being close to the initi
al total density
lambda <- 1.5 # growth rate, also "relatively small"
N_init <- 1000 # initial total density
c <- -2 # complexity, less than -1
mu <- 0.01 # mutation rate, given
# we will define later r as the relative density à savoir N/mean(K)

# population initiale
population <- data.frame(K=rep(K, N_init), lambda=rep(lambda, N_init), c=rep(c, N_init))
```

We define a function that calculates the fitness value from the given traits:

Hide

```
# calculate fitnesses
calc_fitness <- function(N, K, lambda, c) {
  # make sure we're not accidentally dividing by 0
  if (any(lambda == 1)) {
    lambda <- 1.0000000001
  }
  res <- lambda / (1 + (lambda - 1)*((N/K)**((1-c)*lambda/(lambda-1))))
  return(res)
}
# test
# with(population[1,], calc_fitness(N_init, K, lambda, c))
```

We calculte the initial fitness values for our initial population:

Hide

```
# run
fitness <- with(population[1,], calc_fitness(N_init, K, lambda, c))
population$fitness <- rep(fitness, N_init)
```

We define a function that creates the offspring from one individual

Hide

```
# offspring per individual without mutation
offspring <- function(individual) {
  n_offspring <- rpois(1, individual[4])
  if (is.na(n_offspring)) {
    return(vector())
  } else {
    offspring <- data.frame(K=rep(individual[1], n_offspring), lambda=rep(individual[2], n_offspring), c=rep(individual[3], n_offspring), fitness=rep(individual[4], n_offspring))
    return(offspring)
  }
}
# test
# offspring(population[1,])

# also, an optimised fitness-calculation for vectorising the operations is needed:
vector_fitness <- function(input, N) {
  lambda = input[2]
  if (any(lambda == 1)) {
    lambda <- 1.0000000001
  }
  res <- lambda / (1 + (lambda - 1)*((N/input[1])**((1-input[3])*lambda/(lambda-1))))
  return(res)
}
```

We define a function that computes the next generation for a given population, using the offspring function. At this point, mutations are not taken into account yet (wait for it).

Hide

```
# next generation
next_generation <- function(population){
  next_gen <- apply(population, 1, offspring)
  next_gen <- bind_rows(next_gen)
  next_gen$fitness <- apply(next_gen, 1, vectorised_fitness, N=nrow(next_gen))
  return(next_gen)
}
# test
# next_generation(population)
```

TADAAAAA mutation appears:

Hide

```

next_generation_with_mutation <- function(population){
  next_gen <- next_generation(population)
  n_mutations <- rpois(1, nrow(next_gen)*mu)
  mutants <- sample(nrow(next_gen), n_mutations, replace=FALSE)
  if(length(mutants) > 0) {
    for(i in 1:(ncol(next_gen)-1)) {
      next_gen[mutants,i] <- next_gen[mutants, i] + rnorm(1, 0, i*0.04)
    }
    next_gen[mutants,4] <- with(next_gen[mutants,], calc_fitness(nrow(next_gen), K, lambda,
c))
  }
  return(next_gen)
}

```

Just like before, we create the offspring for each individual of the population. Then, out of this newly created generation, we draw the number of mutants from a poisson distribution with a probability of 0.01, pick random mutants from the new generation and modify their traits accordingly.

Here, we define functions that run the model over a given number of generations:

[Hide](#)

```

# run over x generations and plot evolution of population size etc
run <- function(x, population) {
  generations <- population[1,]
  generations$N <- nrow(population)
  # without mutation
  for (i in 1:(x-1)) {
    population <- next_generation(population)
    population$N[1] <- nrow(population)
    generations <- rbind(generations, population[1,])
  }
  return(generations)
}

```

Same thing with mutations:

[Hide](#)

