# Input-Output Database for the Models of the EvolTree Modelling Platform – IA1.4
# MetaPop Model Data Structure

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# 1 MetaPop Model

MetaPop is written in C language.

## 1.1 MetaPop Data Files' Structure

MetaPop is based on text data files: as input, the model requires some parameter settings defined in three kinds of files and as output, several files can be generated.

### 1.1.1 Input Files

Three data files are involved in this step:

- **Parameter file**

The "param" file is used as pre-processing to produce the "conf" file in generating data throughout random processes.

- **Configuration file** *(cf.* "*Annex 1 – Configuration File*")

The configuration file is mandatory for the model as it contains the required parameter settings. It is created on the basis of the previous "param" file.

- **Type of results file** *(cf.* "*Annex 2 – Type of Results File*")

The "type" file contains a list of outputs requested by the user.

- **Genotype file of the last simulated year** *(cf.* "*Annex 3 – Genotype File of the Last Simulated Year*")

The "save" file contains the genotype of all individual trees at the last simulated year. This file is not mandatory, if it is loaded (option "-I" in the command line), it permits to initialise the allelic frequencies.

### 1.1.2 Output Files

MetaPop generates the results in the "res.txt" file; two other optional files can be produced.

- **Result file** *(cf.* "*Annex 4 – Result File*")

The simulation outputs requested in the "type.txt" file are generated in the "res.txt" file.

- **Sample file** *(cf.* "")

A "sample" file contains the genotype of a certain number of individual trees per population at a given simulated year. This output has to be requested in the "type.txt" file.

- **Genotype file of the last simulated year** *(cf.* "*Annex 3 – Genotype File of the Last Simulated Year*")

The "save" file contains the genotype of all individual trees at the last generation of the simulation. That file can be an input file as well as an output one; it is generated if the option "-S" is indicated in the command line.

### 1.1.3 MetaPop's Files Summary

The following table (*cf. Tableau 1*) summarises the potential files involved in the MetaPop process.

***Tableau 1:*** *Data files potentially generated by the MetaPop model (current -> expected)*

| Step | File name | File format | Generated by | File Status |
|---|---|---|---|---|
| IN | param | txt -> xml | Hand made -> MetapopConf<br>-> TreeMBase | Preprocessing |
| | conf | txt | quanticreconf -> MetapopConf<br>-> TreeMBase | Mandatory for the model |
| | type | txt | Hand made -> MetapopConf<br>-> TreeMBase | Mandatory for the model |
| | save | txt | MetaPop model (option "-I") | Loaded if "-I" command line is filled in |

| | | | | |
|---|---|---|---|---|
| OUT | res | txt | MetaPop model (option “-R”) | Always generated |
| | sample | txt | MetaPop model (option in “type.txt”) | Generated if requested in the “type.txt” file |
| | save | txt | MetaPop model (option “-S”) | Generated if “-S” command line is filled in |

## 1.2 MetaPop Model Processing

The MetaPop data processing is in evolution and more particularly the parameter settings’ part. Please read below the notes dated from the 01/04/08.

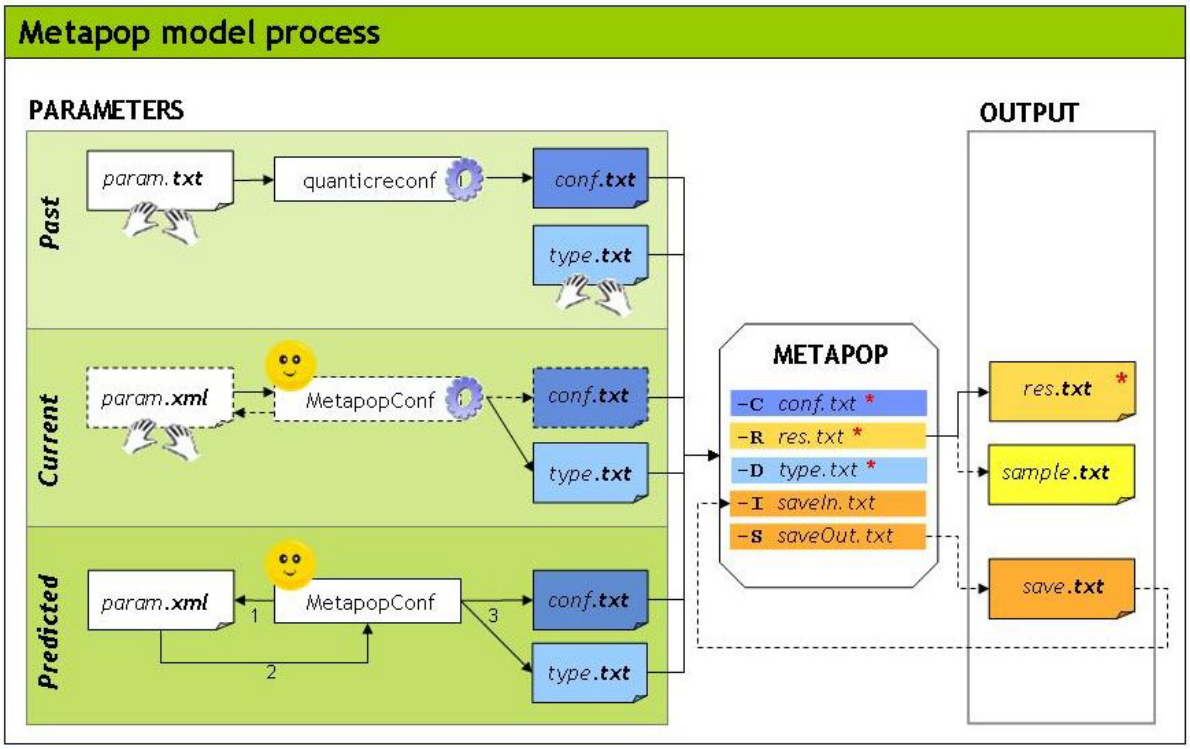



***Figure 1*** *: MetaPop – past, current and predicted – data structure*

### 1.2.1 Development Status

01/04/08: As the data file structure is still in evolution, the “param” file won’t be taken into account as its data are reused in the “conf” file.

- **In the Past**

The “quanticreconf” tool used the “param” file as input to produce the “conf” one in generating data throughout random processes.

The “param” and the “type” files were hand made.

- **Currently**

A Graphical User Interface called “MetapopConf” is in development to help the user in initialising the model settings. The interface is developed in C++ with the Qt library.

The “param” file is no more in a text format; it is currently converted in an xml one. The structure and content are not immobilised yet.

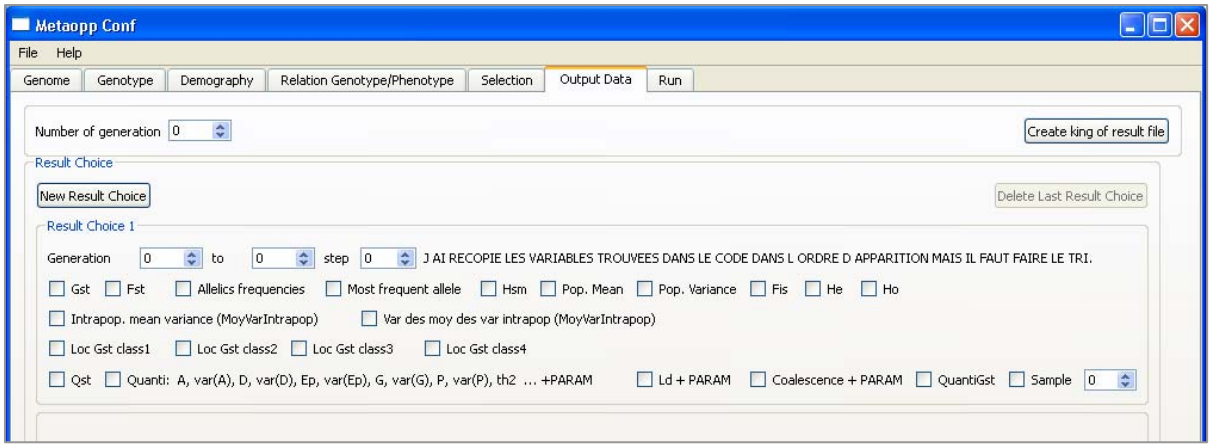



***Figure 2:*** *Metapopconf GUI with a tab per data concepts; the current one permits to define the requested outputs and create the corresponding "type.txt" file*

- **Predicted**

The procedure will be the following:

- "MetapopConf" will read, modify and generate the "param.xml" file.
- "MetapopConf" will generate the "conf.txt" file.
- "MetapopConf" will generate the "type.txt" file.

### 1.2.2 Model Functioning

The model is launched in a bat mode with the following settings:

```
Metapop -Cconf.txt -Rres.txt -Dtype.txt -Ifile_[…].txt -Sfile_sce_[…].txt
```

***Tableau 2:*** *Command lines of the MetaPop model*

| Command | Description | Status |
|---|---|---|
| -C | Indicate the settings file name (conf.txt) | required |
| -R | Indicate the output file name (res.txt) | required |
| -D | Indicate the type of outputs file name (type.txt) | required |
| -I | Indicate the input "save" file name (save.txt) | optional |
| -S | Indicate the output "save" file name (save.txt) | optional |

The model requires the parameter settings ("conf.txt"), the detail of outputs to obtain ("type.txt") and the name of the output file where the results will be generated ("res.txt").

In option, the genotype of all individual trees ("save.txt") can be loaded as input. The same file containing the genotype of all individual trees at the last generation can be produced as output.

The process is detailed in *Figure 3*.

