Data simulation (including genomics) QMSim software

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QMSim: why to use it ?

- ✓To simulate data mimicking livestock species
  - ✓Phenotypes, pedigree, genotypes
- ✓A wide variety of genome architectures
  - ✓From single-locus to infinitesimal model
- ✓It is a user-friendly tool for simulating data
- ✓Computationally efficient in terms of time and memory

QMSim[†]: where to find it ?

[†]Sargolzaei & Schenkel (2009), Bioinformatics 25:680-681.

The code is written in C++ language

Executable files are freely available for Windows, Linux, and Mac at: **(Last update: July 12, 2013)**

http://www.aps.uoguelph.ca/~msargol/qmsim/

How the simulation is carried out ?

In 2 steps:

✓ *First step:* **Historical Population**

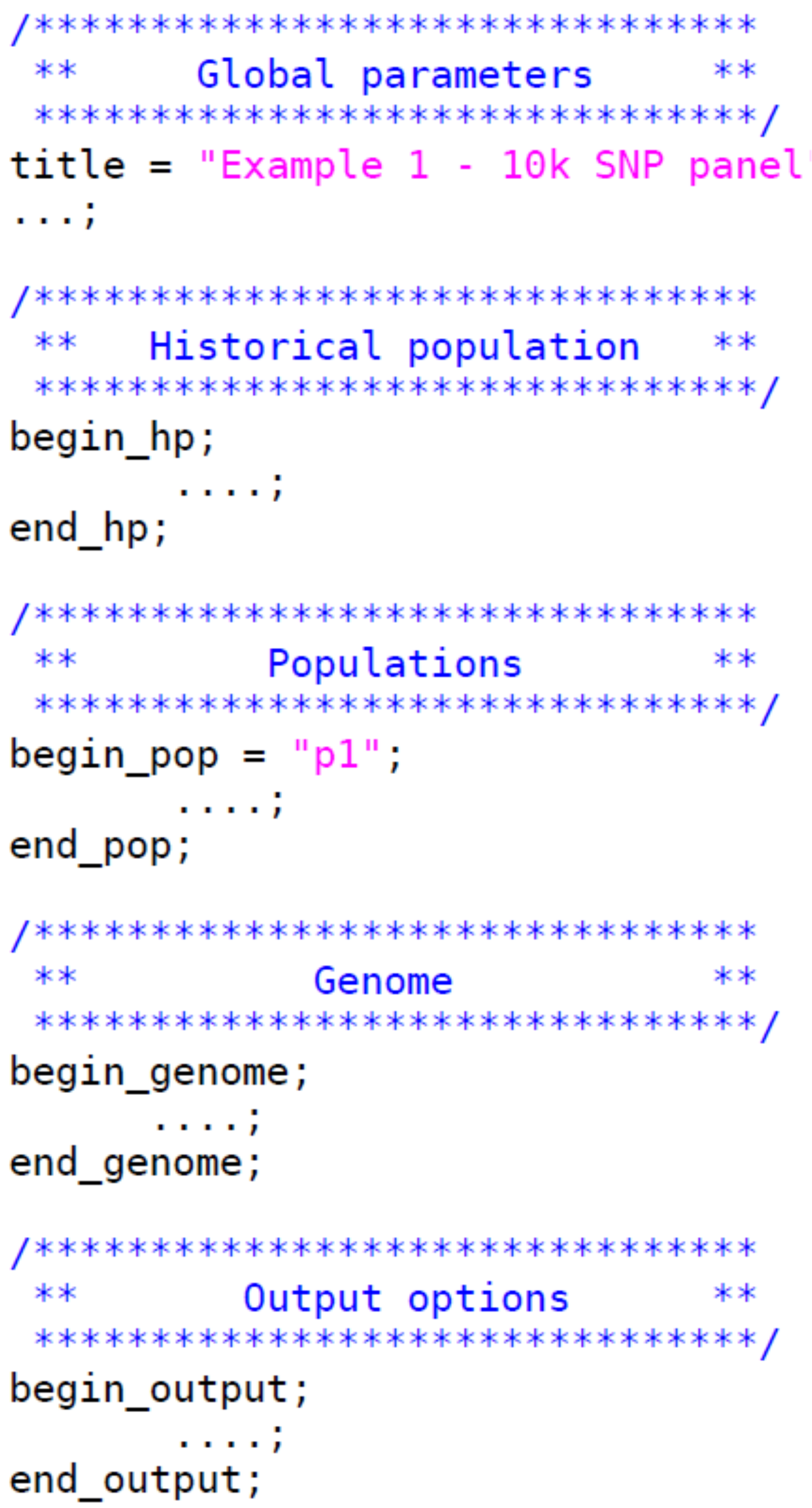
- to create initial LD
- to establish mutation-drift equilibrium
- expansion and contraction of the population

✓ *Second step:* **Recent Population**

- Pedigree
- Phenotypes
- Genotypes

Parameter file

- ✓It must be in ASCII format
- ✓It consists of **five** main sections
- ✓The order of commands within each section is not important
- ✓All commands end with a semicolon
- ✓No semicolon → error message and program exits



```
/*******************************
 **      Global parameters      **
 *******************************/
title = "Example 1 - 10k SNP panel
...;

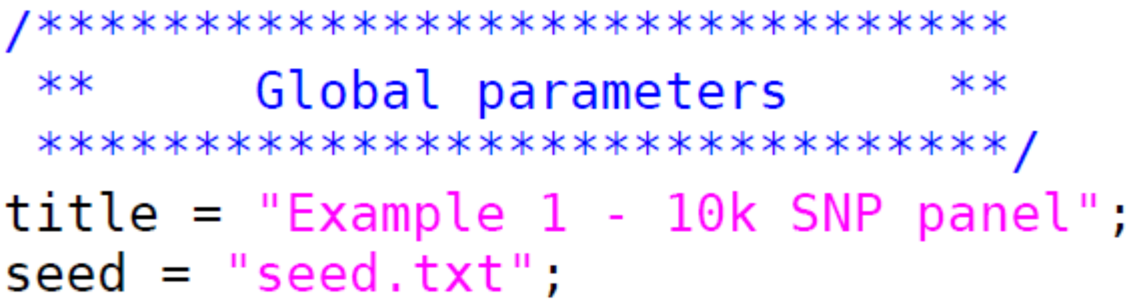
/*******************************
 **    Historical population    **
 *******************************/
begin_hp;
       ....;
end_hp;

/*******************************
 **         Populations         **
 *******************************/
begin_pop = "p1";
       ....;
end_pop;

/*******************************
 **           Genome            **
 *******************************/
begin_genome;
      ....;
end_genome;

/*******************************
 **       Output options        **
 *******************************/
begin_output;
       ....;
end_output;
```

1. Global parameters section



```
/********************************
 **     Global parameters     **
 ********************************/
title = "Example 1 - 10k SNP panel";
seed = "seed.txt";
```

An arbitrary title

The random number generator (RNG*) requires a seed file.

If it is not specified → RNG will be seeded from the system clock

For each run the initial seed numbers will be backed up in output folder → This allows to repeat the run !

Parameter file: ex01.prm

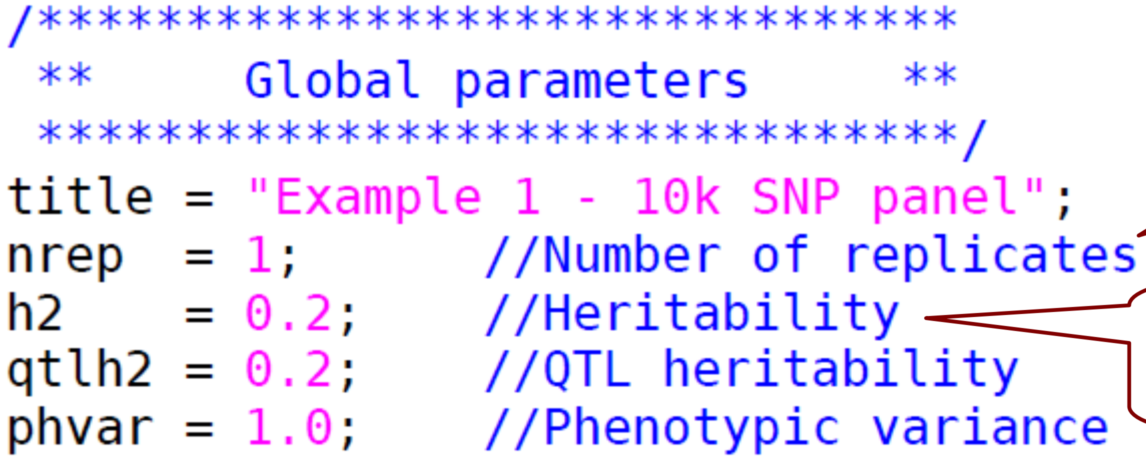
Output folder: r_ex01/

Output

```
.---------------------------------.
| Example 1 - 10k SNP panel |
`---------------------------------'
Initial seed is backed up in [r_ex01/seed].
parameter file is backed up in [r_ex01/ex01.prm].
```

