

# *Runaway*

*demogenetic model for sexual selection*

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**Capsis 4**



# *Runaway Model*

- 1) Objective of Runaway
- 2) Choices for modelling
- 3) Example of simulation

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# 1) Objective of Runaway

To study the co-evolution of traits and genome architecture under sexual selection.

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To study the co-evolution of traits and genome architecture under sexual selection.

## **sexual selection :**

- differences in mating and reproductive success caused by competition over mate and related to the expression of traits.
- result in the evolution of this traits ( it can be morphological and behavioural traits)
- distinction between sexual and other natural selection

*“ Sexual selection... depends, not on a struggle for existence, but on a struggle between the males for possession of females: the result is not death to the unsuccessful competitor, but few or no offspring”*

Darwin 1859, p. 88

# 1) Objective of Runaway

To study the co-evolution of traits and genome architecture under sexual selection.

## **Why this study?**

- sexual selection have a strong impact on the evolution on morphological and behavioural traits
- genetic basis of these traits : the polygeny, the pleiotropy, and the spatial location in the genome (implying possible physical linkage) affect the evolution of these traits

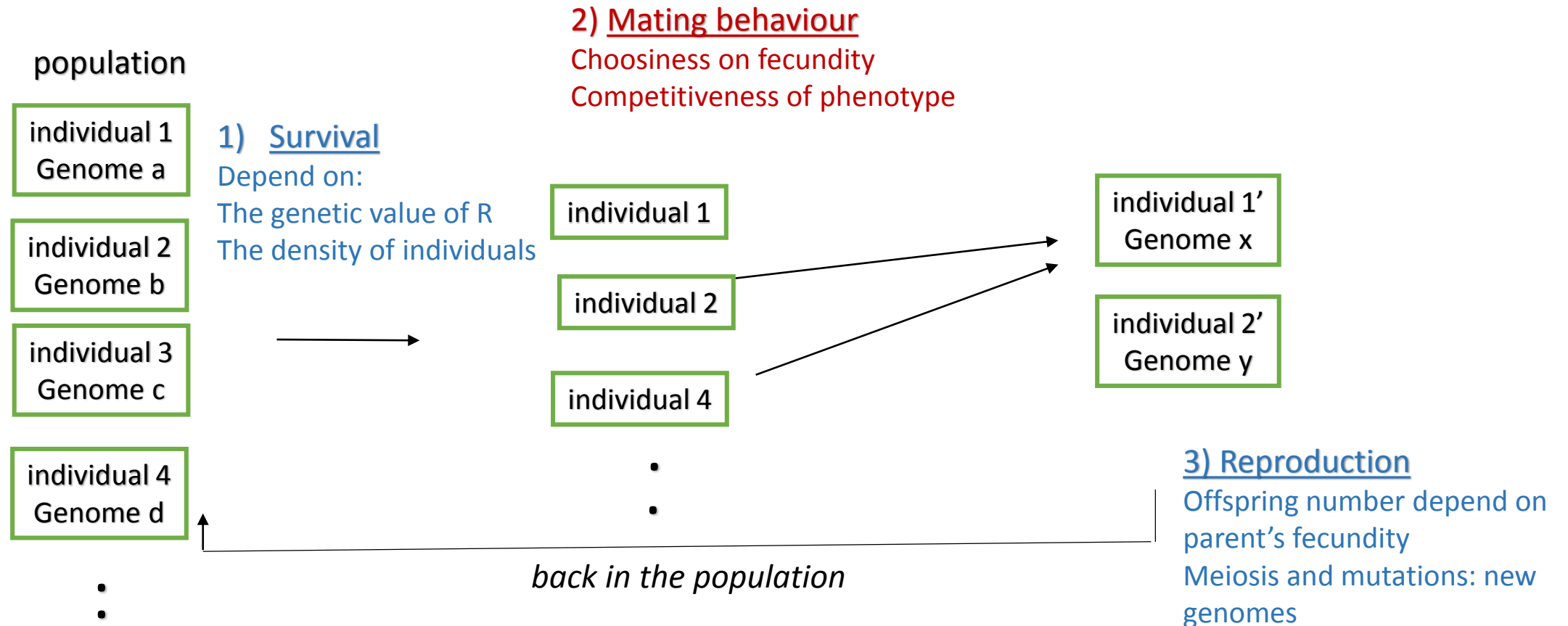
# *Runaway Model*

- 1) Objective of Runaway
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## 2) Choices for modelling

### a) demogenetic cycle

When demogenetic meet behavioural ecology...



Time step: 1 generation.

The age of individual is a number of generations and depend on survival



## 2) Choices for modelling

### b) Traits under sexual selection

When demogenetic meets behavioural ecology...

The genome of each individual is coding for 4 traits:

- $R$  : energy invested in reproduction
- $Ig$  : gametic investment (i.e. fecundity)
- $Pr$  : choosiness on the  $Ig$
- $Ph$  : competitiveness for mating

$$R = Ig + Pr + Ph$$

$$S = \frac{1}{(1 + R) * (1 + \frac{N}{C})}$$

$S$  : survival  
 $N$  : nombre d'individus  
 $C$  : carrying capacity

## 2) Choices for modelling

c) How to model mating behaviours?

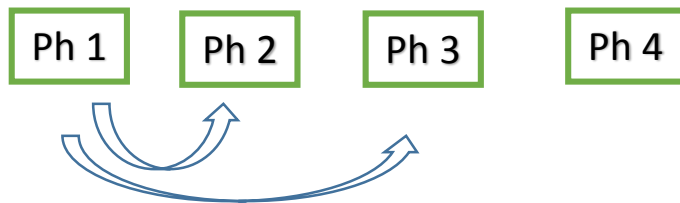
1. Mate choice between individuals is mutual
2. Individuals express a choosiness on the fecundity (trait  $I_g$ ) of their partner
3. Some individuals are more competitive for mating because they are more efficient at finding a partner or more conspicuous by others

## 2) Choices for modelling

c) How to model mating behaviours?