```
run_with_mutation <- function(x, population, verbose=FALSE) {
  population_with_mutation <- population
  if (verbose) {
    print(c("Generation", "Number of individuals"))
    print(c(1, nrow(population_with_mutation)))
  }
  # with mutation
  generations_with_mutation <- data.frame(N=nrow(population_with_mutation), K_means=mean(population_with_mutation$K), K_sd=sd(population_with_mutation$K), lambda_means=mean(population_with_mutation$lambda), lambda_sd=sd(population_with_mutation$lambda), c_means=mean(population_with_mutation$c), c_sd=sd(population_with_mutation$c), fitness_means=mean(population_with_mutation$fitness), fitness_sd=sd(population_with_mutation$fitness))
  for (i in 1:(x-1)) {
    population_with_mutation <- next_generation_with_mutation(population_with_mutation)
    if (verbose) {
      print(c(i+1, nrow(population_with_mutation)))
    }
    generations_with_mutation <- rbind(generations_with_mutation, c(nrow(population_with_mutation), mean(population_with_mutation$K), sd(population_with_mutation$K), mean(population_with_mutation$lambda), sd(population_with_mutation$lambda), mean(population_with_mutation$c), sd(population_with_mutation$c), mean(population_with_mutation$fitness), sd(population_with_mutation$fitness)))
  }
  generations_with_mutation$r <- generations_with_mutation$N / generations_with_mutation$K_means
  return(generations_with_mutation)
}
```

Execute:

Hide

```
x <- 20
generations <- run(x, population)
generations_with_mutation <- run_with_mutation(x, population)
```

Now plot:

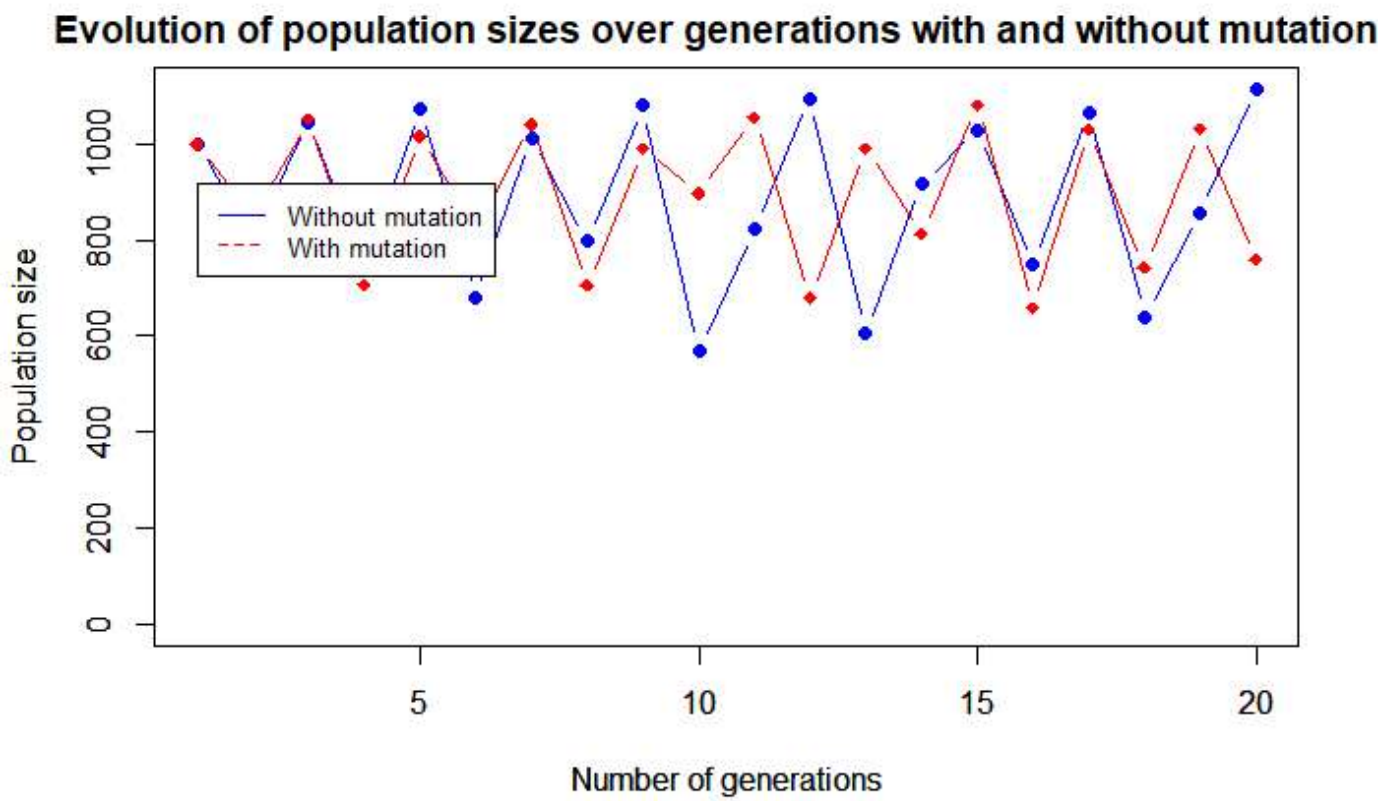
Hide