* Mersenne Twister algorithm (Matsumoto & Nishimura, 1998)

1. Global parameters section

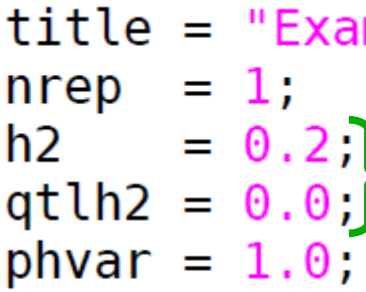


```
/*******************************
 **     Global parameters     **
 *******************************/
title = "Example 1 - 10k SNP panel";
nrep  = 1;      //Number of replicates
h2    = 0.2;    //Heritability
qtlh2 = 0.2;    //QTL heritability
phvar = 1.0;    //Phenotypic variance
```

Range: 0 - 10,000

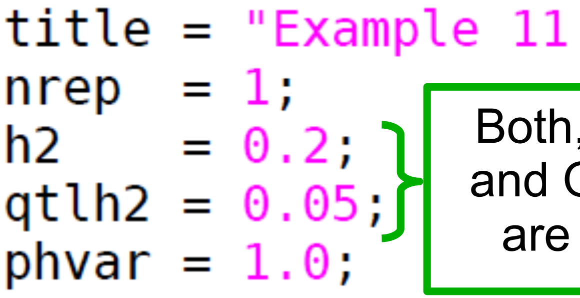
Overall heritability (Polygenic + QTL)

QTL effect is simulated



```
title = "Example 8
nrep  = 1;
h2    = 0.2;
qtlh2 = 0.0;
phvar = 1.0;
```

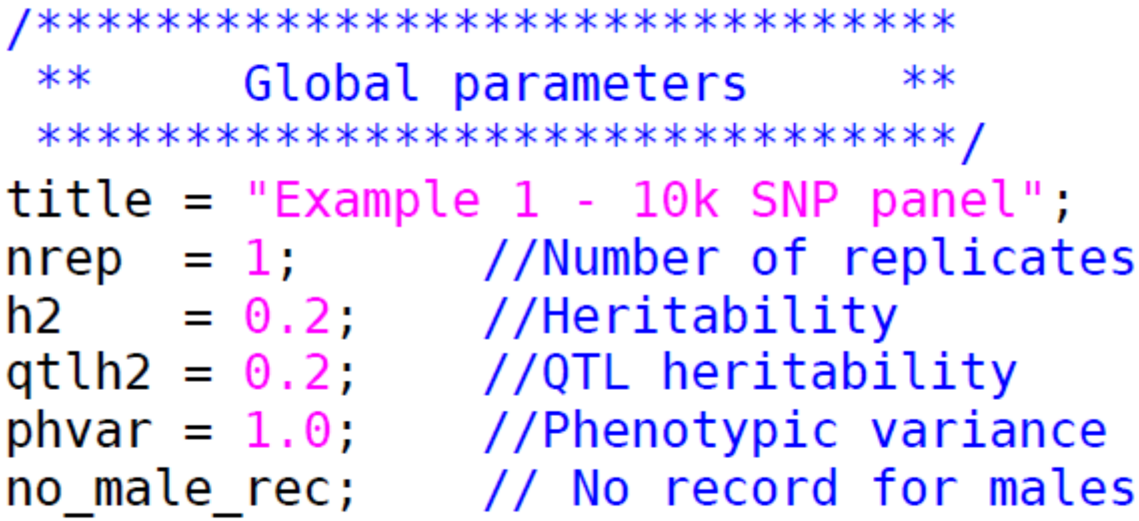
Only polygenic effect is simulated



```
title = "Example 11
nrep  = 1;
h2    = 0.2;
qtlh2 = 0.05;
phvar = 1.0;
```

Both, polygenic and QTL effects are simulated

1. Global parameters section



```
/*******************************
 **      Global parameters    **
 *******************************/
title = "Example 1 - 10k SNP panel";
nrep  = 1;      //Number of replicates
h2    = 0.2;    //Heritability
qtlh2 = 0.2;    //QTL heritability
phvar = 1.0;    //Phenotypic variance
no_male_rec;    // No record for males
```

A sex limited trait like milk yield

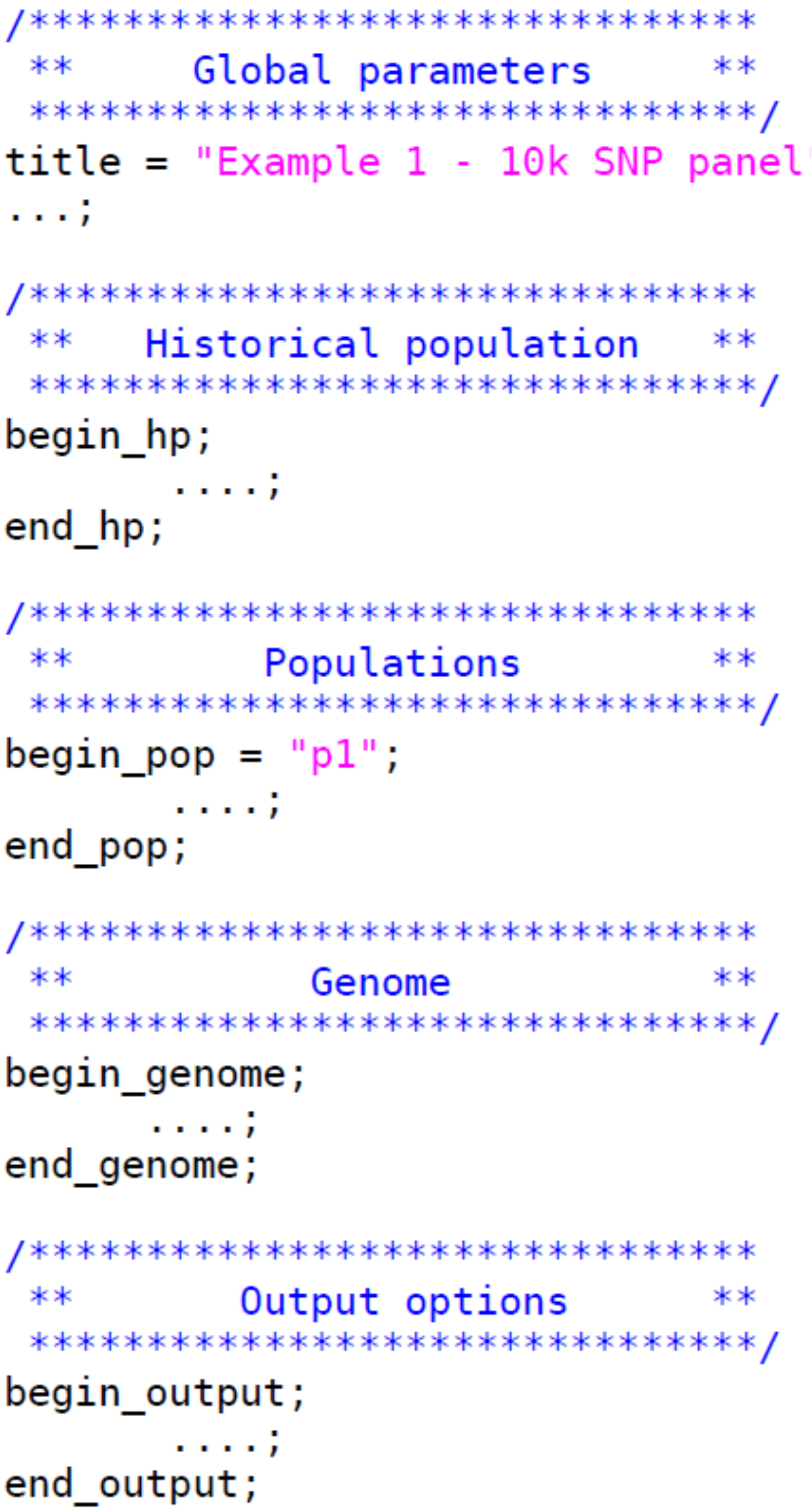
When males do not have records, but selection or culling are based on