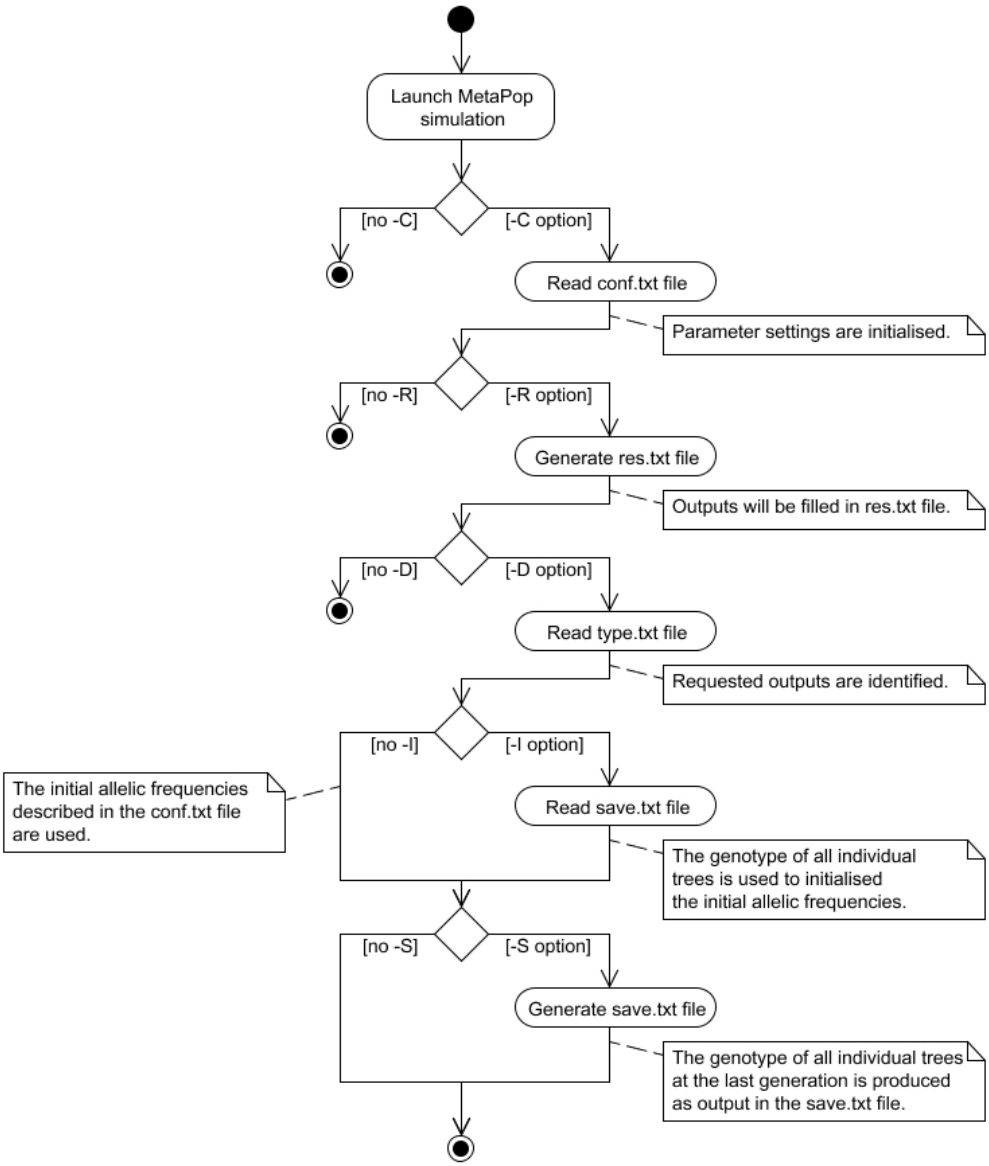



***Figure 3**: MetaPop functioning*

## 1.3 Order of Magnitude

MetaPop deals with huge sets of data as the order of magnitude of the concepts is large. Following orders of magnitude are given as information; it corresponds to the maximum values simulated yet. Only the maximum number of loci is fixed.

To be able to make comparisons with other models of the Modelling Platform, we agreed on not storing huge simulations.

***Tableau 3**: MetaPop concepts' orders of magnitude*

| **Concepts** | **Order of magnitude** |
|---|---|
| Number of simulated years (= "generation" term in MetaPop sense) | 1000 – several 100000 |
| Number of populations | 50 |
| Number of classes | 300 |
| Number of individuals | 10000 – 100000 |
| Number of loci | 1000 |
| Number of alleles per locus | 255 (fixed) |

# 2 Annex 1 – Configuration File

## 2.1 File format

- The parameters are ordered.
- The number of words which composed the label of each line is very important (the ":" symbol counts for a word)
- Decimal are expressed with a dot.

The "fscanf" C++ function reads data from the stream. The function reads and ignores any whitespace characters (blank spaces, newline and tabulation character) which are encountered before the next non-whitespace character.

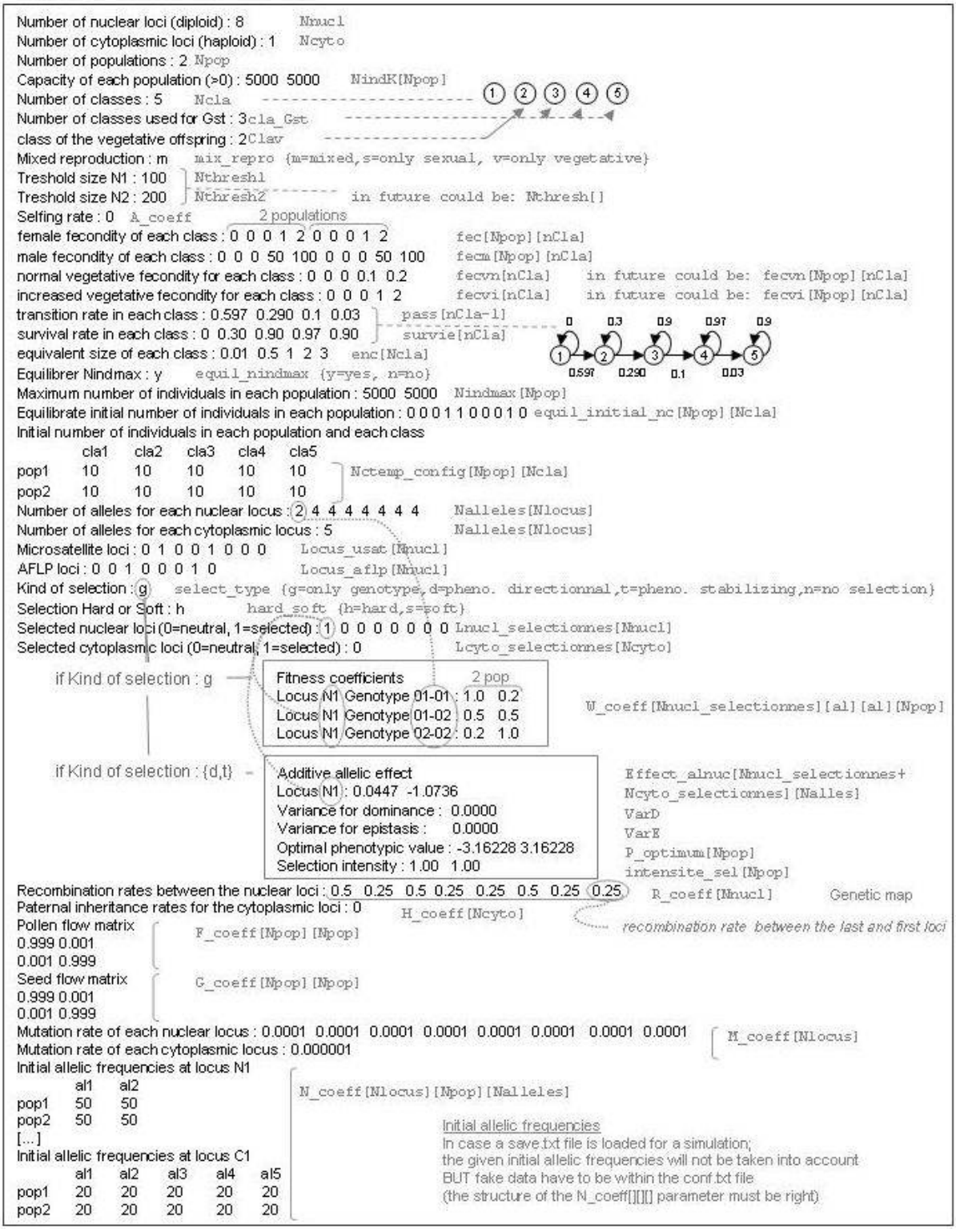



***Figure 4**: "conf.txt" file described with the parameter names*

## 2.2 Number of Loci

### 2.2.1 Number of nuclear loci

| `Number of nuclear loci (diploid) : Nnucl` |
|---|
| `Number of nuclear loci (diploid) : 8` |

### 2.2.2 Number of cytoplasmic loci

| `Number of cytoplamic loci (haploid) : Ncyto` |
|---|

```
Number of cytoplamic loci (haploid) : 1
```

## 2.3 Populations' Definition

### 2.3.1 Number of populations

```
Number of populations : Npop
Number of populations : 2
```

### 2.3.2 Population Capacity

Maximum stand basal area per population

```
Capacity of each population (>0) : NindK
Capacity of each population (>0) : 5000 5000
```

## 2.4 Classes' Definition

### 2.4.1 Number of Classes

```
Number of classes : Ncla
Number of classes : 5
```

### 2.4.2 Gst Classes

```
Number of classes used for Gst : cla_Gst
Number of classes used for Gst : 3
```

*E.g.*, the three bigger classes are used for Gst: 


### 2.4.3 Vegetative Offspring Class

```
class of the vegetative offspring : Clav
class of the vegetative offspring : 2
```

*E.g.*, the second class corresponds to the vegetative offspring: 


## 2.5 Type of Reproduction

```
Mixed reproduction : mix_repro
Mixed reproduction : m
```

Three types of reproduction are available:

- s = sexual
- v = vegetative
- m = mixed *i.e.* sexual + vegetative reproductions

## 2.6 Thresholds

Both thresholds are only used in case of mixed reproduction ("mix_repro" = m).

- **Predicted Update**

More thresholds are predicted to be added.

### 2.6.1 First Threshold

```
Threshold size N1 : Nthresh1
Threshold size N1 : 100
```

### 2.6.2 Second Threshold

```
Threshold size N2 : Nthresh2
Threshold size N2 : 200
```

## 2.7 Selfing Rate

```
Selfing rate : A_coeff
Selfing rate : 0
```

## 2.8 Class Fecundity Definition

### 2.8.1 Female Fecundity

```
female fecondity of each class : fec
female fecondity of each class : 0 0 0 1 2 0 0 0 1 2
```

Relative quantity of seeds *e.g.* the seeds has twice as many chances to come from the class 5 than from the class 4.

### 2.8.2 Male Fecundity

```
male fecondity of each class : fecm
male fecondity of each class : 0 0 0 50 100 0 0 0 50 100
```

Relative quantity of pollen *e.g.* the pollen has twice as many chances to come from the class 5 than from the class 4.

### 2.8.3 Normal Vegetative Fecundity

Normal vegetative fecundity per class when sexual reproduction is present (whatever the population).

```
normal vegetative fecondity for each class : fecvn
normal vegetative fecondity for each class : 0 0 0 0.1 0.2
```

### 2.8.4 Increased Vegetative Fecundity

Increased vegetative fecundity per class when sexual reproduction is absent (whatever the population).