```
plot(1:x, generations$N, type="b", pch=19, col="blue", xlim=c(1, x), ylim=c(0, max(c(generations$N, generations_with_mutation$N))), xlab="Number of generations", ylab="Population size",
  main="Evolution of population sizes over generations with and without mutations")
par(new = T)
```

Hide

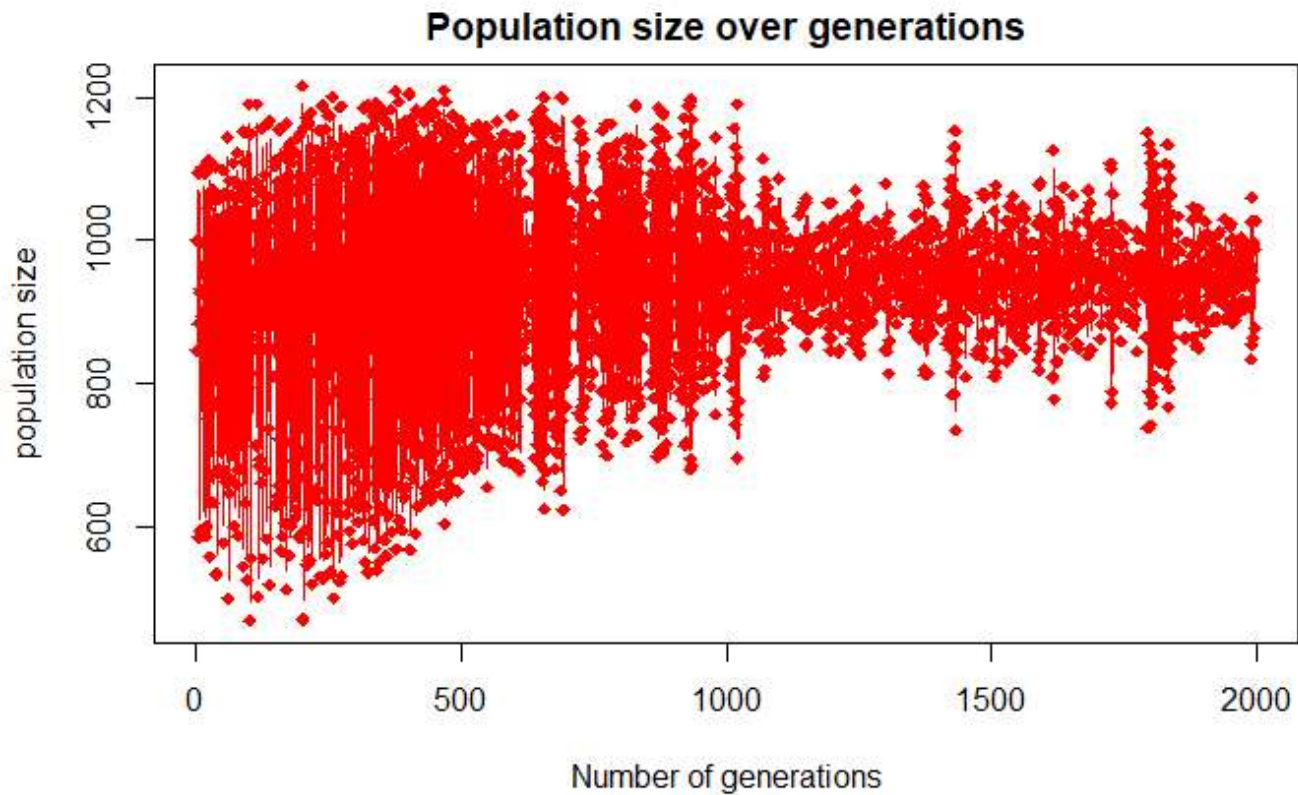
```
plot(1:x, generations_with_mutation$N, type="b", pch=18, col="red", xlim=c(1, x), ylim=c(0, max(c(generations$N, generations_with_mutation$N))), xlab="Number of generations", ylab="Population size")