EBVs → Ok

Phenotypes → Males will be randomly selected or culled

Parameter file

- ✓ It consists of **five** main sections



```
/*****************************
 **      Global parameters    **
 *****************************/
title = "Example 1 - 10k SNP panel"
...;

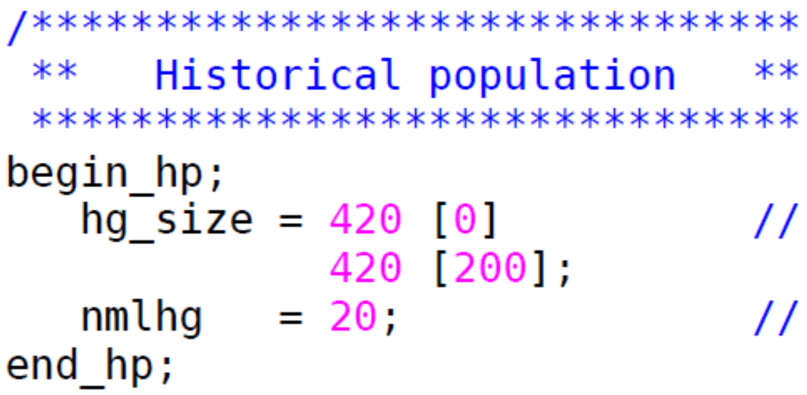
/*****************************
 **   Historical population   **
 *****************************/
begin_hp;
       ....;
end_hp;

/*****************************
 **         Populations       **
 *****************************/
begin_pop = "p1";
       ....;
end_pop;

/*****************************
 **           Genome          **
 *****************************/
begin_genome;
      ....;
end_genome;

/*****************************
 **       Output options      **
 *****************************/
begin_output;
       ....;
end_output;
```

2. Historical population section

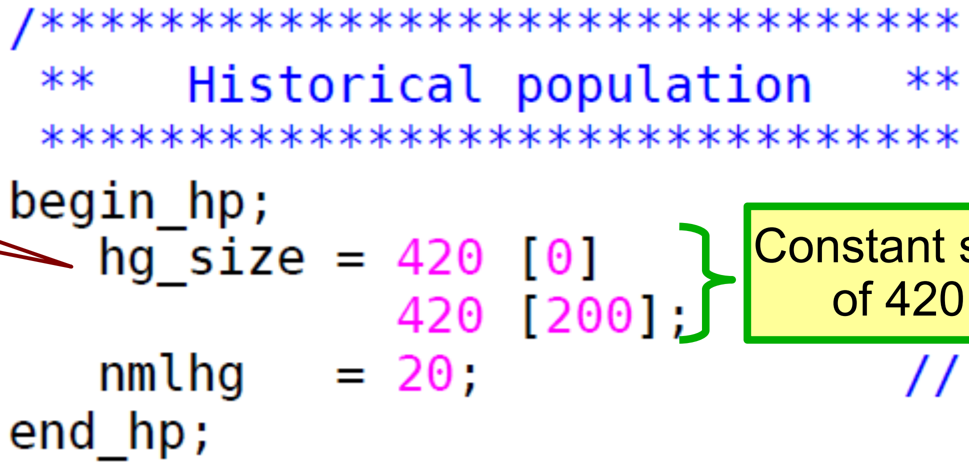


```
/******************************
 **   Historical population   **
 ******************************
begin_hp;
   hg_size = 420 [0]          //
             420 [200];
   nmlhg   = 20;              //
end_hp;
```

- To create initial LD
- Evolutionary forces: mutation and drift (no selection, no migration)
- Random mating: union of gametes randomly sampled from the male and female gametic pools
- Discrete generations
- Only a single historical population

2. Historical population section

Historical generation sizes



```
/*******************************
 **    Historical population    **
 *******************************
begin_hp;
   hg_size = 420 [0]
             420 [200];
   nmlhg   = 20;                 //
end_hp;
```

Constant size of 420

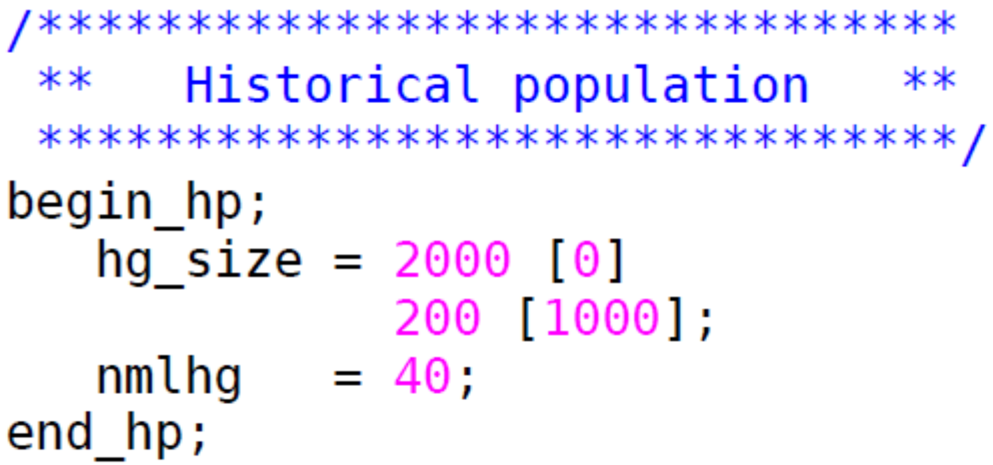
hg_size = **v1** [**v2**]

v1 the historical generation **size**
Range: 2 – 100,000

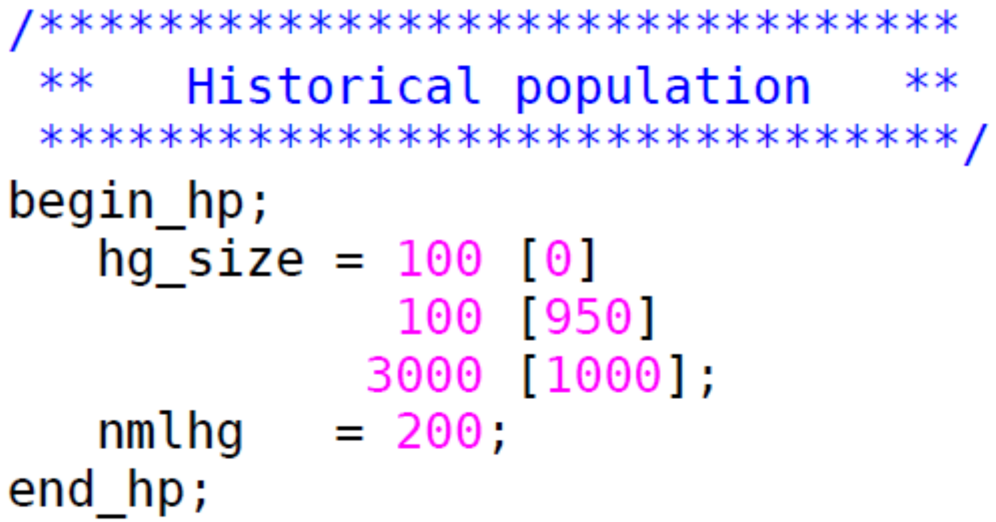
v2 the historical generation **number**
Range: 0 – 150,000

2. Historical population section

Historical **bottleneck** or **expansion** can be simulated



```
/*******************************
 **   Historical population   **
 *******************************/
begin_hp;
   hg_size = 2000 [0]
             200 [1000];
   nmlhg   = 40;
end_hp;
```



```
/*******************************
 **   Historical population   **
 *******************************/
begin_hp;
   hg_size = 100 [0]
             100 [950]
            3000 [1000];
   nmlhg   = 200;
end_hp;
```

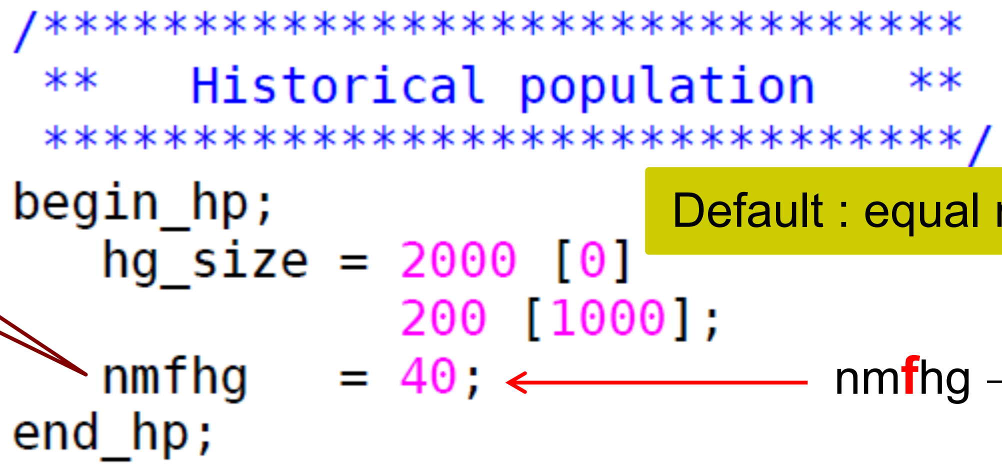
Gradual decrease in size from 2000 to 200