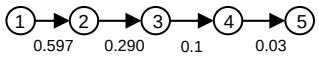
```
increased vegetative fecondity for each class : fecvi
increased vegetative fecondity for each class : 0 0 0 1 2
```

## 2.9 Classes' Definition bis

### 2.9.1 Transition Rate

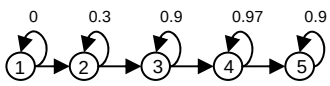
```
transition rate in each class : pass
transition rate in each class : 0.597 0.290 0.1 0.03
```

*E.g.*:




### 2.9.2 Survival Rate

```
survival rate in each class : survie
survival rate in each class : 0 0.30 0.90 0.97 0.90
```




*E.g.*:

### 2.9.3 Class Size

Equivalent size per class (size occupied by all individuals of a class).

```
equivalent size of each class : enc
equivalent size of each class : 0.01 0.5 1 2 3
```

## 2.10 Equilibrate Maximum Number

Equilibrate or not the maximum number of individuals per population (=y equilibrate; =n not equilibrate).

```
Equilibrer Nindmax : equil_nindmax
Equilibrer Nindmax : y
```

## 2.11 Maximum Number of Individuals

Maximum number of individuals per population

```
Maximum number of individuals in each population : Nindmax
Maximum number of individuals in each population : 5000 5000
```

## 2.12 Equilibrate Initial Number

Equilibrate the initial number of individuals per population (=0 don't equilibrate the class; =1 equilibrate the class)

```
Equilibrate initial number of individuals in each population : equil_initial_nc
Equilibrate initial number of individuals in each population : 0 0 0 1 1 0 0 0 1 0
```

## 2.13 Initial Number Setting

### 2.13.1 Label

Line label.

```
Initial number of individuals in each population and each class
```

### 2.13.2 Class Header

Class header.

```
cla1   cla2   cla3   cla4   cla5
```

### 2.13.3 Initial Number per population and class

For each population and class, the initial number of individuals is set.

```
pop# Nctemp_config
pop# 10  10  10  10  10
```

With # as ongoing number of population

## 2.14 Number of Alleles

Number of alleles for each locus – nuclear then cytoplasmic. The number of alleles is fixed to 256 per locus.

### 2.14.1 Number of Nuclear Alleles

```
Number of alleles for each nuclear locus : Nalleles
Number of alleles for each nuclear locus : 2 4 4 4 4 4 4 4
```

### 2.14.2 Number of Cytoplasmic Alleles

```
Number of alleles for each cytoplasmic locus : Nalleles
Number of alleles for each cytoplasmic locus : 5
```

## 2.15 Nuclear Locus Definition

Definition of the nuclear loci: microsatellite or AFLP.

### 2.15.1 Microsatellite Locus

0= not a microsatellite locus; 1= microsatellite locus

```
Microsatellite loci : Locus_usat
Microsatellite loci : 0  1  0  0  1  0  0  0
```

### 2.15.2 AFLP Locus

0= not an AFLP locus; 1= AFLP locus

```
Microsatellite loci : Locus_aflp
Microsatellite loci : 0  0  1  0  0  0  1  0
```

## 2.16 Selection Settings

### 2.16.1 Kind of Selection

Different kinds of selection are available:

- g = only genotype
- d = phenotypic directional
- t = phenotypic stabilizing
- n = no selection

```
Kind of selection : select_type
Kind of selection : g
```

According to the defined kind of selection, different results are generated (*cf. Figure 5*):

- kind of selection = “g” : refer to lines -33 and -34
- kind of selection = “d” or “t” : refer to lines from -35 to -40

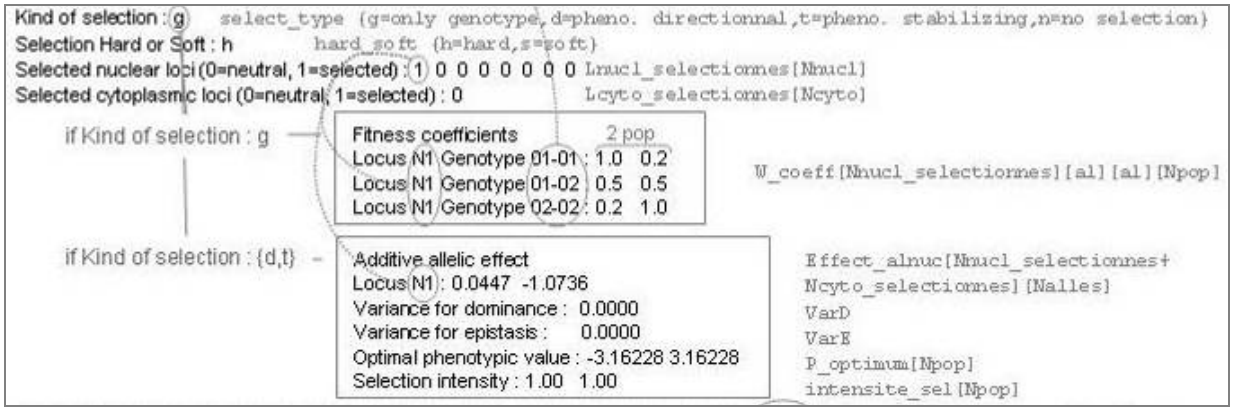



***Figure 5:*** *Extract of the “conf” file focused on the kind of selection and respective settings*

### 2.16.2 Selection

Hard or soft selection:

- h = hard
- s = soft

```
Selection Hard or Soft : hard_soft
Selection Hard or Soft : h
```

### 2.16.3 Nuclear Locus Selection

0= neutral; 1=selected

```
Selected nuclear loci (0=neutral, 1=selected) : Lnucl_selectionnes
Selected nuclear loci (0=neutral, 1=selected) : 1  0  0  0  0  0  0  0
```

### 2.16.4 Cytoplasmic Locus Selection

0= neutral; 1=selected

```
Selected nuclear loci (0=neutral, 1=selected) : Lcyto_selectionnes
Selected cytoplasmic loci (0=neutral, 1=selected) : 0
```

## 2.17 Fitness Coefficients Settings

If the kind of selection is genotypic (line -30), the fitness coefficients are generated for the selected nuclear loci (line -31).

#### 2.17.1 Label

```
Fitness coefficients
```

#### 2.17.2 Fitness Coefficients

```
Locus N1 Genotype 01-01 : W_coeff
Locus N1 Genotype 01-01 : 1.0    0.2
Locus N1 Genotype 01-02 : 0.5    0.5
Locus N1 Genotype 02-02 : 0.2    1.0
```

*E.g*. only the first nuclear locus is selected (defined in line -31) with two alleles (line -25); that's why fitness coefficients are defined only for the "Locus N1" with two values.

### 2.18 Additive Allelic Effects Settings

If the kind of selection is not genotypic (defined in line -30), the additive allelic effects are generated for the selected nuclear loci (line -31).

#### 2.18.1 Label

```
Additive allelic effect
```

#### 2.18.2 Additive Allelic Effects

Additive allelic effect for each allele of each selected locus (nuclear and then cytoplasmic)

```
Locus N1 : Effect_alnuc
Locus N1 : 0.0447   -1.0736
```

*E.g*. only the first nuclear locus is selected (line -31) with two alleles (line -25); that's additive allelic effects are defined only for the "Locus N1" with two values.

### 2.19 Variances

Variances are taken into account only if different from zero.

#### 2.19.1 Variance for Dominance

```
Variance for dominance :  VarD
Variance for dominance :  0.0000
```

#### 2.19.2 Variance for Epistasis

```
Variance for epistasis :  VarE
Variance for epistasis :  0.0000
```

### 2.20 Optimal Phenotypic Value

Optimal phenotypic value per population

```
Optimal phenotypic value : P_optimum
Optimal phenotypic value : -3.16228 3.16228
```

### 2.21 Selection Intensity

```
Selection intensity : intensite_sel
Selection intensity : 1.00   1.00
```

### 2.22 Genetic Map

Recombination rates between the nuclear loci:

- the first value corresponds to the rate between the 1st and 2nd loci *e.g.* "0,5"
- the last value corresponds to the rate between the last and the 1st loci

```
Recombination rates between the nuclear loci : R_coeff
Recombination rates between the nuclear loci : 0.5 0.25 0.5 0.25 0.25 0.5 0.25 0.25
```

The default value could be set at "0.5"; a validation is required.

## 2.23 Cytoplasmic inheritance

Paternal inheritance rates for the cytoplasmic loci:

- 0 = maternal inheritance
- 1 = paternal inheritance
- 0.2 = 20% chance being paternal inherited

```
Paternal inheritance rates for the cytoplasmic loci : H_coeff
```

```
Paternal inheritance rates for the cytoplasmic loci : 0
```

In practice, for each cytoplasmic locus, when a descendant is built, a random number is generated between 0 and 1; if that number is less than the "H_coeff" of the locus, the allele code from the father is taken; else it's the maternal one.

## 2.24 Pollen Flow Matrix

### 2.24.1 Label

```
Pollen flow matrix
```

### 2.24.2 Pollen Flow Matrix

```
F_coeff
```

```
0.999 0.001
0.001 0.999
```

## 2.25 Seed Flow Matrix

### 2.25.1 Label

```
Seed flow matrix
```

### 2.25.2 Seed Flow Matrix

```
G_coeff
```

```
0.999 0.001
0.001 0.999
```

## 2.26 Mutation Rates

Mutation rates of each locus – nuclear then cytoplasmic.

### 2.26.1 Nuclear Locus Mutation Rates

```
Mutation rate of each nuclear locus : M_coeff
```

```
Mutation rate of each nuclear locus : 0.0001  0.0001  0.0001  0.0001  0.0001
0.0001   0.0001  0.0001
```

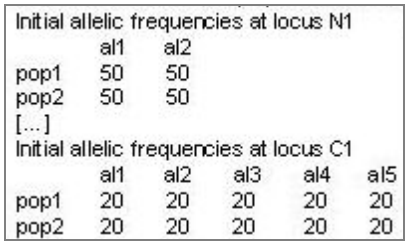
### 2.26.2 Cytoplasmic Locus Mutation Rates

```
Mutation rate of each cytoplasmic locus : M_coeff
```

```
Mutation rate of each cytoplasmic locus : 0.000001
```

## 2.27 Initial Allelic Frequencies Settings

In case a "save.txt" file is loaded at the simulation initialisation, the given initial allelic frequencies settings will not be taken into account but fake data have to be within the "conf.txt" file: the structure of the "N_coeff" parameter must be right.



Initial allelic frequencies at locus N1

| | al1 | al2 |
|---|---|---|
| pop1 | 50 | 50 |
| pop2 | 50 | 50 |

[...]