- Encounters between individuals

- Mating groups are done by drawing a given number of individuals (the size of the group can be chosen in the user interface)
- Mating can occur between two individuals from the same mating group
- individuals are sorted according to their phenotypic values ( decreasing order)



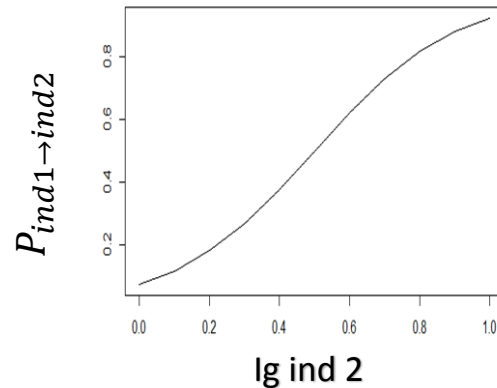
Ph 1 meet each individual until mutual choice  
He is the first to choose his partner or the first to be presented  
to a potential partner

## 2) Choices for modelling

c) How to model mating behaviours?

- Mating between individuals

Probability that ind. 1 agrees to mate with ind. 2 : logit function of  $Ig$  and  $Pr$



$$P_{ind1 \rightarrow ind2} = \frac{\exp(pr1(a.Ig2 - b))}{1 + \exp(pr1(a.Ig2 - b))}$$

*pr1: choosiness value for ind 1*

*Ig2: gametic investment for ind 2*

*a et b: parameters to adjust the shape of the function*

$$\text{Mating} \leftrightarrow \begin{cases} \text{random number 1} \geq P_{ind1 \rightarrow ind2} \\ \text{random number 2} \geq P_{ind2 \rightarrow ind1} \end{cases}$$

## 2) Choices for modelling

c) How to model mating behaviours?

- Mating between individuals

The choosiness is adjusted according to mate quality distribution ( $Ig$  values) in the mating group

$$Ig\ ind1 = \frac{Ig\ ind1 - Ig\ min}{Ig\ min - Ig\ max}$$

*$Ig\ min$ : lower value of gametic investment in the mating group*

*$Ig\ max$ : higher value of gametic investment in the mating group*

## 2) choices for modelisation

d) How to model genetic basis of traits?

- Genetical architecture:

Using library Genetics

- fixed number of genes
- diploid DNA
- sexual chromosomes and cytoplasmic DNA are not modeled
- recombinaison probability map can be tuned
- fixed number of potential alleles

## 2) Choices for modelisation

d) How to model genetic basis of traits?

- Allelic expression

Each allele can code for each of the traits (pleiotropy)

Allelic effects for each traits : random draw from beta distributions

Trait value : sum of allelic effects over all loci

$$T_j = \sum_{l=1}^n a_{lj}$$

$T$  = trait value

$n$  = loci number

$a_{lj}$  = value of the allele  $l$  for the trait  $j$  at the locus  $l$

## 2) Choices for modelisation

d) How to model genetic basis of traits?

- Reproduction

Number of offspring =  $\min(\lg \text{ ind a}, \lg \text{ ind b}) \times \alpha$        $\alpha$  demographic constant

New genomes are created :

- meioses and fecundation processes (library genetics)
- Mutation : random draw of a new allele from the pool of existing alleles defined by the user



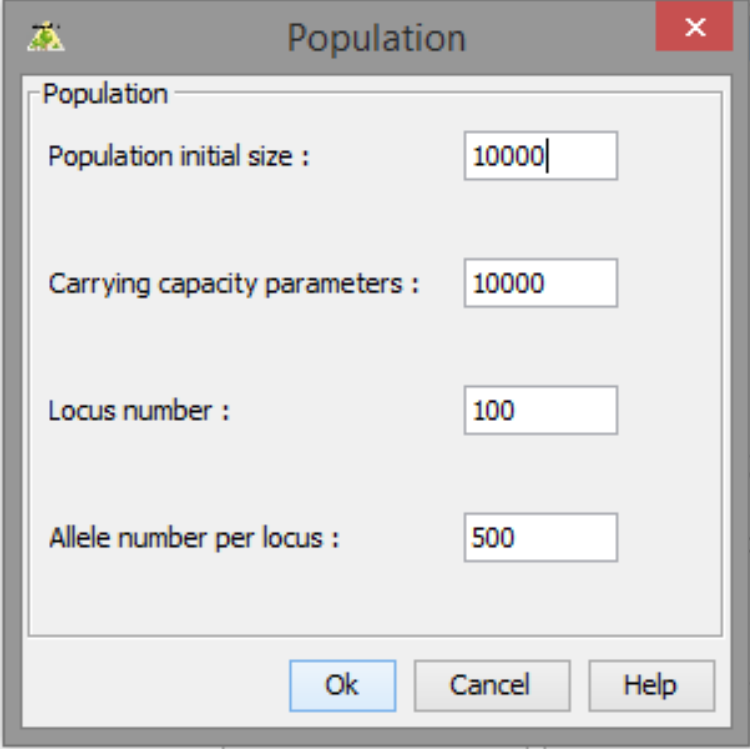
# *Runaway Model*

- 1) Objective of Runaway
- 2) Choices for modelling
- 3) Example of simulation

### 3) Example of simulation

a) interface user and choices for scenarios

- Population size
- Carrying capacity
- Number of genes
- Number of potential alleles



The image shows a software dialog box titled "Population". It contains four input fields with the following labels and values:

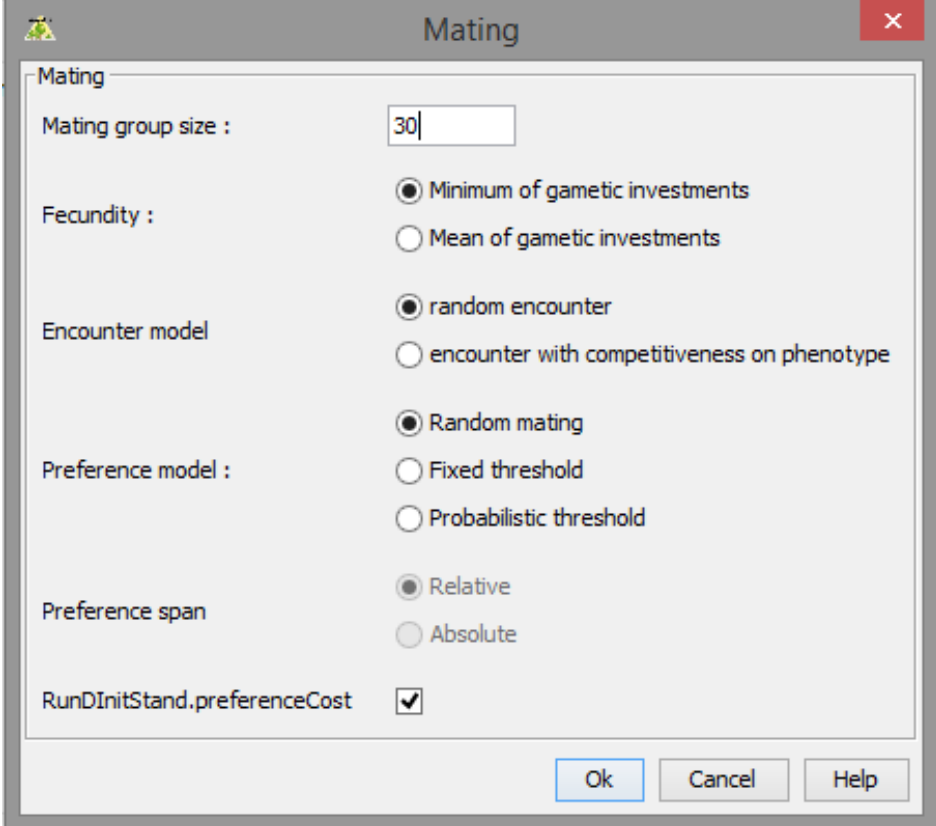
Label	Value
Population initial size :	10000
Carrying capacity parameters :	10000
Locus number :	100
Allele number per locus :	500

At the bottom of the dialog box are three buttons: "Ok", "Cancel", and "Help".

### 3) Example of simulation

#### a) interface user and choices for scenarios

- Mating group size
- Type of encounter
- Type of preference



The screenshot shows a 'Mating' dialog box with the following settings:

- Mating group size : 30
- Fecundity : ☒ Minimum of gametic investments, ☐ Mean of gametic investments
- Encounter model : ☒ random encounter, ☐ encounter with competitiveness on phenotype
- Preference model : ☒ Random mating, ☐ Fixed threshold, ☐ Probabilistic threshold
- Preference span : ☒ Relative, ☐ Absolute
- RunDInitStand.preferenceCost : ☒

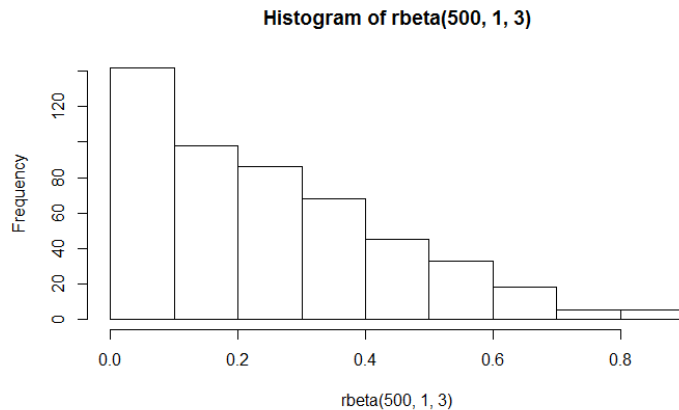
Buttons at the bottom: Ok, Cancel, Help.

### 3) Example of simulation

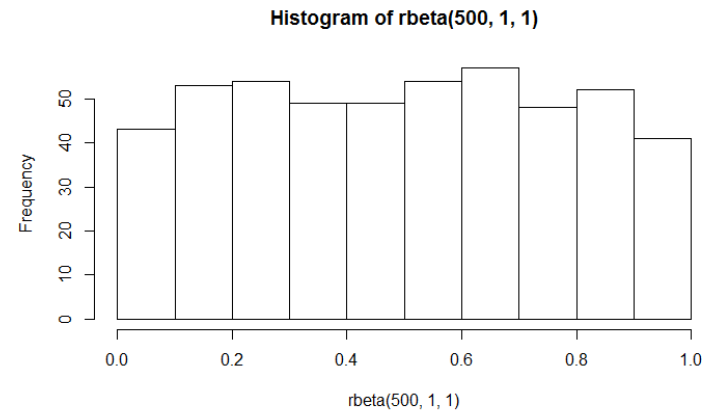
#### a) interface user and choices for scenarios

- Mutation rate
- Allelic effects for traits

Allelic effects for Pr, Ph and Ig :  
random draw from a beta (1,3) distribution



Allelic effects for R :  
random draw from a beta (1,1) distribution



Population

Population

Mutation rate :

☐ RunDInitStand.economicalMutation ☒ RunDInitStand.realisticMutation

RunDInitStand.allelesEffectsMutation

Resource

Second beta parameter for resource :

First beta parameter for resource :

Investment

Second beta parameter for investment :

First beta parameter for investment :

Phenotype

Second beta parameter for phenotype :

First beta parameter for phenotype :

Preference

Second beta parameter for preference :

First beta parameter for preference :