legend(1, max(c(generations$N, generations_with_mutation$N))-200, legend=c("Without mutation", "With mutation"), col=c("blue", "red"), lty=1:2, cex=0.8)
```

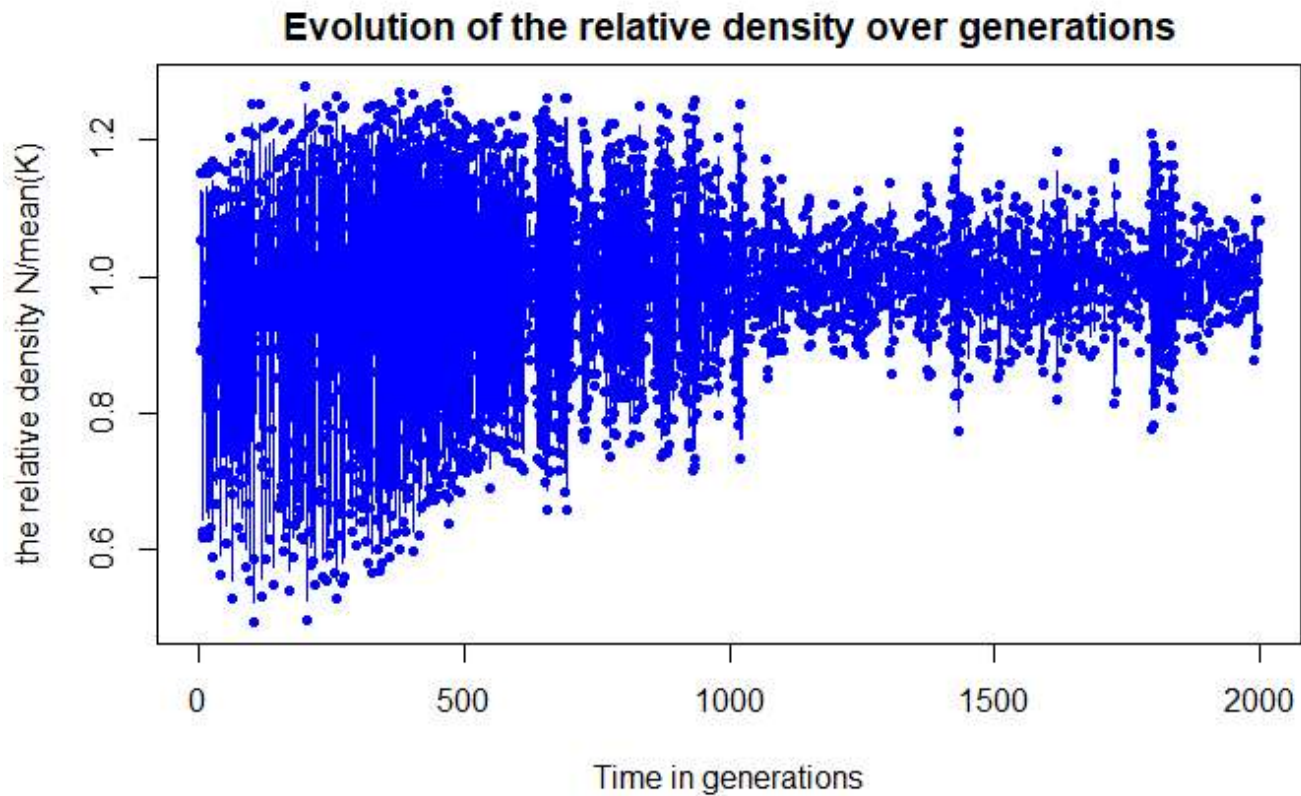


# Some plots:

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



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



Comparing with the paper, we noticed that the relative density should eventually become equal to 1 for large times. Unfortunately, over the small time span we covered, this is not the case for us.