Initial allelic frequencies at locus C1

| | al1 | al2 | al3 | al4 | al5 |
|---|---|---|---|---|---|
| pop1 | 20 | 20 | 20 | 20 | 20 |
| pop2 | 20 | 20 | 20 | 20 | 20 |

***Figure 6:*** *Extract of the "conf" file focused on the initial allelic frequencies settings*

### 2.27.1 Label

For each locus – nuclear and then cytoplasmic

```
Initial allelic frequencies at locus N1
```

### 2.27.2 Header of Alleles

For each allele defined for the given locus, refer to line -25 for the allele number definition per locus.

```
                al1       al2
```

### 2.27.3 Initial Allelic Frequencies

Initial allelic frequencies displayed per locus, alleles and populations

```
N_coeff
pop1       50    50
pop2       50    50
```

# 3 Annex 2 – Type of Results File

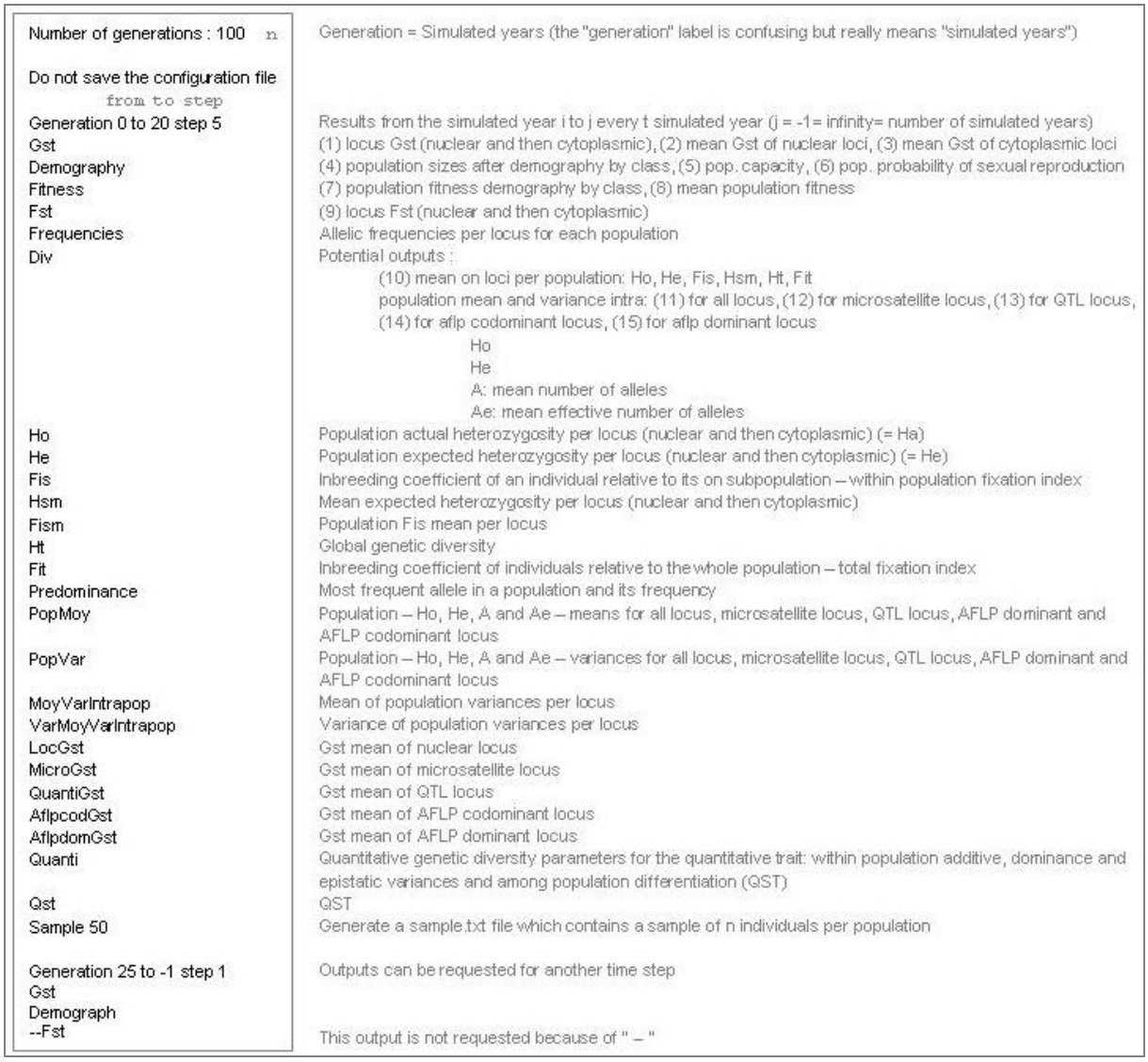



***Figure 7**: "type.txt" file*

File read by "resultd.c" file in C++ code.

## 3.1 File Format

- Lines are not numbered; a line is recognised throughout its label and more over, the number of words or characters that composed the label.
- Empty lines don't matter.
- Lines beginning with "--" are not taken into account.

## 3.2 Number of generations

Total number of simulated years (equivalent to the "ngenerationmax" parameter)

| `Number of generations : n` |
|---|
| `Number of generations : 100` |

## 3.3 Save Settings

| `Do not save the configuration file` |
|---|

This line is not mandatory.

Per default, the configuration file ("conf.txt") is saved. On the contrary, the configuration file is not saved if this line is defined.

## 3.4 Results' Structure

A structure of results corresponds to the list of types of results requested for a set of simulated years. Maximum 30 structures of results can be defined.

### 3.4.1 Results' Structure Settings

| `Generation from to to step step` |
|---|
| `Generation from 0 to 20 step 5` |

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| from | Simulated year from which the outputs are displayed | 1 |
| to | Simulated year to which the outputs are displayed<br>If "to" = -1, requested outputs are displayed for all simulated years | 2 |
| step | Outputs are displayed every "steo" simulated years | 3 |

### 3.4.2 List of Types of Results

| Type of result name | Description |
|---|---|
| Gst | Display locus Gst (nuclear and then cytoplasmic), mean Gst of nuclear loci and mean Gst of cytoplasmic loci |
| Demography | Display population sizes after demography by class, population capacity and population probability of sexual reproduction |
| Fitness | Display population fitness demography by class and mean population fitness |
| Fst | Display locus Fst (nuclear and then cytoplasmic) |
| Frequencies | Display allelic frequencies per locus for each population |
| Ho | Display the population observed heterozygosity per locus (nuclear and then cytoplasmic) (= Ha) |
| He | Display the population expected heterozygosity per locus (nuclear and then cytoplasmic) (= He) |
| Fis | Display the inbreeding coefficient of an individual relative to its subpopulation – within population fixation index |
| Hsm | Display mean expected heterozygosity per locus (nuclear and then cytoplasmic) |
| Fism | Display population Fis mean per locus |
| Ht | Display the global genetic diversity |
| Fit | Display the inbreeding coefficient of individuals relative to the whole population – total fixation index |
| Predominance | Display the most frequent allele in a population and its frequency (as this type of result is useful, it can be kept) |
| Div | Display: mean on loci per population for potential outputs (Ho, He, Fis, Hsm, Ht and Fit) and mean and variance intra per population for all locus, for microsatellite, for QTL, for aflp codominant and for aflp dominant |
| PopMoy | Display population – Ho, He, A and Ae – means for all locus, microsatellite locus, QTL locus, AFLP dominant and AFLP codominant locus |
| PopVar | Display population – Ho, He, A and Ae – variances for all locus, microsatellite locus, QTL locus, AFLP dominant and AFLP codominant locus |
| MoyVarIntrapop | Display mean of population variances per locus |
| VarMoyVarIntrapop | Display variance of population variances per locus |
| LocGst | Display Gst mean of nuclear locus |
| MicroGst | Display Gst mean of microsatellite locus |
| QuantiGst | Display Gst mean of QTL locus |
| AflpcodGst | Display Gst mean of AFLP codominant locus |
| AflpdomGst | Display Gst mean of AFLP dominant locus |
| Quanti | Display quantitative genetic diversity parameters for the quantitative trait: within population additive, dominance and epistatic variances and among population differentiation ($Q_{ST}$) |
| Qst | Display the $Q_{ST}$ |
| Ld | Display linkage disequilibrium (not validated yet, to be added in the MetaPop |

| | |
|---|---|
| | GUI) |
| Sample [sample_size] | Generate a “sample.txt” file which contains a sample of “sample_size” individuals per population<br>Example:<br>`Generation 0 to 10 step 5`<br>`Sample 50`<br>In that case, 3 sample files will be generated: “sample0.txt”, “sample5.txt” and “sample10”.txt. |

# 4 Annex 3 – Genotype File of the Last Simulated Year

The source file “ind.c” permits to load and save the “save.txt” file.

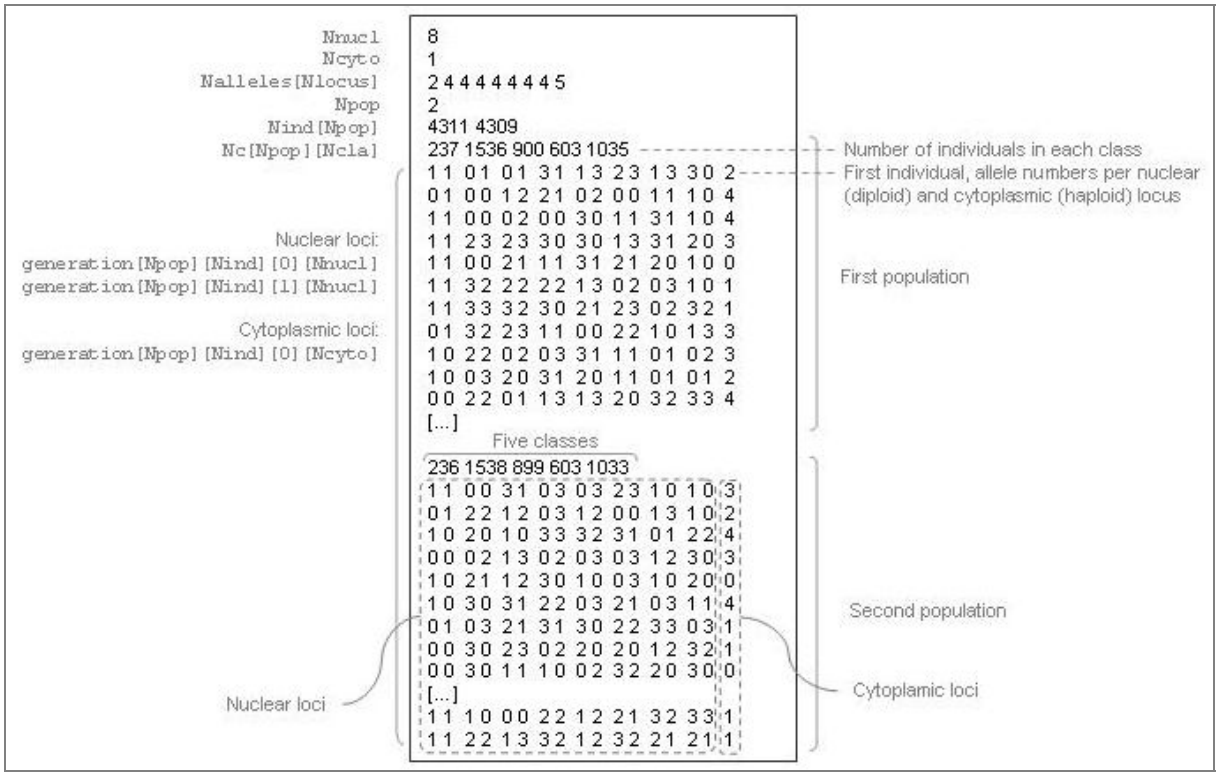



***Figure 8**: “save.txt” file*

## 4.1 File Format

- The parameters are ordered one after the other.