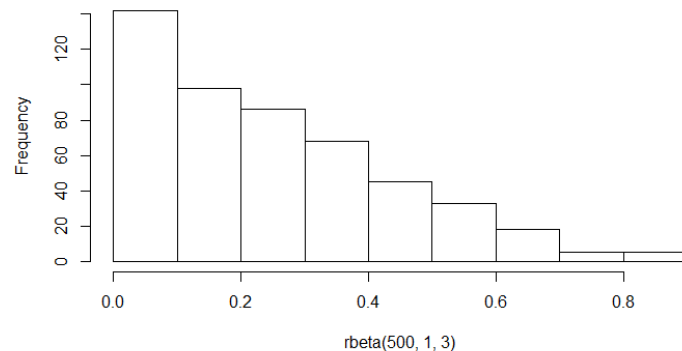
### 3) Instances of simulation

b) outputs: data extractor and Stand viewer

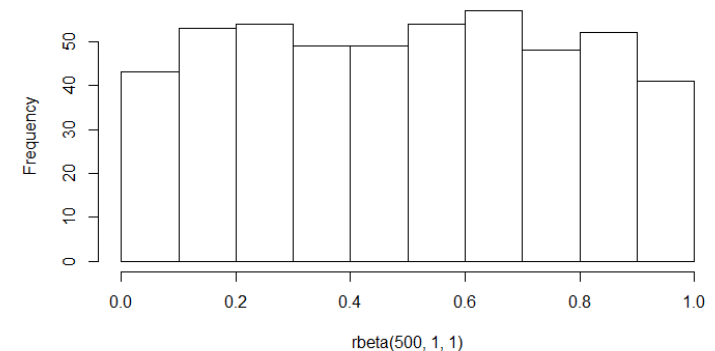
#### Scenario :

- Population size and carrying capacity : 10000
- Mating group size : 30
- Encounter with competitiveness on phenotype and mate choice with choosiness on Ig
- 100 genes, 500 potential alleles per loci
- Allelic effects for traits

Allelic effects distribution for Pr, Ph and Ig



Allelic effects distribution for R

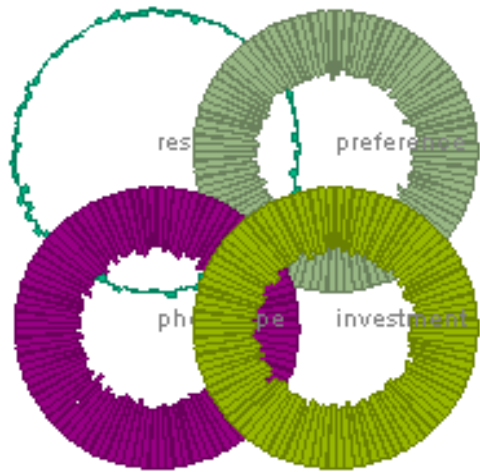


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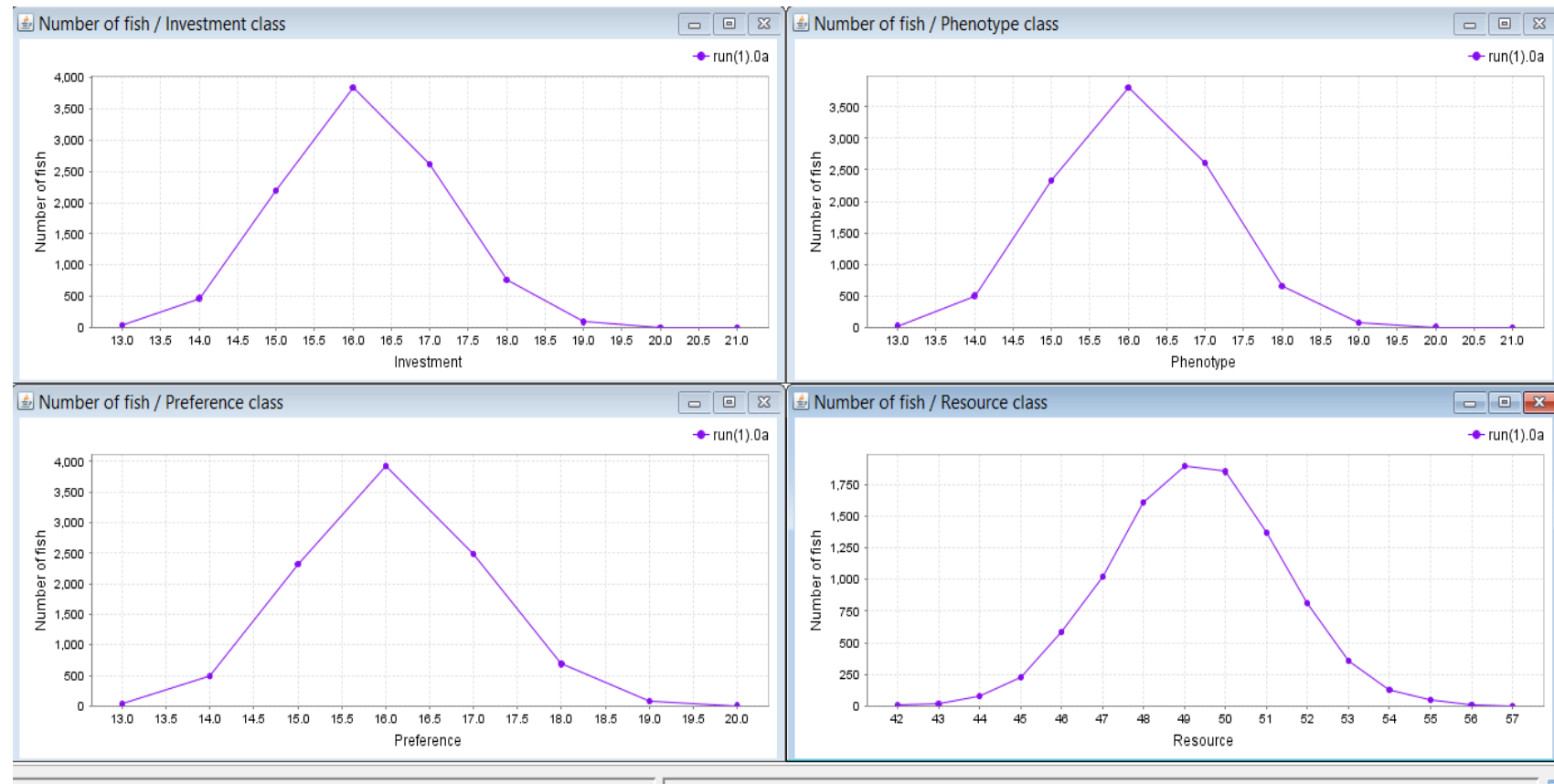
b) outputs: data extractor and Stand viewer