Hide

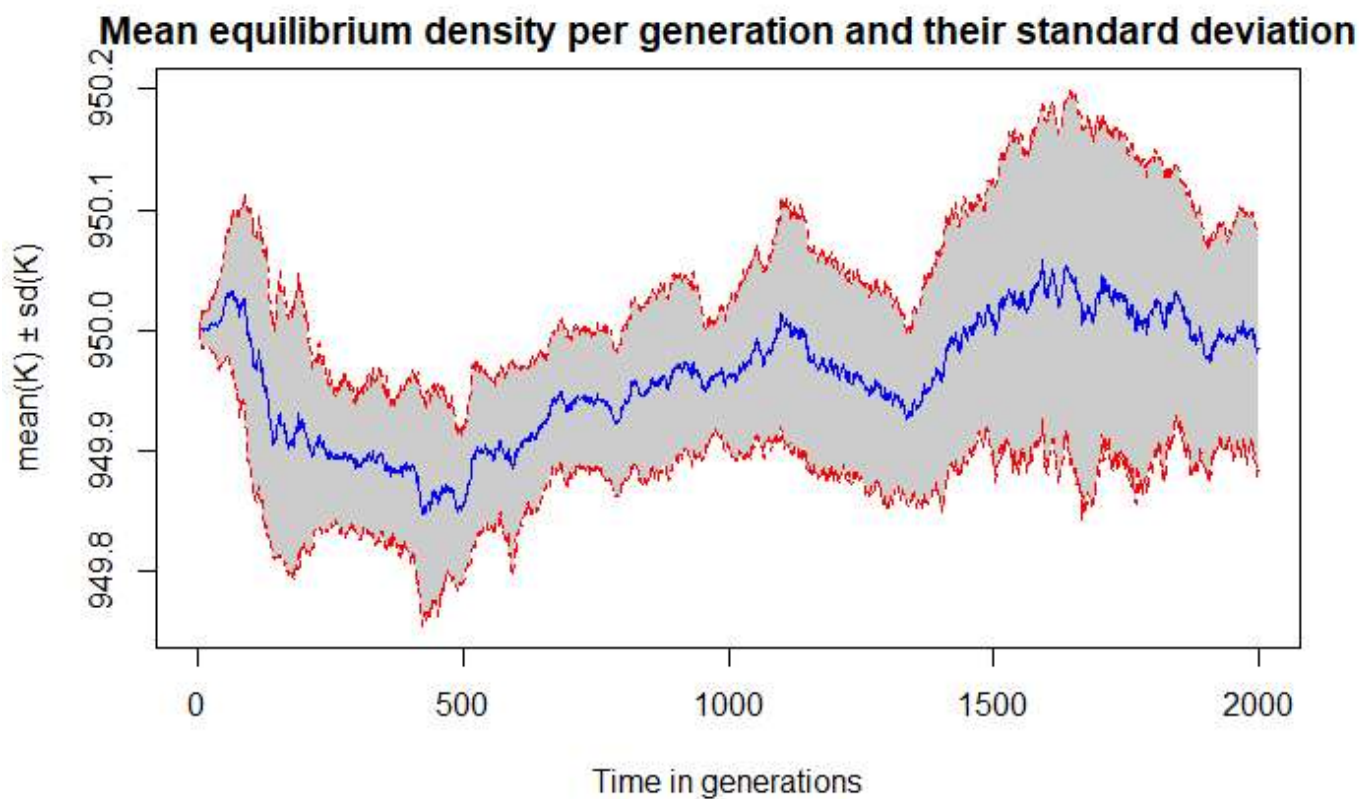
```
plot(1:x, gen$K_means, type = 'l', col="blue", ylim=c(min(gen$K_means-gen$K_sd), max(gen$K_means+gen$K_sd)), xlab="Time in generations", ylab="mean(K) \u00B1 sd(K)", main="Mean equilibrium density per generation and their standard deviation")
# add fill
polygon(c(x:1, 1:x), c(rev(gen$K_means-gen$K_sd), gen$K_means+gen$K_sd), col = 'grey80', border = NA)
```

Hide