Expansion in the last historical generation from 100 to 3000

LD in livestock extends over longer distances than in humans

2. Historical population section

Number of males

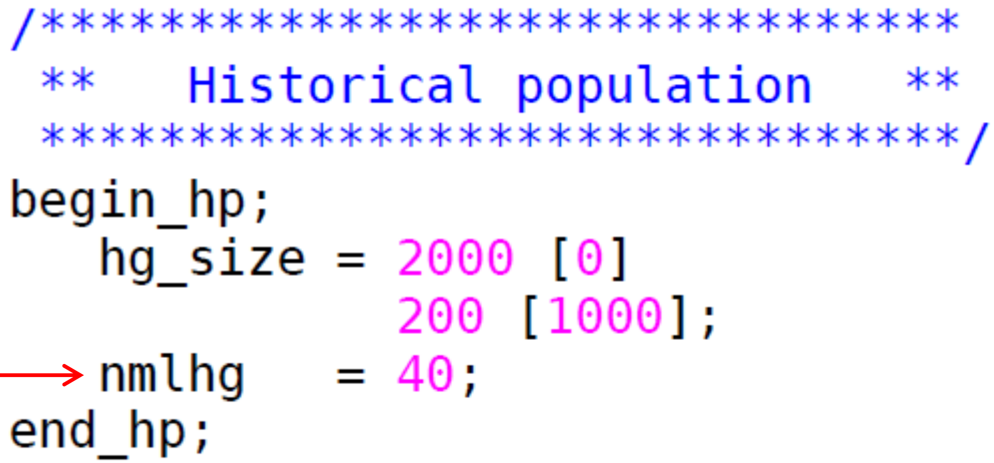


```
/******************************
 **   Historical population   **
 ******************************/
begin_hp;
   hg_size = 2000 [0]
             200 [1000];
   nmfhg   = 40;
end_hp;
```

Default : equal number of males and females

nmfhg → **first** historical generation

Sex ratio will be constant across historical generations. It can be changed in the last generation

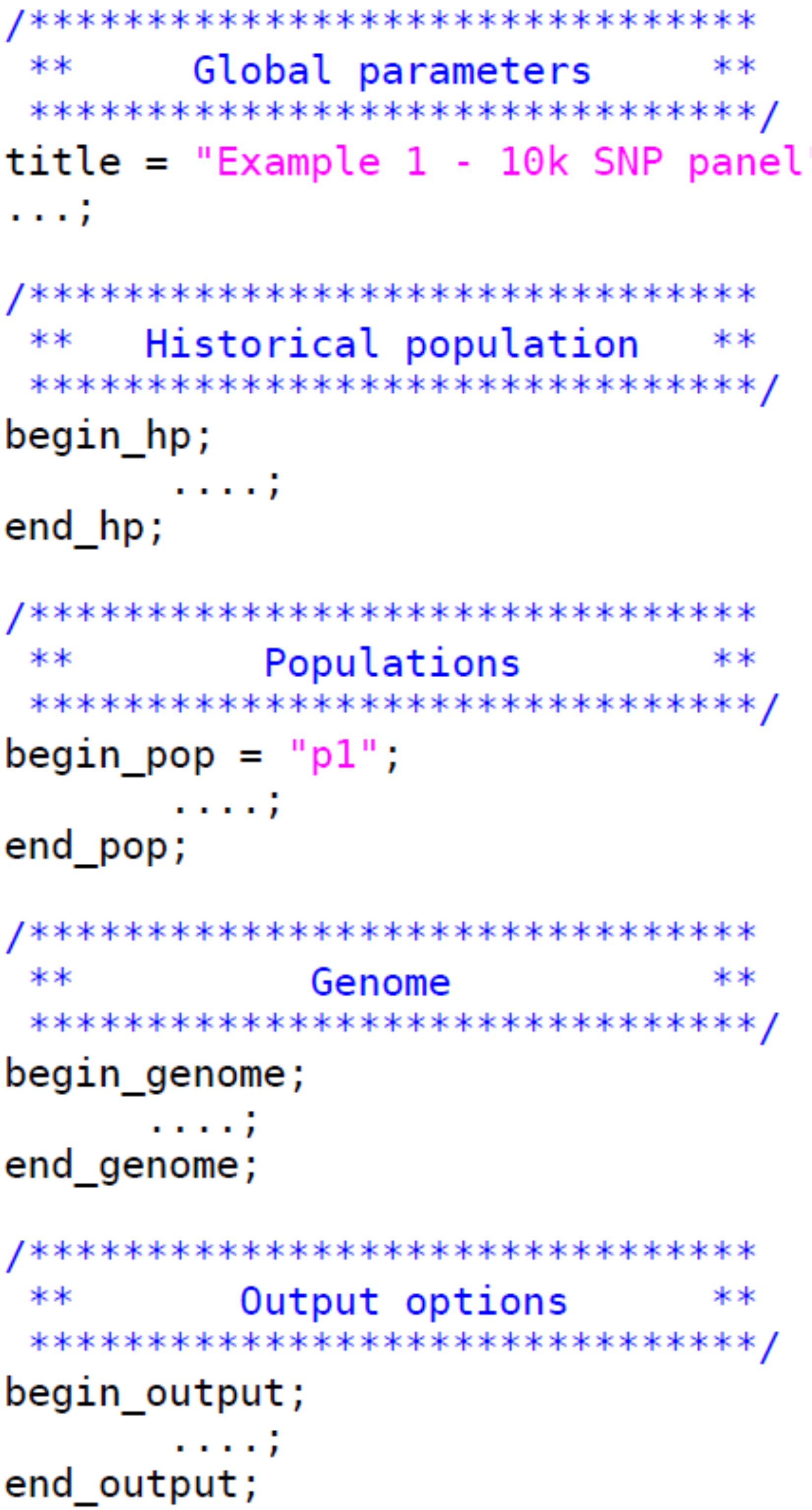


```
/******************************
 **   Historical population   **
 ******************************/
begin_hp;
   hg_size = 2000 [0]
             200 [1000];
   nmlhg   = 40;
end_hp;
```

nmlhg → **last** historical generation

Parameter file

✓It consists of **five** main sections



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 **      Global parameters     **
 *****************************/
title = "Example 1 - 10k SNP panel
...;

/*****************************
 **    Historical population   **
 *****************************/
begin_hp;
       ....;
end_hp;

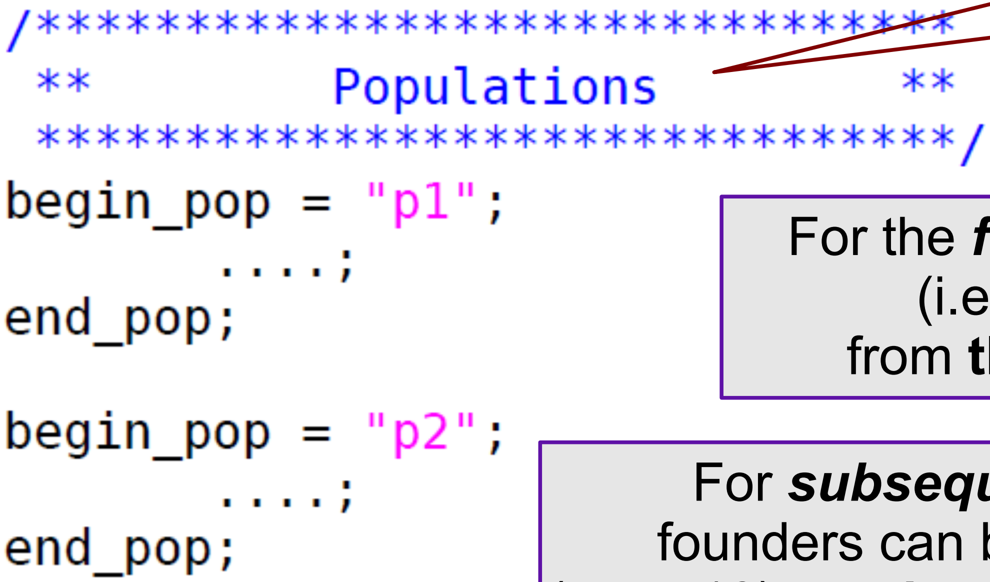
/*****************************
 **         Populations        **
 *****************************/
begin_pop = "p1";
       ....;
end_pop;

/*****************************
 **           Genome           **
 *****************************/
begin_genome;
      ....;
end_genome;

/*****************************
 **       Output options       **
 *****************************/
begin_output;
       ....;
end_output;
```

3. Population section

One or multiple recent populations