Initial stand

- Trait distribution
- genome viewer



The mean allelic effect for Pr Ph and Ig is rather low for every loci

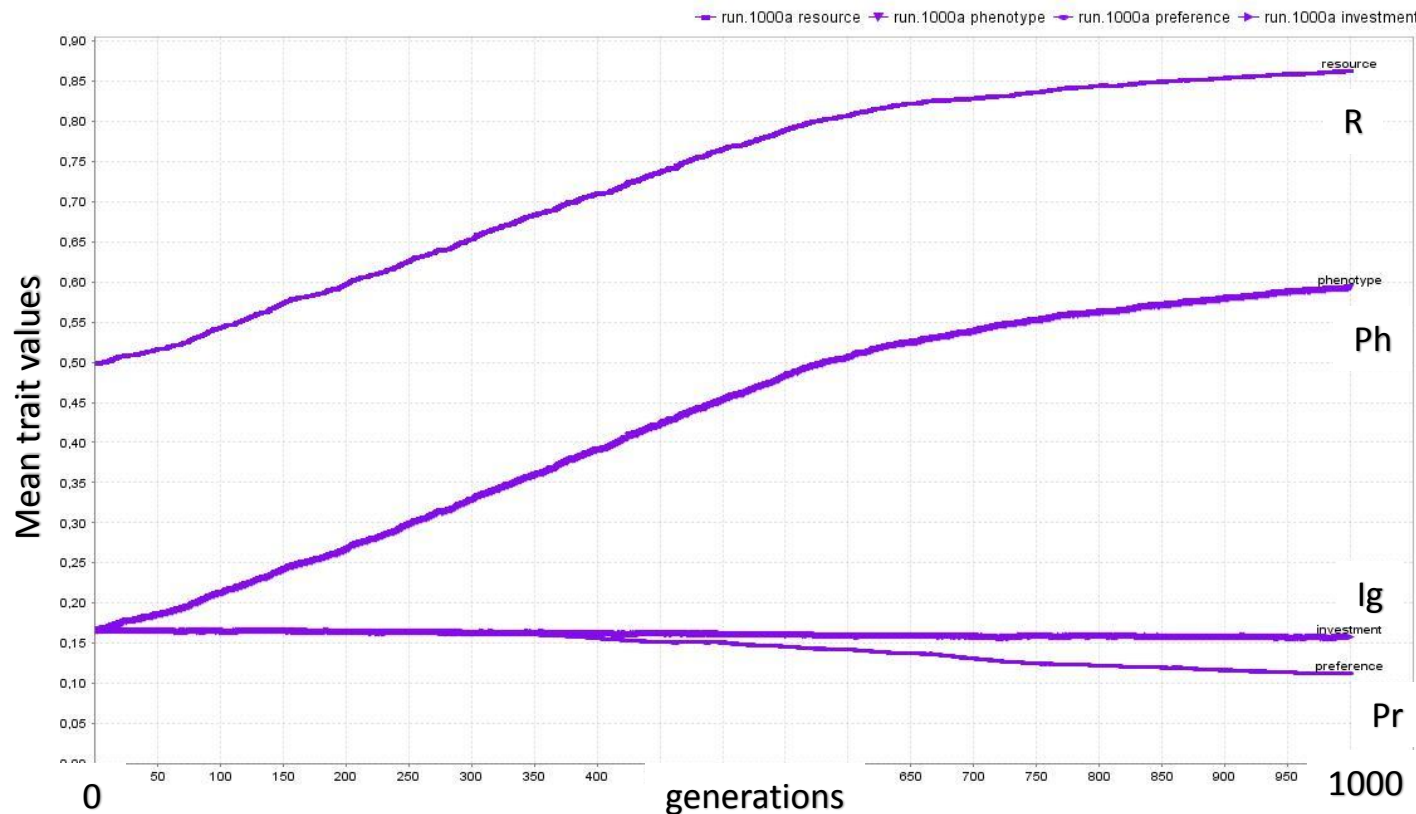


### 3) Instances of simulation

b) outputs: data extractor and Stand viewer

## Evolution over 1000 generations

- Mean trait values in the population



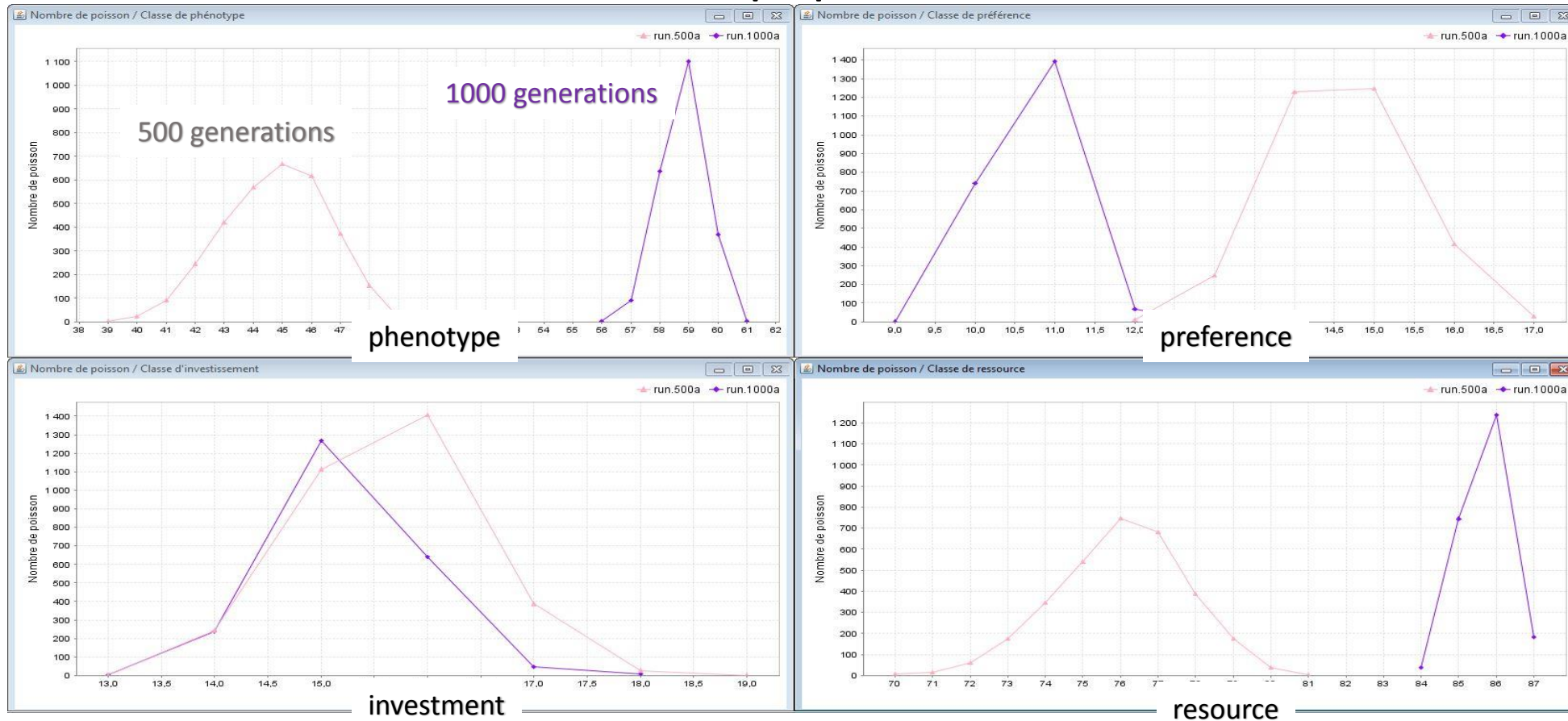
Mean value of trait R is increasing because of increasing value of phenotype while gametic investment remain constant and preference is decreasing.