```
lines(1:x, gen$K_means, col="blue")
# intervals
lines(1:x, gen$K_means-gen$K_sd, lty = 'dashed', col = 'red')
```

Hide

```
lines(1:x, gen$K_means+gen$K_sd, lty = 'dashed', col = 'red')
```



Hide

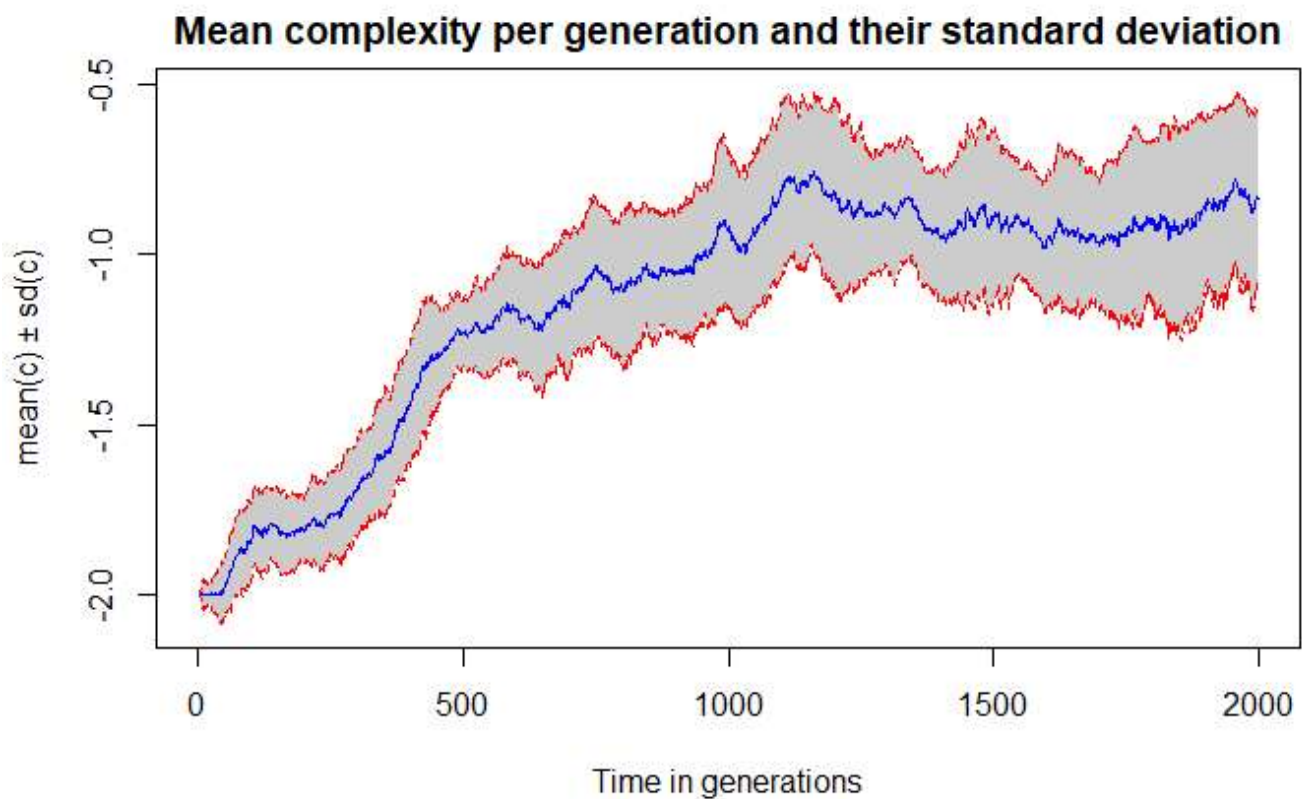
```
plot(1:x, gen$c_means, type = 'l', col="blue", ylim=c(min(gen$c_means-gen$c_sd), max(gen$c_means+gen$c_sd)), xlab="Time in generations", ylab="mean(c) \u00B1 sd(c)", main="Mean complexity per generation and their standard deviation")
# add fill
polygon(c(x:1, 1:x), c(rev(gen$c_means-gen$c_sd), gen$c_means+gen$c_sd), col = 'grey80', border = NA)
```

Hide

```
lines(1:x, gen$c_means, col="blue")
# intervals
lines(1:x, gen$c_means-gen$c_sd, lty = 'dashed', col = 'red')
```

Hide