## 4.2 Number of Loci

### 4.2.1 Number of Nuclear Loci

| Nnucl |
|---|
| 8 |

### 4.2.2 Number of Cytoplasmic Loci

| Ncyto |
|---|
| 1 |

## 4.3 Number of Alleles

Setting of the number of alleles per locus – nuclear and then cytoplasmic

| Nalleles |
|---|
| 2 4 4 4 4 4 4 4 5 |

## 4.4 Number of Populations

| Npop |
|---|
| 2 |

## 4.5 Number of Individuals

Number of individuals in each population at a given simulated year

| Nind |
|---|
| 4311 4309 |

## 4.6 Individuals' Definition

To define the individuals at the last simulated year, for each population,

- A first line is generated to indicate the number of individuals in each class of that population
- Just below, one line per individual of that population is dedicated to its genotype (allele codes of nuclear and cytoplasmic loci).

### 4.6.1 Number of Individuals

Number of individuals in each class and population

| Nc |
|---|
| 237 1536 900 603 1035 |

### 4.6.2 Genotype

Allele codes of each locus (nuclear and then cytoplasmic) for each individual of each population at a given simulated year

| generation |
|---|
| 1 1  0 1  0 1  3 1  1 3  2 3  1 3  3 0  2 |

*E.g.* the 16 first values corresponds to the alleles codes of the 8 nuclear loci; the last value "2" corresponds to the allele code in the single cytoplasmic locus.

For print:

- 1 space between nuclear allele codes
- 2 spaces between nuclear allele codes and cytoplasmic allele code

# 5 Annex 4 – Result File

The procedure "Compute_results" in "resultd.c" MetaPop source file permits to compute the results.

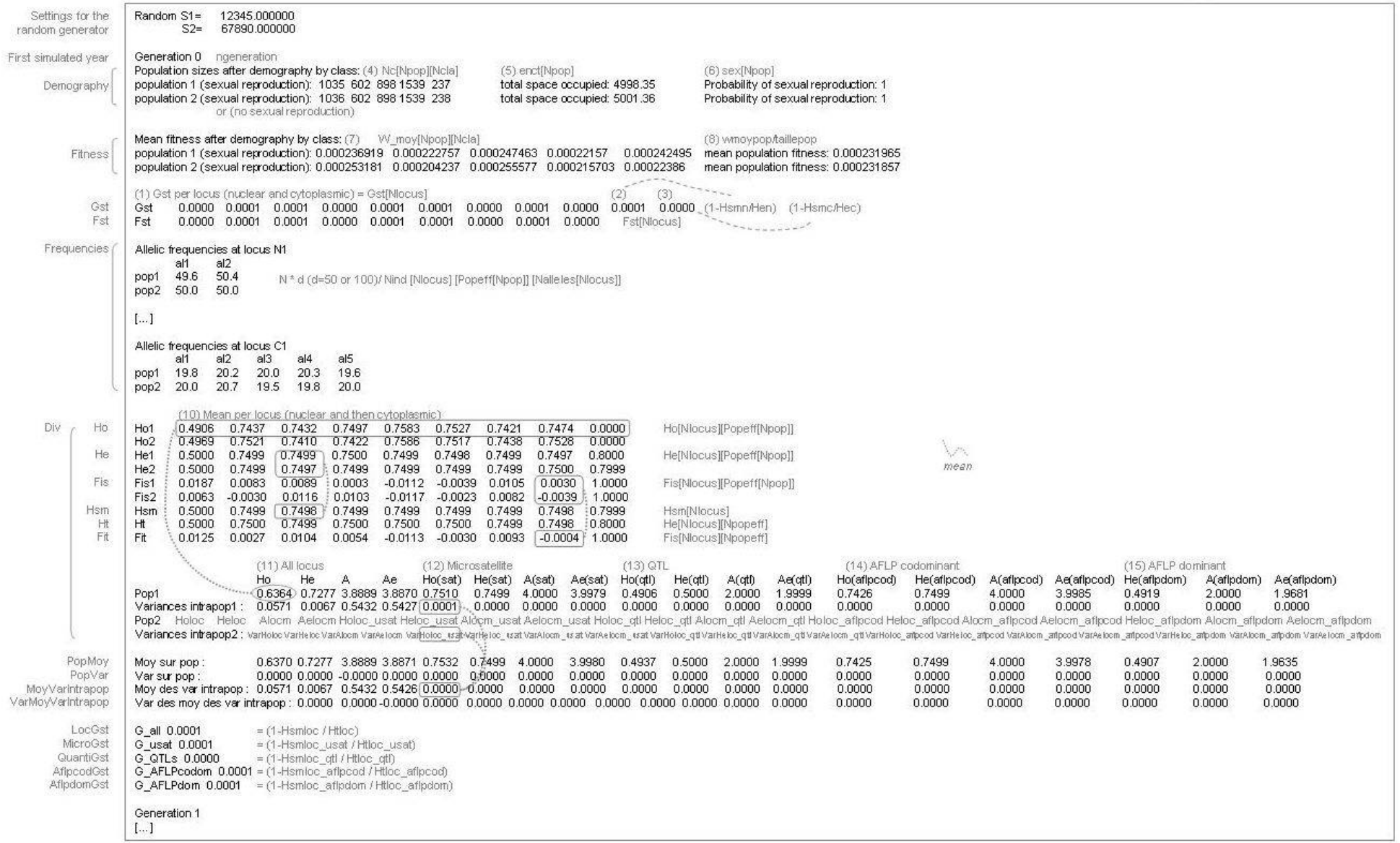



***Figure 9**: "res.txt" file*

## 5.1 File Format

- Decimal are expressed with a dot.
- Results are displayed according to the user request defined in the “type.txt” file.

## 5.2 Random Generator Settings

“void Srandom” in “proba.c” file

The random generator settings permit to reproduce a simulation using the same list of random numbers, etc.

### 5.2.1 First Random Generator Setting

```
Random S1= S1
Random S1= 12345.000000
```

### 5.2.2 Second Random Generator Setting

```
       S2= S2
       S2= 67890.000000
```

## 5.3 Current Simulated Year

The ongoing simulated year to which the results are computed is displayed next to the “Generation” label.

```
Generation ngeneration
Generation 0
```

## 5.4 Demography Results

Those lines are only generated if the “Demography” type of results is requested in the “type.txt” file.

“void Print_demo_cla” in “demo_migr.c” file

The first line is the header of the demographical results; then, one line is dedicated to each population for displaying the “Nc”, “enct” and “sex” parameters.

### 5.4.1 Label

```
Population sizes after demography by class:
```

### 5.4.2 Demographical Results per Class

```
population pop (sexual reproduction): Nc                  total space occupied:
enct         Probability of sexual reproduction: sex
population 1 (sexual reproduction): 1035 602 898 1539 237  total space occupied:
4998.35      Probability of sexual reproduction: 1
```

- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: “population” | | 1 |
| pop | Ongoing population number (MetaPop local parameter) | 2 |
| Label different given the “repsex” parameter:<br>“(no sexual reproduction)” for “repsex”=0 or<br>“(sexual reproduction)” for “repsex”=1 | | 3 |
| Nc | Number of individuals per population and per class | 4 |
| Label: “total space occupied:” | | 5 |
| enct | Total stand basal area per population | 6 |
| Label: “Probability of sexual reproduction:” | | 7 |
| sex | Probability of sexual reproduction | 8 |

## 5.5 Fitness Demographical Results

Those lines are only generated if the “Fitness” type of results is requested in the “type.txt” file.

The first line is the header; then, one line is dedicated to each population for displaying the population fitness demography by class and the mean population fitness.

### 5.5.1 Label

```
Mean fitness after demography by class:
```

### 5.5.2 Fitness Demographical Results per Class

```
population pop (sexual reproduction): W_moy   mean population fitness:
wmoypop/taillepop
population 1 (sexual reproduction): 0.000236919   0.000222757   0.000247463
0.00022157     0.000242495       mean population fitness: 0.000231965
```

- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: “population” | | 1 |
| pop | Ongoing population number (MetaPop local parameter) | 2 |
| Label different given the “repsex” parameter:<br>“(no sexual reproduction)” for “repsex”=0 or<br>“(sexual reproduction)” for “repsex”=1 | | 3 |
| W_moy | Mean population fitness per population and per class | 4 |
| Label: “mean population fitness :” | | 5 |
| TreeMBase_mean_pop_fitness | Mean population fitness = wmoypop / taillepop | 6 |

- “TreeMBase_mean_pop_fitness” parameter is created to represent the parameter composed of the “wmoypop” and “taillepop” MetaPop local parameters.

| | | |
|---|---|---|
| wmoypop | Total fitness per population (MetaPop local parameter) | 6 |
| taillepop | Total number of individuals per population (MetaPop local parameter) | 6 |

## 5.6 Gst Results

That line is only generated if the “Gst” type of results is requested in the “type.txt” file.

```
Gst  Gst     1-Hsmn/Hen    1-Hsmc/Hec
Gst  0.0000 0.0001 0.0001 0.0000 0.0001 0.0001 0.0000 0.0001 0.0000   0.0001 0.0000
```

- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: “Gst” | | 1 |
| Gst | Gst per locus (nuclear and then cytoplasmic) | 2 |
| TreeMBase_mean_gstn | Mean Gst of nuclear loci | 3 |
| TreeMBase_mean_gstc | Mean Gst of cytoplasmic loci | 4 |