### 3) Instances of simulation

b) outputs: data extractor and Stand viewer

Evolution over 1000 generations

- Traits distribution in the population



Unimodal distributions  
Reduced variation

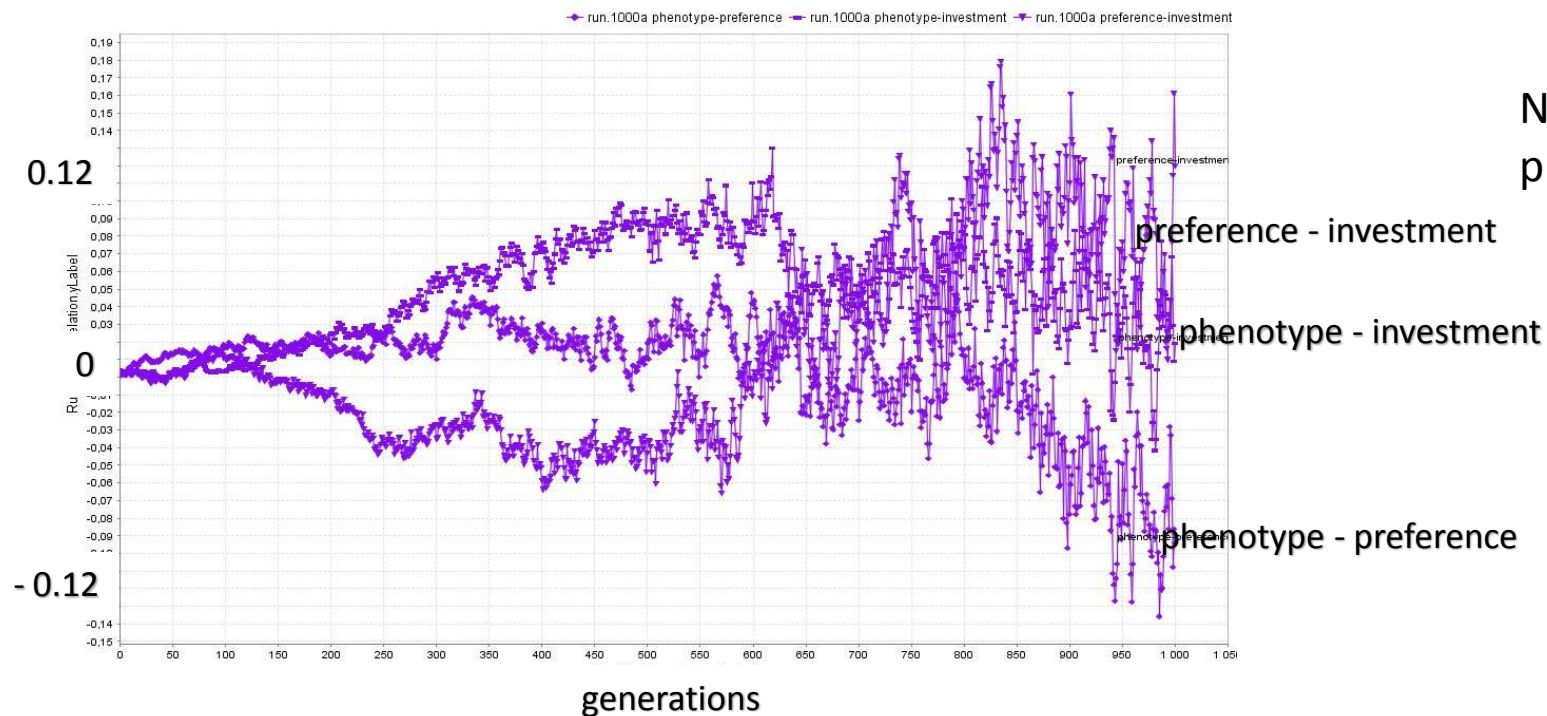


### 3) Instances of simulation

b) instance of output: data extractor and Stand viewer

Evolution over 1000 generations

- Computing the correlation between traits



Negative correlation between phenotype and preference