```
lines(1:x, gen$c_means+gen$c_sd, lty = 'dashed', col = 'red')
```



Hide

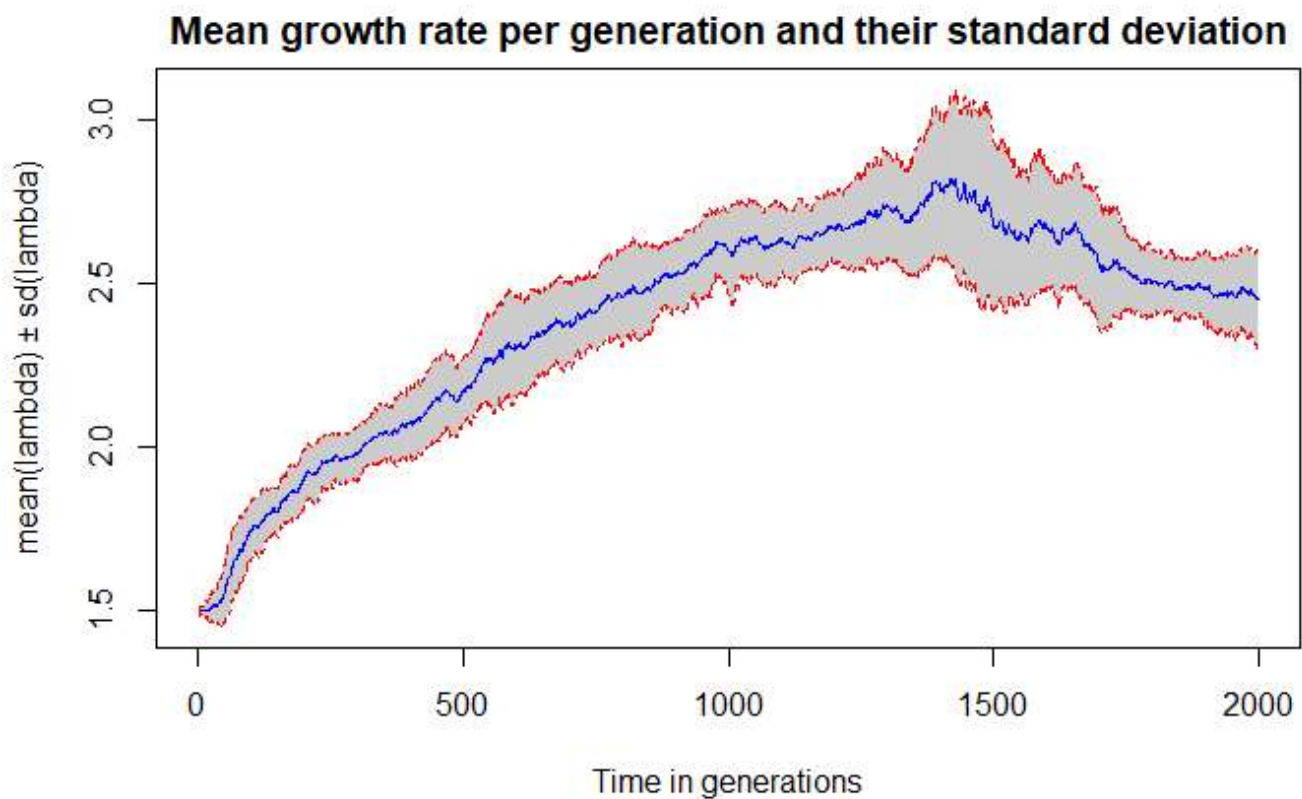
```
plot(1:x, gen$lambda_means, type = 'l', col="blue", ylim=c(min(gen$lambda_means-gen$lambda_sd), max(gen$lambda_means+gen$lambda_sd)), xlab="Time in generations", ylab="mean(lambda) \u00B1 sd(lambda)", main="Mean growth rate per generation and their standard deviation")
# add fill
polygon(c(x:1, 1:x), c(rev(gen$lambda_means-gen$lambda_sd), gen$lambda_means+gen$lambda_sd),
  col = 'grey80', border = NA)
```

Hide