```
/*******************************
 **        Populations        **
 *******************************/
begin_pop = "p1";
       ....;
end_pop;

begin_pop = "p2";
       ....;
end_pop;
```

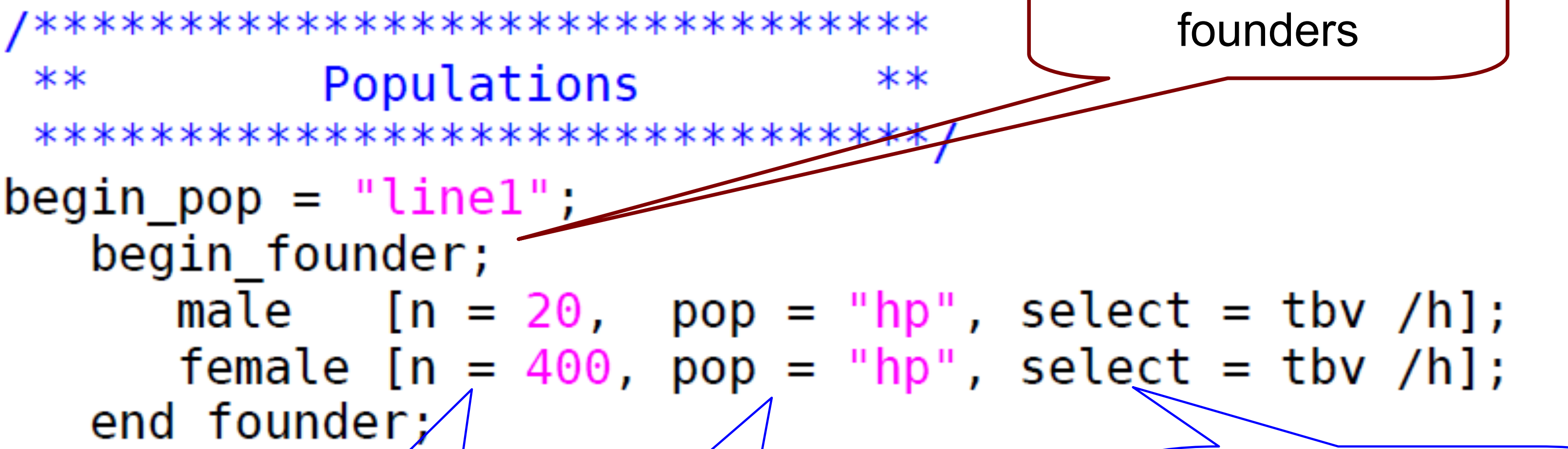
For the ***first defined recent population*** (i.e. p1), founders must come from **the last historical population**

For ***subsequent populations*** (i.e. p2), founders can be chosen from one or more (up to 10) **previously defined populations** (i.e. p1)

Multiple recent populations can be analyzed separately (one pedigree for each population) or jointly (by creating one pedigree for all populations) for inbreeding and EBV

3. Population section

Choosing founders for a population



```
/*******************************
 **         Populations       **
 *******************************/
begin_pop = "line1";
   begin_founder;
      male   [n = 20,  pop = "hp", select = tbv /h];
      female [n = 400, pop = "hp", select = tbv /h];
   end founder;
```

Parameters for the founders

Number of male/female to be selected

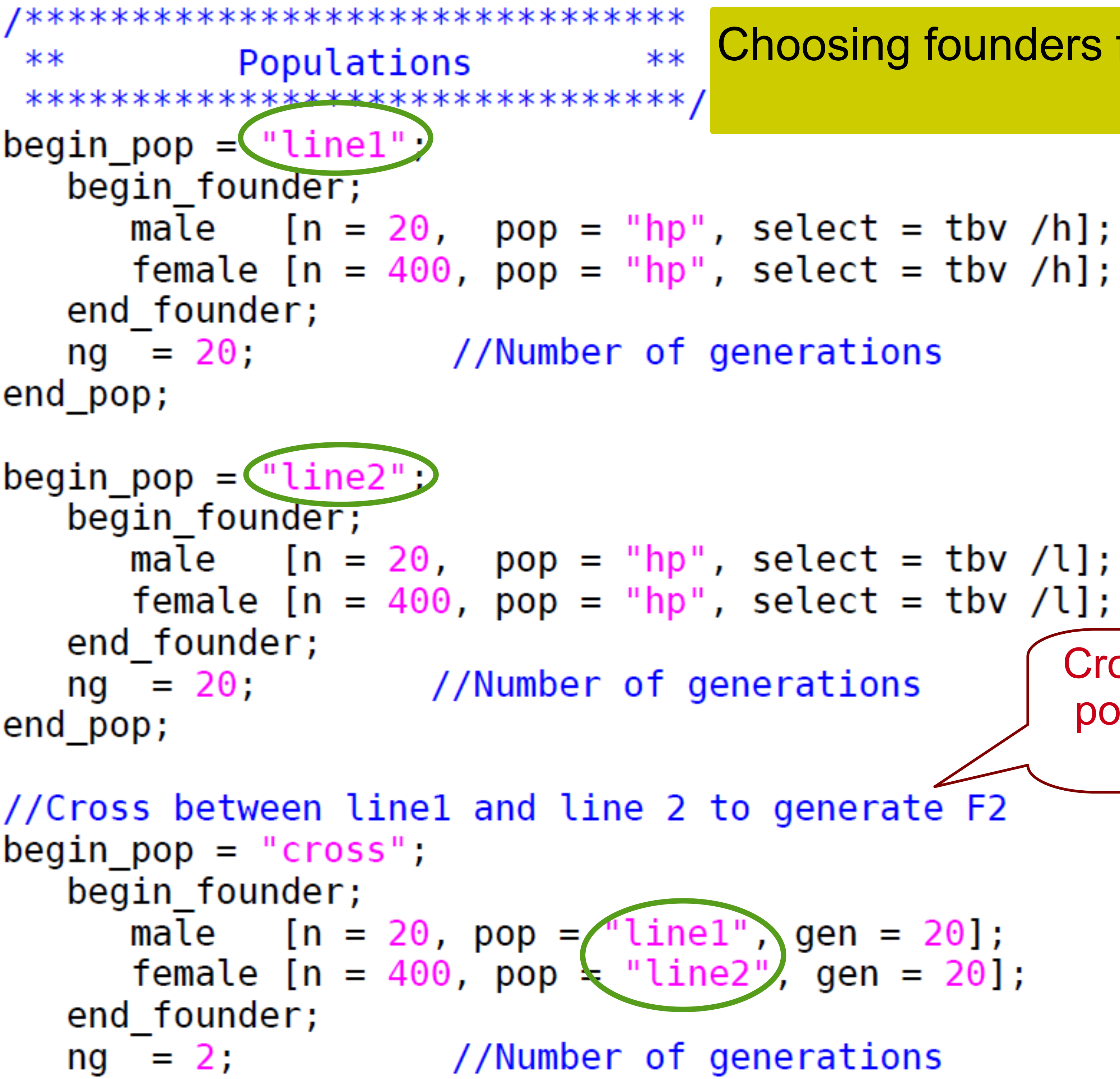
It indicates from which population the base animals must be selected

Type of selection

select: rnd (default), phen, tbv and ebv
/l : to select low values
/h : to select high values

hp: historical population (last historical generation)

Choosing founders for a population for F2 design



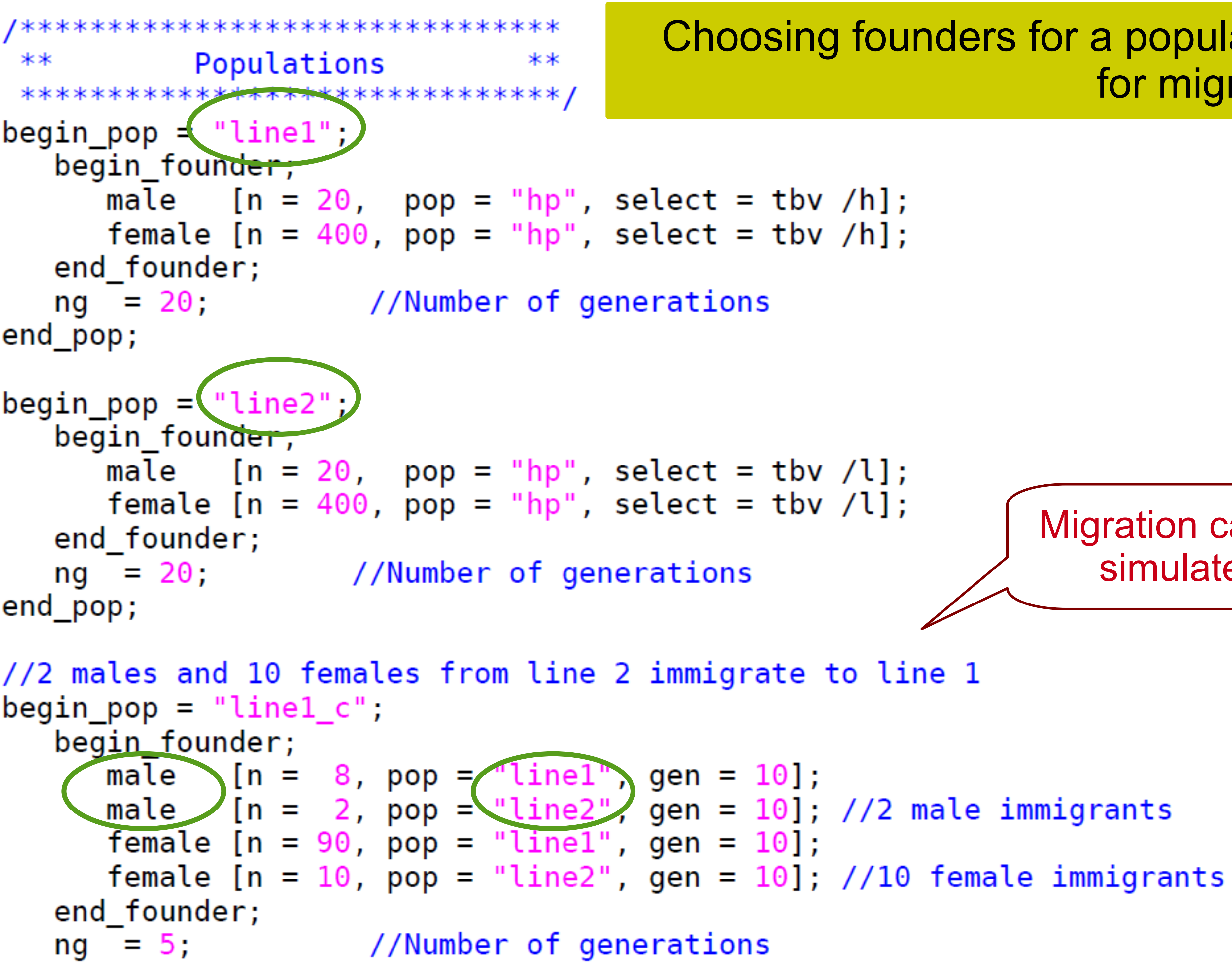
```
/*******************************
 **        Populations        **
 *******************************/
begin_pop = "line1";
   begin_founder;
      male   [n = 20,  pop = "hp", select = tbv /h];
      female [n = 400, pop = "hp", select = tbv /h];
   end_founder;
   ng  = 20;         //Number of generations
end_pop;