preference - investment

phenotype - investment

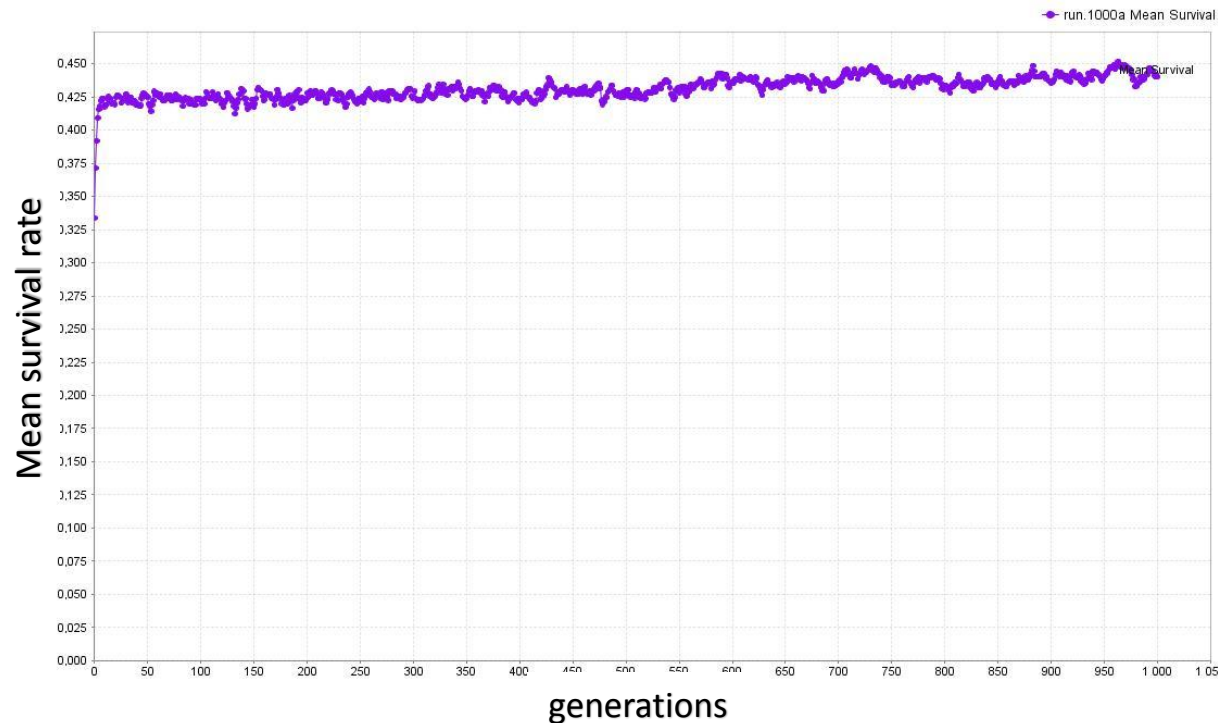
phenotype - preference

### 3) Instance of simulation

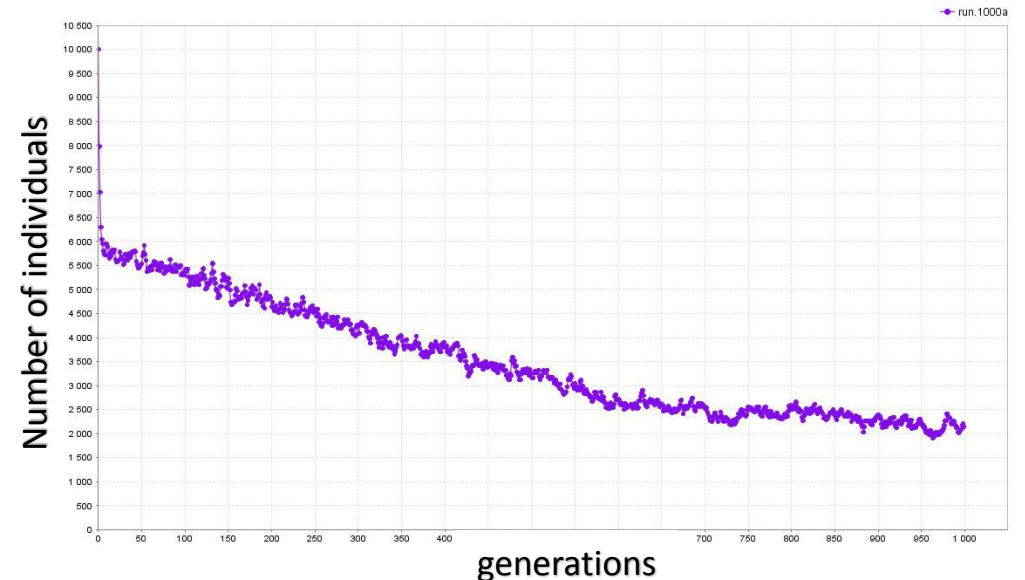
b) outputs: data extractor and Stand viewer

Evolution over 1000 generations

- Demography : survival depend on resource trait value and on density



Mean survival rate in the population remain constante  
Because R mean value is increasing while the population size is decreasing