- “TreeMBase_mean_gstn” parameter is created to represent the calculation: 1-Hsmn/Hen.
- “TreeMBase_mean_gstn” parameter is created to represent the calculation: 1-Hsmc/Hec.

| | | |
|---|---|---|
| Hsmn | Cumulative Hsm[Nnucl] | 3 |
| Hen | Cumulative He[Nnucl][Npopeff] | 3 |
| Hsmc | Cumulative Hsm[cytoplasmic loci] | 4 |
| Hec | Cumulative He[cytoplasmic loci][Npopeff] | 4 |

## 5.7 Fst Results

That line is only generated if the “Fst” type of results is requested in the “type.txt” file.

```
Fst   Fst
Fst   0.0000   0.0001   0.0001   0.0000   0.0001  0.0001   0.0000   0.0001   0.0000
```

- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: “Fst” | | 1 |
| Fst | Fst per locus (nuclear and then cytoplasmic) | 2 |

## 5.8 Allelic Frequencies

The allelic frequencies are only generated if the “Frequencies” type of results is requested in the “type.txt” file.

```
Allelic frequencies at locus N1
        al1     al2
pop1     49.6    50.4
pop2     50.0    50.0

Allelic frequencies at locus N2
        al1     al2     al3     al4
pop1     25.3    24.4    25.7    24.5
pop2     24.2    24.8    25.3    25.7

Allelic frequencies at locus N3
        al1     al2     al3     al4
pop1     25.1    25.2    25.5    24.3
pop2     24.2    24.1    26.1    25.6
```

[…]

```
Allelic frequencies at locus N8
        al1     al2     al3     al4
pop1     26.4    25.1    24.8    23.8
pop2     25.4    25.3    24.8    24.5

Allelic frequencies at locus C1
        al1     al2     al3     al4     al5
pop1     19.8    20.2    20.0    20.3    19.6
pop2     20.0    20.7    19.5    19.8    20.0
```

***Figure 10 :*** *Extract of the “res” file focused on the allelic frequencies*

### 5.8.1 Labels

Two lines are displayed before the allelic frequencies:

- The first line permits to identify the locus with a letter (“N” for nuclear and “C” for cytoplasmic) plus an identifying number.
- The second line lists the allele codes corresponding to the current locus.

```
Allelic frequencies at locus N1
       al1    al2
```

### 5.8.2 Allelic Frequencies Values

```
Poppop  N * d / Nind
pop1    49.6   50.4
pop2    50.0   50.0
```

- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: “pop” | | 1 |
| pop | Ongoing population number (MetaPop local parameter) | 2 |
| TreeMBase_frequencies | Allele frequency per locus, per population and per allele expressed as percentage | 3 |

- “TreeMBase_frequencies” parameter is created to represent the calculation: N * d / Nind.

| | | |
|---|---|---|
| N | Number of allele copies per locus, per population and per allele | 3 |
| d | d = 50 or 100 | 3 |
| Nind | Number of individuals per population | 3 |

## 5.9 Potential Outputs – Mean per Locus and Population

Means on loci per population can be displayed for potential outputs – Ho, He, Fis, Hsm, Ht, Fit – only if the "Div" type of results is requested in the "type.txt" file. Mean and variance intra per population are also generated.

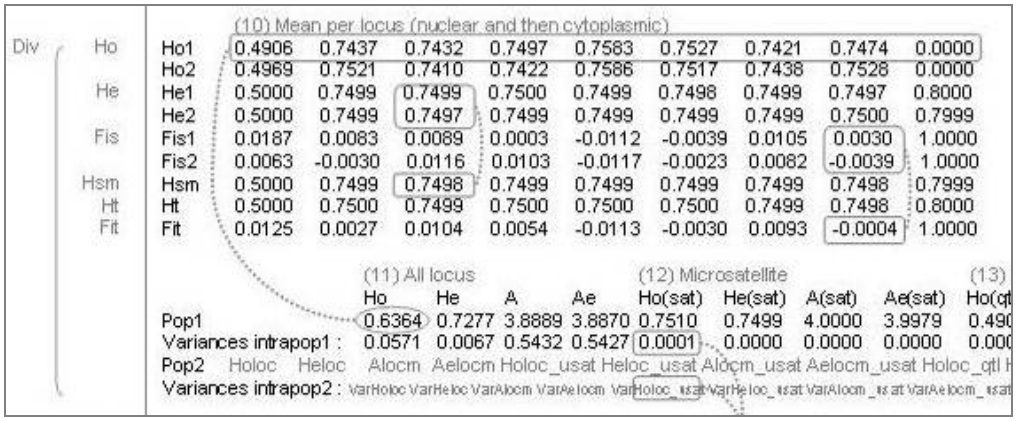



***Figure 11 :*** *Extract of the "res" file focused on the potential outputs (mean per locus and population)*

### 5.9.1 Ho – Actual Heterozygosity

A line is displayed for each population; as many values as number of loci (nuclear and then cytoplasmic) are generated.

```
Hopop Ho
Ho1 0.4906   0.7437   0.7432   0.7497   0.7583   0.7527   0.7421   0.7474   0.0000
```

- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: "Ho" | | 1 |
| pop | Ongoing population number (MetaPop local parameter) | 2 |
| Ho | Observed heterozygosity per locus in each population | 3 |

### 5.9.2 He – Expected Heterozygosity

A line is displayed for each population; as many values as number of loci (nuclear and then cytoplasmic) are generated.

```
Hepop He
He1 0.5000   0.7499   0.7499   0.7500   0.7499   0.7498   0.7499   0.7497   0.8000
```

- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: "He" | | 1 |
| pop | Ongoing population number (MetaPop local parameter) | 2 |
| He | Expected heterozygosity per locus in each population | 3 |

### 5.9.3 Fis – Within Population Fixation Index

A line is displayed for each population; as many values as number of loci (nuclear and then cytoplasmic) are generated.

```
Fispop Fis
Fis1 0.0187   0.0083   0.0089  0.0003  -0.0112  -0.0039  0.0105   0.0030   1.0000
```

- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: "Fis" | | 1 |
| pop | Ongoing population number (MetaPop local parameter) | 2 |
| Fis | Within population fixation index per locus in each population | 3 |

### 5.9.4 Hsm – Mean Expected Heterozygosity

A single line is displayed to display to means across populations of the previous "He" calculations; as many values as number of loci (nuclear and then cytoplasmic) are generated.

```
Hsm Hsm
Hsm  0.5000   0.7499   0.7498   0.7499  0.7499   0.7499   0.7499   0.7498   0.7999
```

- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: "Hsm" | | 1 |
| Hsm | Mean expected heterozygosity per locus across population | 2 |

### 5.9.5 Ht – Global Genetic Diversity

A single line is displayed; as many values as number of loci (nuclear and then cytoplasmic) are generated.

```
Ht TreeMBase_Ht
Ht  0.5000   0.7500   0.7499   0.7500  0.7500   0.7500   0.7499   0.7498   0.8000
```

- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: "Ht" | | 1 |
| TreeMBase_Ht | Global genetic diversity | 2 |

- "TreeMBase_Ht" parameter is created to represent the calculation: He[Nlocus][Npopeff].

| | | |
|---|---|---|
| He | Expected heterozygosity per locus in each population | 2 |
| Nlocus | Number of loci (nuclear loci + cytoplasmic loci) | 2 |
| Npopeff | Number of populations with at least 10 individuals | 2 |

### 5.9.6 Fit – Total Fixation Index

A single line is displayed to display to means across populations of the previous "Fis" calculations; as many values as number of loci (nuclear and then cytoplasmic) are generated.

```
Fit TreeMBase_Fit
Fit 0.0125   0.0027   0.0104   0.0054   -0.0113  -0.0030  0.0093   -0.0004  1.0000
```

- **Parameters**

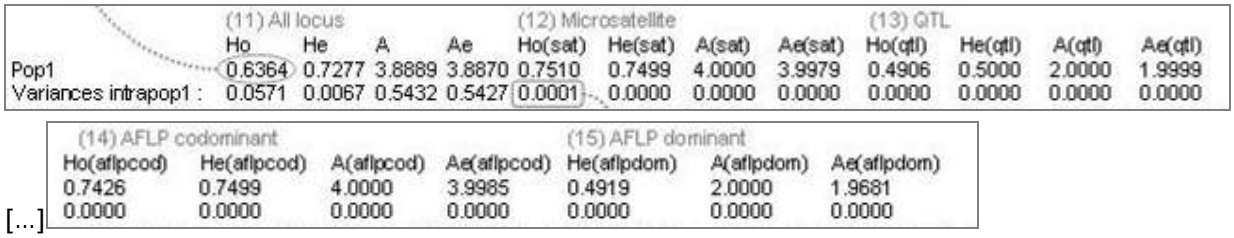
| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: "Fit" | | 1 |
| TreeMBase_Fit | Total fixation index | 2 |

- "TreeMBase_Fit" parameter is created to represent the calculation: Fis[Nlocus][Npopeff].

| | | |
|---|---|---|
| Fis | Within population fixation index per locus in each population | 2 |
| Nlocus | Number of loci (nuclear loci + cytoplasmic loci) | 2 |
| Npopeff | Number of populations with at least 10 individuals | 2 |

### 5.9.7 Mean and Variance Intra per Population

Per population, a line is dedicated to the population means and another one for the variances intra (*cf. Figure 12*). The results are always generated for all loci and, if defined, possibly for microsatellite, QTL, AFLP codominant and AFLP dominant loci.



| | (11) All locus | | | | (12) Microsatellite | | | | (13) QTL | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | Ho | He | A | Ae | Ho(sat) | He(sat) | A(sat) | Ae(sat) | Ho(qtl) | He(qtl) | A(qtl) | Ae(qtl) |
| Pop1 | 0.6364 | 0.7277 | 3.8889 | 3.8870 | 0.7510 | 0.7499 | 4.0000 | 3.9979 | 0.4906 | 0.5000 | 2.0000 | 1.9999 |
| Variances intrapop1 : | 0.0571 | 0.0067 | 0.5432 | 0.5427 | 0.0001 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 | 0.0000 |



[...]