begin_pop = "line2";
   begin_founder;
      male   [n = 20,  pop = "hp", select = tbv /l];
      female [n = 400, pop = "hp", select = tbv /l];
   end_founder;
   ng  = 20;        //Number of generations
end_pop;

//Cross between line1 and line 2 to generate F2
begin_pop = "cross";
   begin_founder;
      male   [n = 20, pop = "line1", gen = 20];
      female [n = 400, pop = "line2", gen = 20];
   end_founder;
   ng  = 2;          //Number of generations
```

Crossing between populations/lines is allowed

Choosing founders for a population for migration



```
/********************************
 **        Populations         **
 *******************************/
begin_pop = "line1";
   begin_founder;
      male   [n = 20,  pop = "hp", select = tbv /h];
      female [n = 400, pop = "hp", select = tbv /h];
   end_founder;
   ng  = 20;         //Number of generations
end_pop;

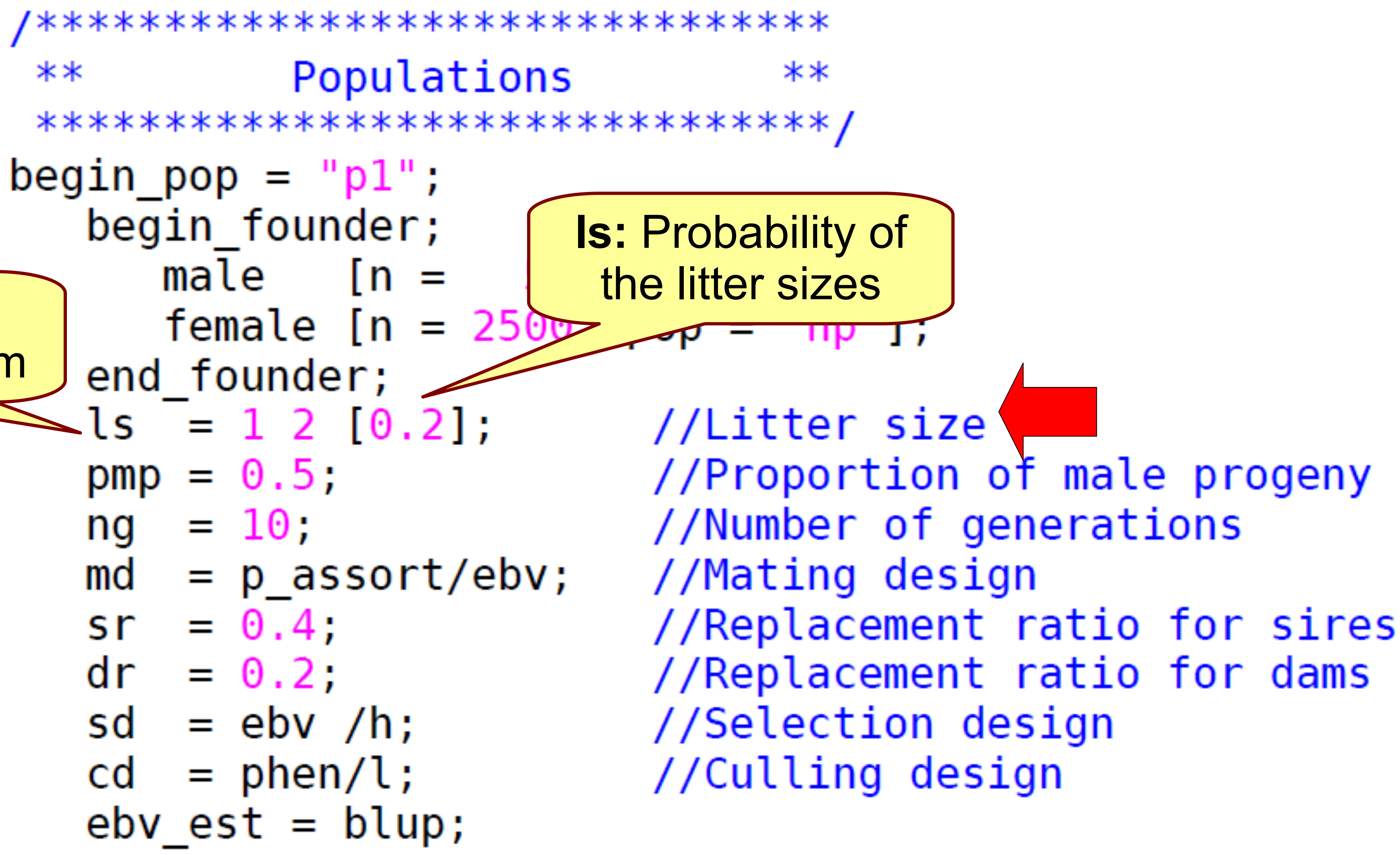
begin_pop = "line2";
   begin_founder;
      male   [n = 20,  pop = "hp", select = tbv /l];
      female [n = 400, pop = "hp", select = tbv /l];
   end_founder;
   ng  = 20;        //Number of generations
end_pop;