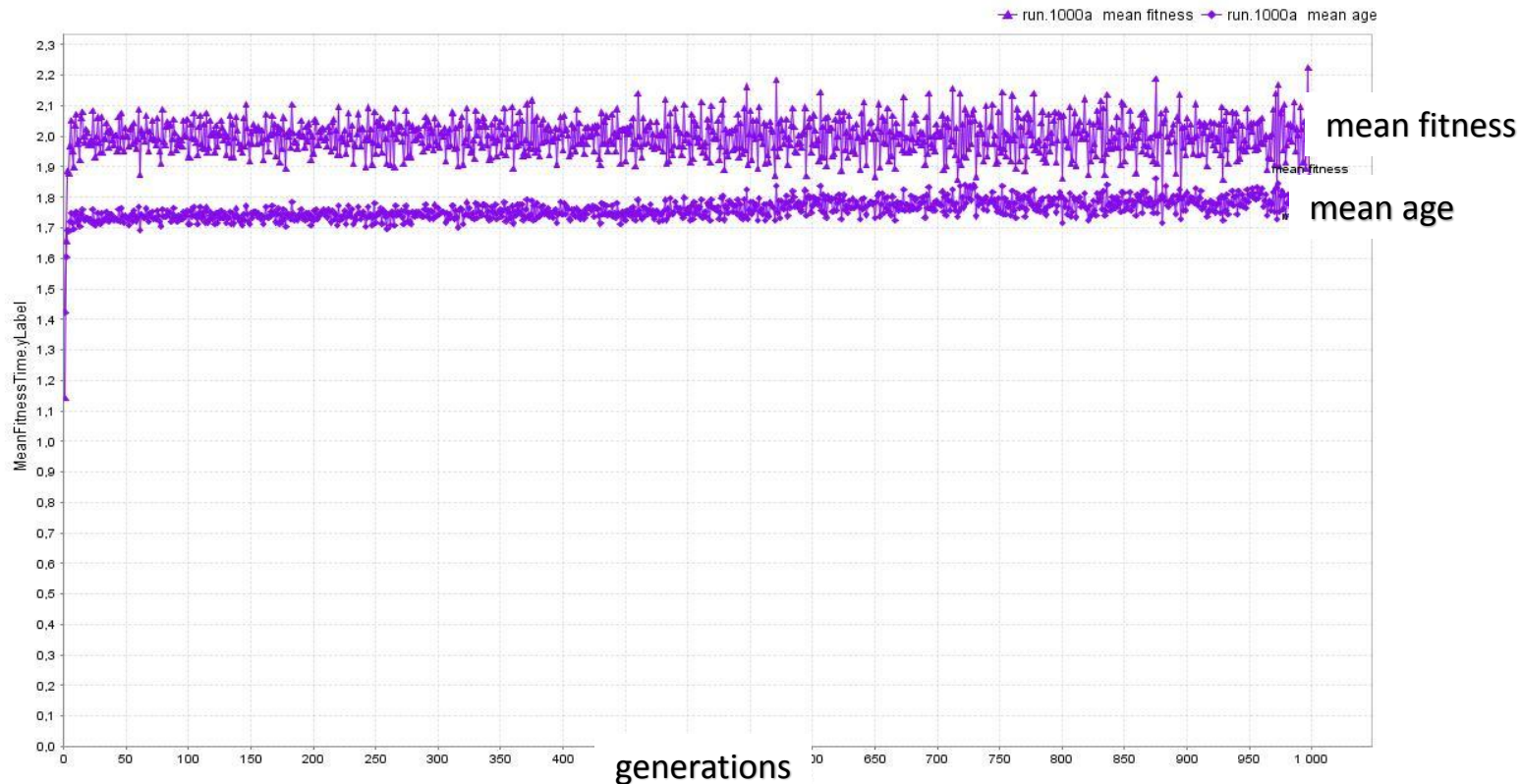


### 3) Instance of simulation

b) outputs : data extractor and Stand viewer

Evolution over 1000 generations

- Mean fitness in the population : lifetime reproductive success



Two offsprings per individual on average

### 3) Instance of simulation

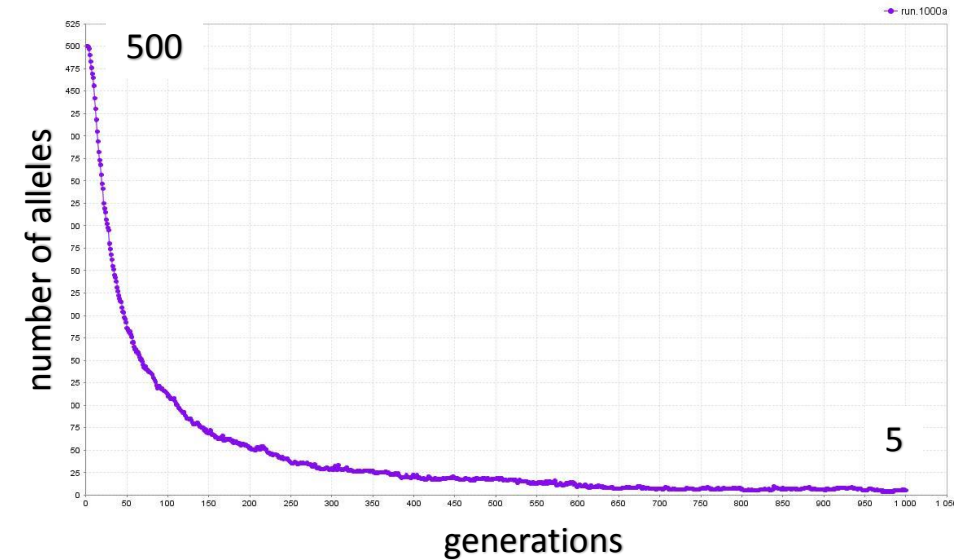
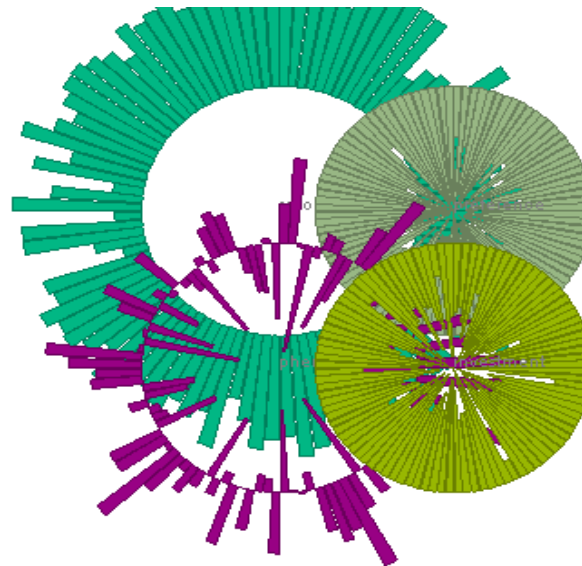
b) outputs: data extractor and Stand viewer

Evolution over 1000 generations

- Genome structure

Number of allele

Mean allelic effect per locus



- Loss of allelic diversity

*a work in progress..*

- It was just an example for a given combination of parameters..
- Several simulations are currently running in order to make a first sensitivity analysis.
  - 972 combinations of parameters
  - 30 simulations for each combination of parameters
  - evolution over 3000 generations
- To understand how the different assumption influence the course of evolution and to compare the behaviour of the model with already published analytical models

Thank you for your attention !

*Any questions?*