***Figure 12 :*** *Extract of the "res" file focused on the population mean and variance intra*

A first line contains the labels.

```
Ho  He  A  Ae  Ho(sat)  He(sat)  A(sat)  Ae(sat)  Ho(qtl)  He(qtl)  A(qtl)  Ae(qtl)
Ho(aflpcod) He(aflpcod) A(aflpcod) Ae(aflpcod) He(aflpdom) A(aflpdom) Ae(aflpdom)
```

The second line displays the population mean results.

```
Pop1 0.6364  0.7277  3.8889  3.8870  0.7510  0.7499  4.0000  3.9979  0.4906  0.5000
2.0000  1.9999  0.7426  0.7499  4.0000  3.9985  0.4919  2.0000  1.9681
```

- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: “Pop” | | 1 |
| pop | Ongoing population number (MetaPop local parameter) | 2 |
| Holoc | Population Ho mean across loci in each population | 3 |
| Heloc | Population He mean across loci in each population | 4 |
| Alocm | Population A across loci in each population | 5 |
| Aelocm | Population Ae across loci in each population | 6 |
| Holoc_usat | Population Ho mean across microsatellite loci in each population | -7 |
| Heloc_usat | Population He mean across microsatellite loci in each population | -8 |
| Alocm_usat | Population A mean across microsatellite loci in each population | -9 |
| Aelocm_usat | Population Ae mean across microsatellite loci in each population | -10 |
| Holoc_qtl | Population Ho mean across QTL loci in each population | -11 |
| Heloc_qtl | Population He mean across QTL loci in each population | -12 |
| Alocm_qtl | Population A mean across QTL loci in each population | -13 |
| Aelocm_qtl | Population Ae mean across QTL loci in each population | -14 |
| Holoc_aflpcod | Population Ho mean across AFLP codominant loci in each population | -15 |
| Heloc_aflpcod | Population He mean across AFLP codominant loci in each population | -16 |
| Alocm_aflpcod | Population A mean across AFLP codominant loci in each population | -17 |
| Aelocm_aflpcod | Population Ae mean across AFLP codominant loci in each population | -18 |
| Heloc_aflpdom | Population Ho mean across AFLP dominant loci in each population | -19 |
| Alocm_aflpdom | Population He mean across AFLP dominant loci in each population | -20 |
| Aelocm_aflpdom | Population A mean across AFLP dominant loci in each population | -21 |

NB: As the order could vary according to the loci definitions (microsatellite, QTL, etc.), ranks in line could be negative.

The third line displays the variance intra results per population.

```
Variances intrapop1 : 0.0571  0.0067  0.5432  0.5427  0.0001  0.0000  0.0000
0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000  0.0000
0.0000  0.0000
```

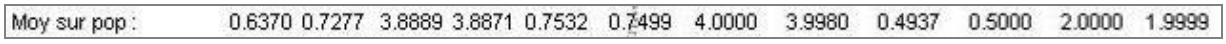
- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: “Variances intrapop” | | 1 |
| pop | Ongoing population number (MetaPop local parameter) | 2 |
| VarHoloc | Population Ae mean across AFLP dominant loci in each population | 3 |
| VarHeloc | Population He variance across loci in each population | 4 |
| VarAlocm | Population A variance across loci in each population | 5 |
| VarAelocm | Population Ae variance across loci in each population | 6 |
| VarHoloc_usat | Population Ho variance across microsatellite loci in each population | -7 |
| VarHeloc_usat | Population He variance across microsatellite loci in each population | -8 |
| VarAlocm_usat | Population A variance across microsatellite loci in each population | -9 |
| VarAelocm_usat | Population Ae variance across microsatellite loci in each population | -10 |
| VarHoloc_qtl | Population Ho variance across QTL loci in each population | -11 |
| VarHeloc_qtl | Population He variance across QTL loci in each population | -12 |
| VarAlocm_qtl | Population A variance across QTL loci in each population | -13 |
| VarAelocm_qtl | Population Ae variance across QTL loci in each population | -14 |
| VarHoloc_aflpcod | Population Ho variance across AFLP codominant loci in each population | -15 |

| | | |
|---|---|---|
| VarHeloc_aflpcod | Population He variance across AFLP codominant loci in each population | -16 |
| VarAlocm_aflpcod | Population A variance across AFLP codominant loci in each population | -17 |
| VarAelocm_aflpcod | Population Ae variance across AFLP codominant loci in each population | -18 |
| VarHeloc_aflpdom | Population He variance across AFLP dominant loci in each population | -19 |
| VarAlocm_aflpdom | Population A variance across AFLP dominant loci in each population | -20 |
| VarAelocm_aflpdom | Population Ae variance across AFLP dominant loci in each population | -21 |

## 5.10 Population Mean

A single line is displayed with the population means on loci – Ho, He, A and Ae; only if the "PopMoy" type of results is requested in the "type.txt" file.




- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: "Moy sur pop :" | | 1 |
| TreeMBase_getmean_Npop_Holoc | Get_mean(Npopeff, Holoc) | 2 |
| TreeMBase_getmean_Npop_Heloc | Get_mean(Npop,Heloc) | 3 |
| TreeMBase_getmean_Npop_Alocm | Get_mean(Npop,Alocm) | 4 |
| TreeMBase_getmean_Npop_Aelocm | Get_mean(Npop,Aelocm) | 5 |
| TreeMBase_getmean_Npop_Holoc_usat | Get_mean(Npoo,Holoc_usat) | -6 |
| TreeMBase_getmean_Npop_Heloc_usat | Get_mean(Npop,Heloc_usat) | -7 |
| TreeMBase_getmean_Npop_Alocm_usat | Get_mean(Npop,Alocm_usat) | -8 |
| TreeMBase_getmean_Npop_Aelocm_usat | Get_mean(Npop,Aelocm_usat) | -9 |
| TreeMBase_getmean_Npop_Holoc_qtl | Get_mean(Npop,Holoc_qtl) | -10 |
| TreeMBase_getmean_Npop_Heloc_qtl | Get_mean(Npop,Heloc_qtl) | -11 |
| TreeMBase_getmean_Npop_Alocm_qtl | Get_mean(Npop,Alocm_qtl) | -12 |
| TreeMBase_getmean_Npop_Aelocm_qtl | Get_mean(Npop,Aelocm_qtl) | -13 |
| TreeMBase_getmean_Npop_Holoc_aflpcod | Get_mean(Npop,Holoc_aflpcod) | -14 |
| TreeMBase_getmean_Npop_Heloc_aflpcod | Get_mean(Npop,Heloc_aflpcod) | -15 |
| TreeMBase_getmean_Npop_Alocm_aflpcod | Get_mean(Npop,Alocm_aflpcod) | -16 |
| TreeMBase_getmean_Npop_Aelocm_aflpcod | Get_mean(Npop,Aelocm_aflpcod) | -17 |
| TreeMBase_getmean_Npop_Heloc_aflpdom | Get_mean(Npop,Heloc_aflpdom) | -18 |
| TreeMBase_getmean_Npop_Alocm_aflpdom | Get_mean(Npop,Alocm_aflpdom) | -19 |
| TreeMBase_getmean_Npop_Aelocm_aflpdom | Get_mean(Npop,Aelocm_aflpdom) | -20 |

- "TreeMBase_getmean_Npop_..." parameters are created to represent the calculation made in the "Get_mean" function.

## 5.11 Population Variance

A single line is displayed with the population variances on loci – Ho, He, A and Ae; only if the "PopVar" type of results is requested in the "type.txt" file.


- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: "Var sur pop :" | | 1 |
| TreeMBase_getvar_Npop_Holoc | Get_var(Npop,Holoc) | 2 |
| TreeMBase_getvar_Npop_Heloc | Get_var(Npop,Heloc) | 3 |
| TreeMBase_getvar_Npop_Alocm | Get_var(Npop,Alocm) | 4 |
| TreeMBase_getvar_Npop_Aelocm | Get_var(Npop,Aelocm) | 5 |
| TreeMBase_getvar_Npop_Holoc_usat | Get_var(Npop,Holoc_usat) | -6 |

| | | |
|---|---|---|
| TreeMBase_getvar_Npop_Heloc_usat | Get_var(Npop,Heloc_usat) | -7 |
| TreeMBase_getvar_Npop_Alocm_usat | Get_var(Npop,Alocm_usat) | -8 |
| TreeMBase_getvar_Npop_Aelocm_usat | Get_var(Npop,Aelocm_usat) | -9 |
| TreeMBase_getvar_Npop_Holoc_qtl | Get_var(Npop,Holoc_qtl) | -10 |
| TreeMBase_getvar_Npop_Heloc_qtl | Get_var(Npop,Heloc_qtl) | -11 |
| TreeMBase_getvar_Npop_Alocm_qtl | Get_var(Npop,Alocm_qtl) | -12 |
| TreeMBase_getvar_Npop_Aelocm_qtl | Get_var(Npop,Aelocm_qtl) | -13 |
| TreeMBase_getvar_Npop_Holoc_aflpcod | Get_var(Npop,Holoc_aflpcod) | -14 |
| TreeMBase_getvar_Npop_Heloc_aflpcod | Get_var(Npop,Heloc_aflpcod) | -15 |
| TreeMBase_getvar_Npop_Alocm_aflpcod | Get_var(Npop,Alocm_aflpcod) | -16 |
| TreeMBase_getvar_Npop_Aelocm_aflpcod | Get_var(Npop,Aelocm_aflpcod) | -17 |
| TreeMBase_getvar_Npop_Heloc_aflpdom | Get_var(Npop,Heloc_aflpdom) | -18 |
| TreeMBase_getvar_Npop_Alocm_aflpdom | Get_var(Npop,Alocm_aflpdom) | -19 |
| TreeMBase_getvar_Npop_Aelocm_aflpdom | Get_var(Npop,Aelocm_aflpdom) | -20 |

- "TreeMBase_getvar_Npop_..." parameters are created to represent the calculation made in the "Get_var" function.

## 5.12 Mean of Population Variance

A single line is displayed with the mean of population variances on loci – Ho, He, A and Ae; only if the "MoyVarIntrapop" type of results is requested in the "type.txt" file.