```
lines(1:x, gen$lambda_means, col="blue")
# intervals
lines(1:x, gen$lambda_means-gen$lambda_sd, lty = 'dashed', col = 'red')
```

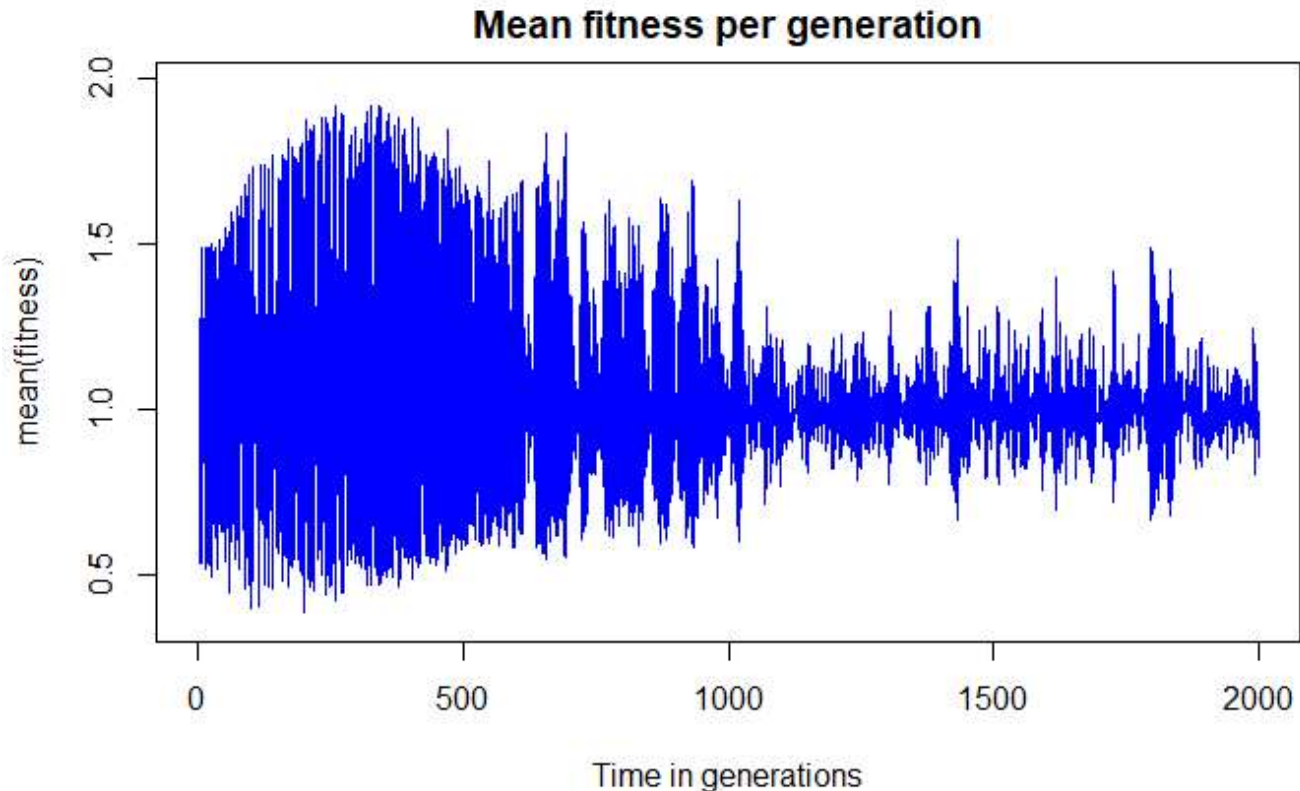
Hide

```
lines(1:x, gen$lambda_means+gen$lambda_sd, lty = 'dashed', col = 'red')
```



Hide

```
plot(1:x, gen$fitness_means, type = 'l', col="blue", ylim=c(min(gen$fitness_means-gen$fitness_sd), max(gen$fitness_means+gen$fitness_sd)), xlab="Time in generations", ylab="mean(fitness)", main="Mean fitness per generation")
```



Hide

```
# add fill
# polygon(c(x:1, 1:x), c(rev(gen$fitness_means-gen$fitness_sd), gen$fitness_means+gen$fitness_sd), col = 'grey80', border = NA)
# lines(1:x, gen$fitness_means, col="blue")
# intervals
# lines(1:x, gen$fitness_means-gen$fitness_sd, lty = 'dashed', col = 'red')
# lines(1:x, gen$fitness_means+gen$fitness_sd, lty = 'dashed', col = 'red')
```