//2 males and 10 females from line 2 immigrate to line 1
begin_pop = "line1_c";
   begin_founder;
      male   [n =  8, pop = "line1", gen = 10];
      male   [n =  2, pop = "line2", gen = 10]; //2 male immigrants
      female [n = 90, pop = "line1", gen = 10];
      female [n = 10, pop = "line2", gen = 10]; //10 female immigrants
   end_founder;
   ng  = 5;          //Number of generations
```

Migration can be simulated

3. Population section

Litter size



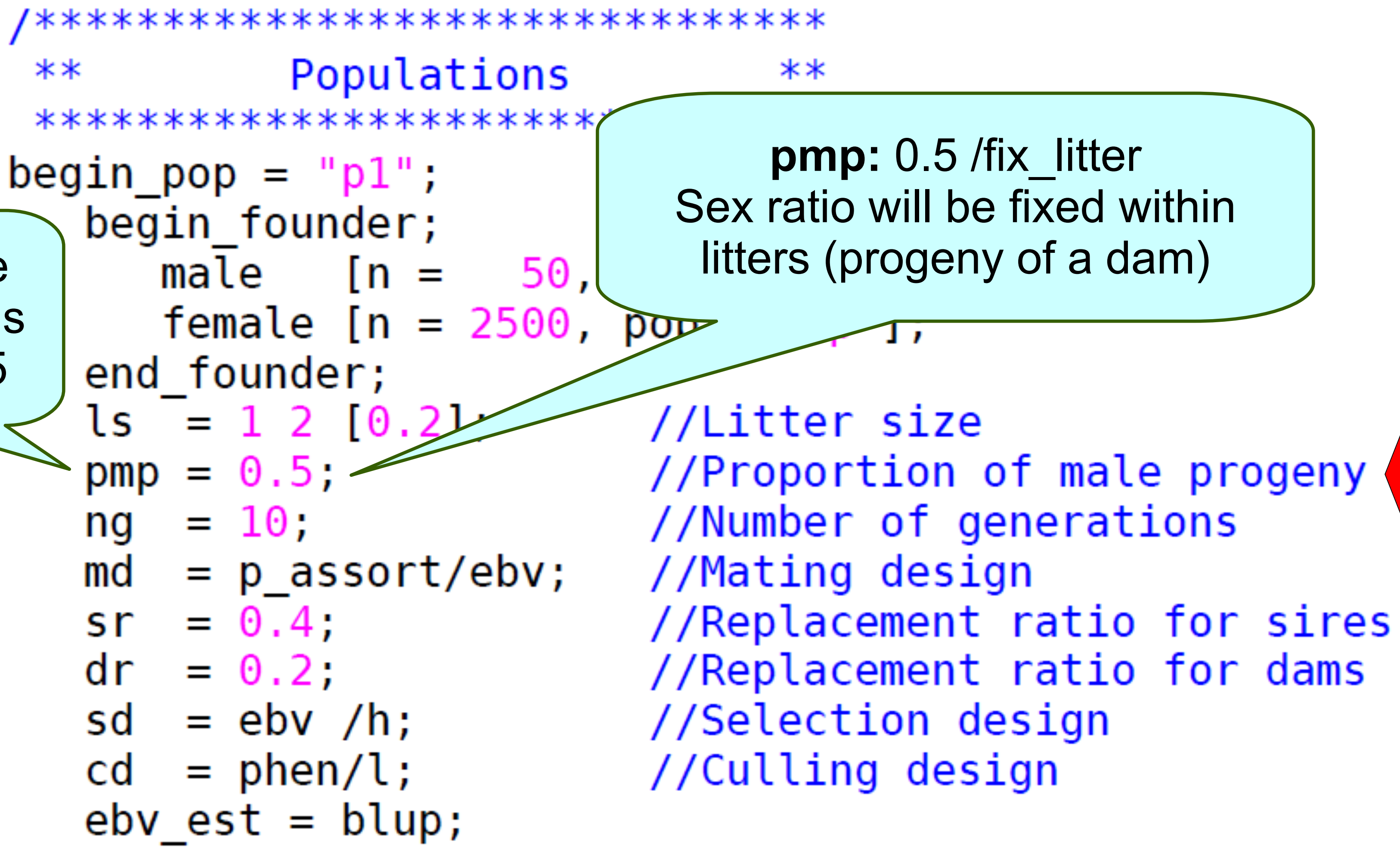
```
/******************************
 **        Populations        **
 ******************************/
begin_pop = "p1";
   begin_founder;
      male    [n =
      female [n = 2500      pop = "np"];
   end_founder;
   ls  = 1 2 [0.2];        //Litter size
   pmp = 0.5;              //Proportion of male progeny
   ng  = 10;               //Number of generations
   md  = p_assort/ebv;     //Mating design
   sr  = 0.4;              //Replacement ratio for sires
   dr  = 0.2;              //Replacement ratio for dams
   sd  = ebv /h;           //Selection design
   cd  = phen/l;           //Culling design
   ebv_est = blup;
```

ls: number of progeny per dam

ls: Probability of the litter sizes

3. Population section

Sex ratio



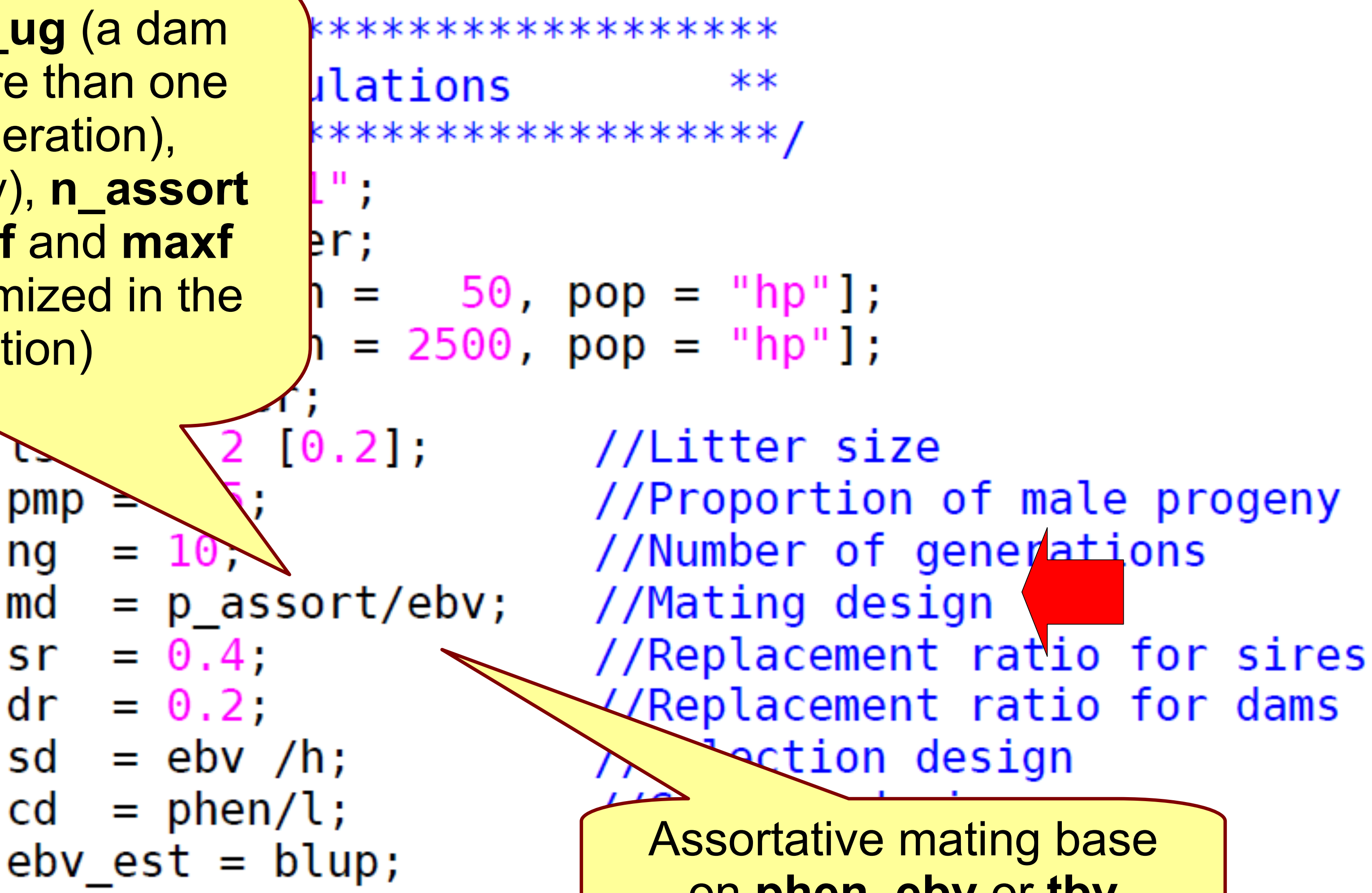
```
/*****************************
 **        Populations        **
 **********************
begin_pop = "p1";
   begin_founder;
      male   [n =   50,
      female [n = 2500, po          ];
   end_founder;
   ls   = 1 2 [0.2];           //Litter size
   pmp = 0.5;                  //Proportion of male progeny
   ng   = 10;                  //Number of generations
   md   = p_assort/ebv;        //Mating design
   sr   = 0.4;                 //Replacement ratio for sires
   dr   = 0.2;                 //Replacement ratio for dams
   sd   = ebv /h;              //Selection design
   cd   = phen/l;              //Culling design
   ebv_est = blup;
```

pmp: range 0-1, default is equal to 0.5

pmp: 0.5 /fix_litter
Sex ratio will be fixed within litters (progeny of a dam)

3. Population section

Matting design



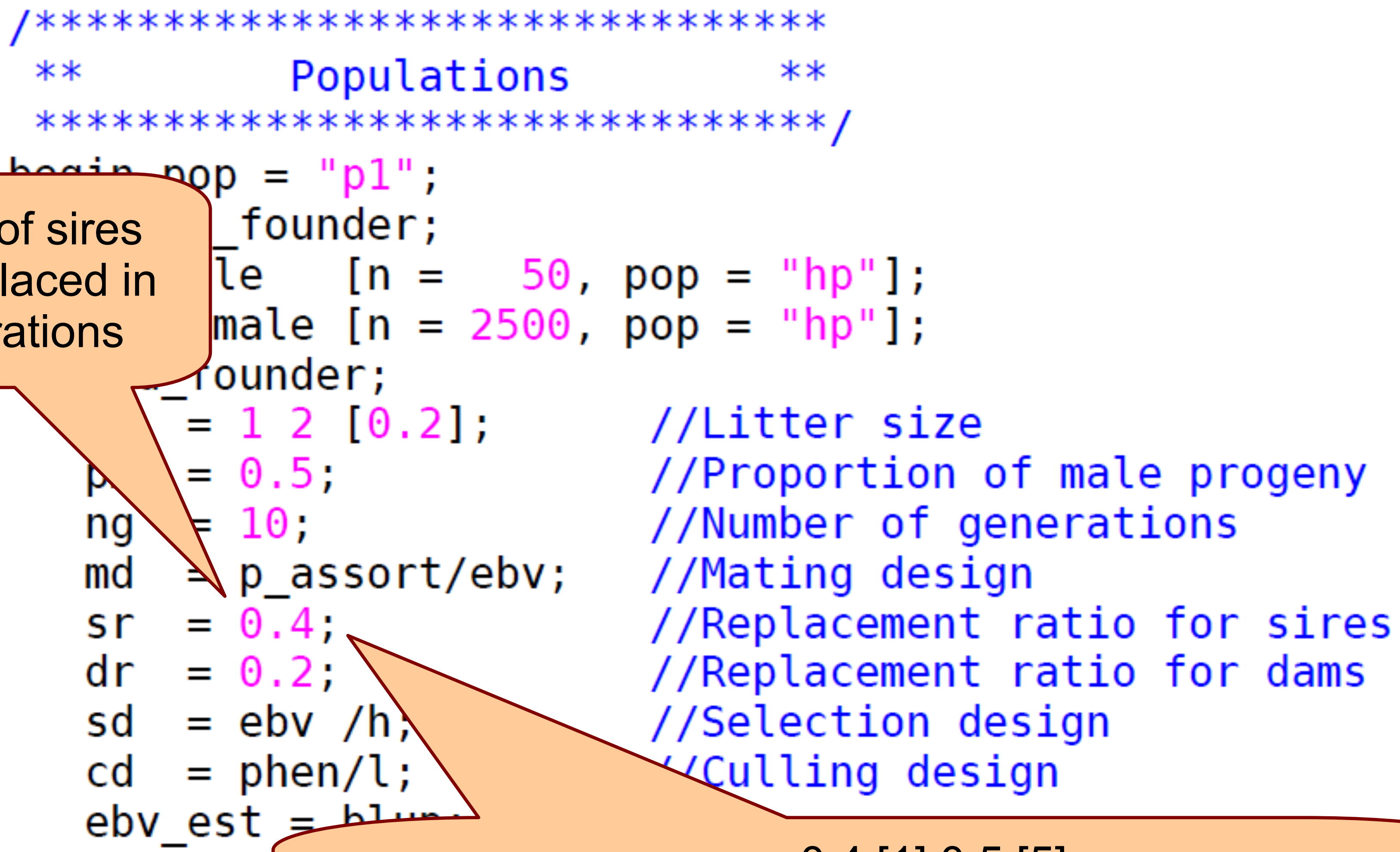
```
*******************
ulations        **
*******************/
l";
er;
n =   50, pop = "hp"];
n = 2500, pop = "hp"];
r;
      2 [0.2];        //Litter size
pmp =      ;          //Proportion of male progeny
ng  = 10;             //Number of generations
md  = p_assort/ebv;   //Mating design
sr  = 0.4;            //Replacement ratio for sires
dr  = 0.2;            //Replacement ratio for dams
sd  = ebv /h;         //  lection design
cd  = phen/l;
ebv_est = blup;
```

rnd (default)**, rnd_ug** (a dam can mate with more than one sire in each generation), **p_assort** (similarity), **n_assort** (dissimilarity), **minf** and **maxf** (inbreeding is minimized in the next generation)

Assortative mating base on **phen**, **ebv** or **tbv**

3. Population section

Replacement