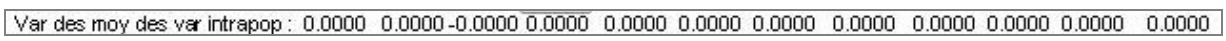

- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: "Moy des var intrapop :" | | 1 |
| TreeMBase_getmean_Npop_VarHoloc) | Get_mean(Npop,VarHoloc) | 2 |
| TreeMBase_getmean_Npop_VarHeloc) | Get_mean(Npop,VarHeloc) | 3 |
| TreeMBase_getmean_Npop_VarAlocm) | Get_mean(Npop,VarAlocm) | 4 |
| TreeMBase_getmean_Npop_VarAelocm) | Get_mean(Npop,VarAelocm) | 5 |
| TreeMBase_getmean_Npop_VarHoloc_usat) | Get_mean(Npop,VarHoloc_usat) | -6 |
| TreeMBase_getmean_Npop_VarHeloc_usat) | Get_mean(Npop,VarHeloc_usat) | -7 |
| TreeMBase_getmean_Npop_VarAlocm_usat) | Get_mean(Npop,VarAlocm_usat) | -8 |
| TreeMBase_getmean_Npop_VarAelocm_usat) | Get_mean(Npop,VarAelocm_usat) | -9 |
| TreeMBase_getmean_Npop_VarHoloc_qtl) | Get_mean(Npop,VarHoloc_qtl) | -10 |
| TreeMBase_getmean_Npop_VarHeloc_qtl) | Get_mean(Npop,VarHeloc_qtl) | -11 |
| TreeMBase_getmean_Npop_VarAlocm_qtl) | Get_mean(Npop,VarAlocm_qtl) | -12 |
| TreeMBase_getmean_Npop_VarAelocm_qtl) | Get_mean(Npop,VarAelocm_qtl) | -13 |
| TreeMBase_getmean_Npop_VarHoloc_aflpcod) | Get_mean(Npop,VarHoloc_aflpcod) | -14 |
| TreeMBase_getmean_Npop_VarHeloc_aflpcod) | Get_mean(Npop,VarHeloc_aflpcod) | -15 |
| TreeMBase_getmean_Npop_VarAlocm_aflpcod) | Get_mean(Npop,VarAlocm_aflpcod) | -16 |
| TreeMBase_getmean_Npop_VarAelocm_aflpcod) | Get_mean(Npop,VarAelocm_aflpcod) | -17 |
| TreeMBase_getmean_Npop_VarHeloc_aflpdom) | Get_mean(Npop,VarHeloc_aflpdom) | -18 |
| TreeMBase_getmean_Npop_VarAlocm_aflpdom) | Get_mean(Npop,VarAlocm_aflpdom) | -19 |
| TreeMBase_getmean_Npop_VarAelocm_aflpdom) | Get_mean(Npop,VarAelocm_aflpdom) | -20 |

- "TreeMBase_getmean_Npop_Var..." parameters are created to represent the calculation made in the "Get_mean" function.

## 5.13 Variance of Population Variance

A single line is displayed with the variance of population variances on loci – Ho, He, A and Ae; only if the "VarMoyVarIntrapop" type of results is requested in the "type.txt" file.




- **Parameters**

| Parameter name | Parameter description | Rank |
|---|---|---|

| | | in line |
|---|---|---|
| Label: “Var des moy des var intrapop :” | | 1 |
| TreeMBase_getvar_Npop_VarHoloc | Get_var(Npop,VarHoloc) | 2 |
| TreeMBase_getvar_Npop_VarHeloc | Get_var(Npop,VarHeloc) | 3 |
| TreeMBase_getvar_Npop_VarAlocm | Get_var(Npop,VarAlocm) | 4 |
| TreeMBase_getvar_Npop_VarAelocm | Get_var(Npop,VarAelocm) | 5 |
| TreeMBase_getvar_Npop_VarHoloc_usat | Get_var(Npop,VarHoloc_usat) | -6 |
| TreeMBase_getvar_Npop_VarHeloc_usat | Get_var(Npop,VarHeloc_usat) | -7 |
| TreeMBase_getvar_Npop_VarAlocm_usat | Get_var(Npop,VarAlocm_usat) | -8 |
| TreeMBase_getvar_Npop_VarAelocm_usat | Get_var(Npop,VarAelocm_usat) | -9 |
| TreeMBase_getvar_Npop_VarHoloc_qtl | Get_var(Npop,VarHoloc_qtl) | -10 |
| TreeMBase_getvar_Npop_VarHeloc_qtl | Get_var(Npop,VarHeloc_qtl) | -11 |
| TreeMBase_getvar_Npop_VarAlocm_qtl | Get_var(Npop,VarAlocm_qtl) | -12 |
| TreeMBase_getvar_Npop_VarAelocm_qtl) | Get_var(Npop,VarAelocm_qtl) | -13 |
| TreeMBase_getvar_Npop_VarHoloc_aflpcod | Get_var(Npop,VarHoloc_aflpcod) | -14 |
| TreeMBase_getvar_Npop_VarHeloc_aflpcod | Get_var(Npop,VarHeloc_aflpcod) | -15 |
| TreeMBase_getvar_Npop_VarAlocm_aflpcod | Get_var(Npop,VarAlocm_aflpcod) | -16 |
| TreeMBase_getvar_Npop_VarAelocm_aflpcod | Get_var(Npop,VarAelocm_aflpcod) | -17 |
| TreeMBase_getvar_Npop_VarHeloc_aflpdom | Get_var(Npop,VarHeloc_aflpdom) | -18 |
| TreeMBase_getvar_Npop_VarAlocm_aflpdom | Get_var(Npop,VarAlocm_aflpdom) | -19 |
| TreeMBase_getvar_Npop_VarAelocm_aflpdom | Get_var(Npop,VarAelocm_aflpdom) | -20 |

- “TreeMBase_getvar_Npop_Var...” parameters are created to represent the calculation made in the “Get_var” function.

## 5.14 Gst Mean of Nuclear Locus

This result is displayed only if the “LocGst” type of results is requested in the “type.txt” file.

```
G_all  0.0001
```

- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: “G_all” | | 1 |
| TreeMBase_getgst_Hsmloc_Htloc | Get_gst(Hsmloc,Htloc) | 2 |

- “TreeMBase_getgst_Hsmloc_Htloc” parameter is created to represent the calculation made in the “Get_gst” function.

## 5.15 Gst Mean of Microsatellite Locus

This result is displayed only if the “MicroGst” type of results is requested in the “type.txt” file.

```
G_usat  0.0001
```

- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: “G_usat” | | 1 |
| TreeMBase_getgst_Hsmloc_usat_Htloc_usat | Get_gst(Hsmloc_usat,Htloc_usat) | 2 |

- “TreeMBase_getgst_Hsmloc_usat_Htloc_usat” parameter is created to represent the calculation made in the “Get_gst” function.

## 5.16 Gst Mean of Microsatellite Locus

This result is displayed only if the “QuantiGst” type of results is requested in the “type.txt” file.

```
G_QTLs  0.0000
```

- **Parameters**

| Parameter name | Parameter description | Rank in |
|---|---|---|

| | | line |
|---|---|---|
| Label: “G_QTLs” | | 1 |
| TreeMBase_getgst_Hsmloc_qtl_Htloc_qtl | Get_gst(Hsmloc_qtl,Htloc_qtl) | 2 |

- “TreeMBase_getgst_Hsmloc_qtl_Htloc_qtl” parameter is created to represent the calculation made in the “Get_gst” function.

### 5.17 Gst Mean of AFLP Codominant Locus

This result is displayed only if the “AflpcodGst” type of results is requested in the “type.txt” file.

```
G_AFLPcodom 0.0001
```

- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: “G_AFLPcodom ” | | 1 |
| TreeMBase_getgst_Hsmloc_aflpcod_Htloc_aflpcod | Get_gst(Hsmloc_aflpcod,Htloc_aflpcod) | 2 |

- “TreeMBase_getgst_Hsmloc_aflpcod_Htloc_aflpcod” parameter is created to represent the calculation made in the “Get_gst” function.

### 5.18 Gst Mean of AFLP Codominant Locus

This result is displayed only if the “AflpdomGst” type of results is requested in the “type.txt” file.

```
G_AFLPdom 0.0001
```

- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| Label: “G_AFLPdom ” | | 1 |
| TreeMBase_getgst_Hsmloc_aflpdom_Htloc_aflpdom | Get_gst(Hsmloc_aflpdom,Htloc_aflpdom) | 2 |

- “TreeMBase_getgst_Hsmloc_aflpdom_Htloc_aflpdom” parameter is created to represent the calculation made in the “Get_gst” function.

## 6 Annex 5 – Sample File

The source file “ind.c” permits to generate a “sample[n].txt” file.

The “sample.txt” file is generated if the option “Sample [sample_size]” (*e.g.* “Sample 50”) is defined in the “type.txt” file where sample_size is the sample size in each population.

The individual trees are randomly sampled in the population.


***Figure 13 :*** *"sample" file*

## 6.1 File Format

- Decimal are expressed with a dot.
- The parameters are ordered one after the other.

## 6.2 Simulated Year of the Sample

The simulated year of the sample corresponds to the settings of the "type.txt" file.

Example:

```
Generation 0 to 10 step 5
Sample 50
```

In that case, three sample files will be generated corresponding to the simulated year 0, 5 and 10.

| ngeneration |
|---|
| 0 |

## 6.3 Number of Populations

```
NPop
25
```

## 6.4 Sample Size

Number of individuals per population; it corresponds to the sample size defined in the “type.txt” file in the setting “Sample #”.

```
Nind
50 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50 50
```

## 6.5 Number of Nuclear and Cytoplasmic Loci

The numbers of nuclear and cytoplasmic loci are defined on a single line.

```
Nnucl Ncyto
209 0
```

## 6.6 Number of Alleles per Locus

The numbers of alleles per locus is defined on a single line.

```
Nalleles
100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 […] 100
```

## 6.7 Number of Alleles per Locus

The numbers of alleles per locus is defined on a single line.

```
Nalleles
100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 100 […] 100
```

## 6.8 Genetic Map

The genetic map (recombination rates) is displayed in one line.

```
R_coeff
0.230769 0.0225564 0.00225056 0.000225006 2.25001e-05 2.25e-06 2.25e-07 2.25e-08
2.5e-09 2.5e-09 2.25e-08 2.25e-07 [...]2.25e-07 2.25e-08 2.5e-09 2.5e-09 2.25e-08
2.25e-07 2.25e-06 2.25001e-05 0.000225006 0.00225056 0.0225564 0.230769
```

## 6.9 Phenotypic Value and Genotype per Individual

A line is displayed per individual of each population: it contains the phenotypic value and the genotype of the individual.

```
pop ind pheno   generation
1    1   -7.1632  30 23 3 3 92 33 7 7 52 52 6 6 88 88 9 9 18 18 85 85 56 56 79 4
57 57 41 41 48 48 12 12 20 20 18 18 64 64 39 39 39 42 91 91 96 96 84 84 85 8 51 51
45 27 38 60 50 50 9 9 1 1 74 2 98 73 5 29 89 89 67 5 94 64 73 73 96 96 42 75 84 69
55 76 73 26 43 43 81 81 76 76 […] 74 21 51 46 30 70 70 88 88 98 65 31 31 59 99
```

- **Parameters**

| Parameter name | Parameter description | Rank in line |
|---|---|---|
| pop | Ongoing population number (MetaPop local parameter) | 1 |
| ind | Ongoing individual number (MetaPop local parameter) | 2 |
| pheno | Phenotypic value per population and individual | 3 |
| generation | Genotype per locus (nuclear and then cytoplasmic) of each individual of each population | 4 |