```
/*******************************
 **        Populations        **
 *******************************/
begin_pop = "p1";
          _founder;
          le    [n =   50, pop = "hp"];
          male [n = 2500, pop = "hp"];
          _founder;
          = 1 2 [0.2];      //Litter size
   p      = 0.5;            //Proportion of male progeny
   ng     = 10;             //Number of generations
   md     = p_assort/ebv;   //Mating design
   sr     = 0.4;            //Replacement ratio for sires
   dr     = 0.2;            //Replacement ratio for dams
   sd     = ebv /h;         //Selection design
   cd     = phen/l;         //Culling design
   ebv_est = blup;
```

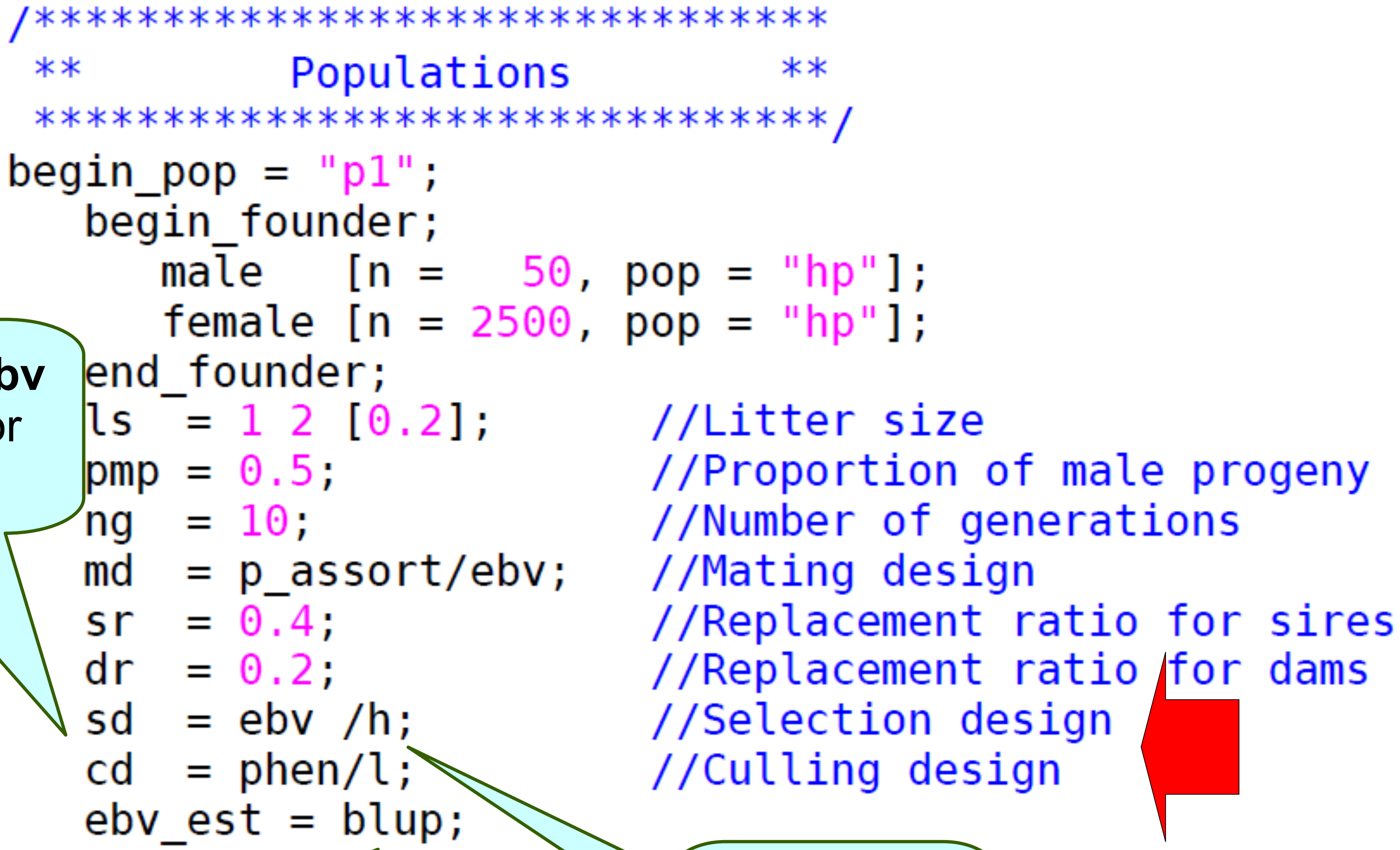
sr : 40% of sires will be replaced in all generations

sr : 0.4 [1] 0.5 [5]
40% of sires will be culled for generation 1 to 5, and 50% from generation 5 to last generation

sr : 1, discrete generations (default)

3. Population section

Selection and culling designs

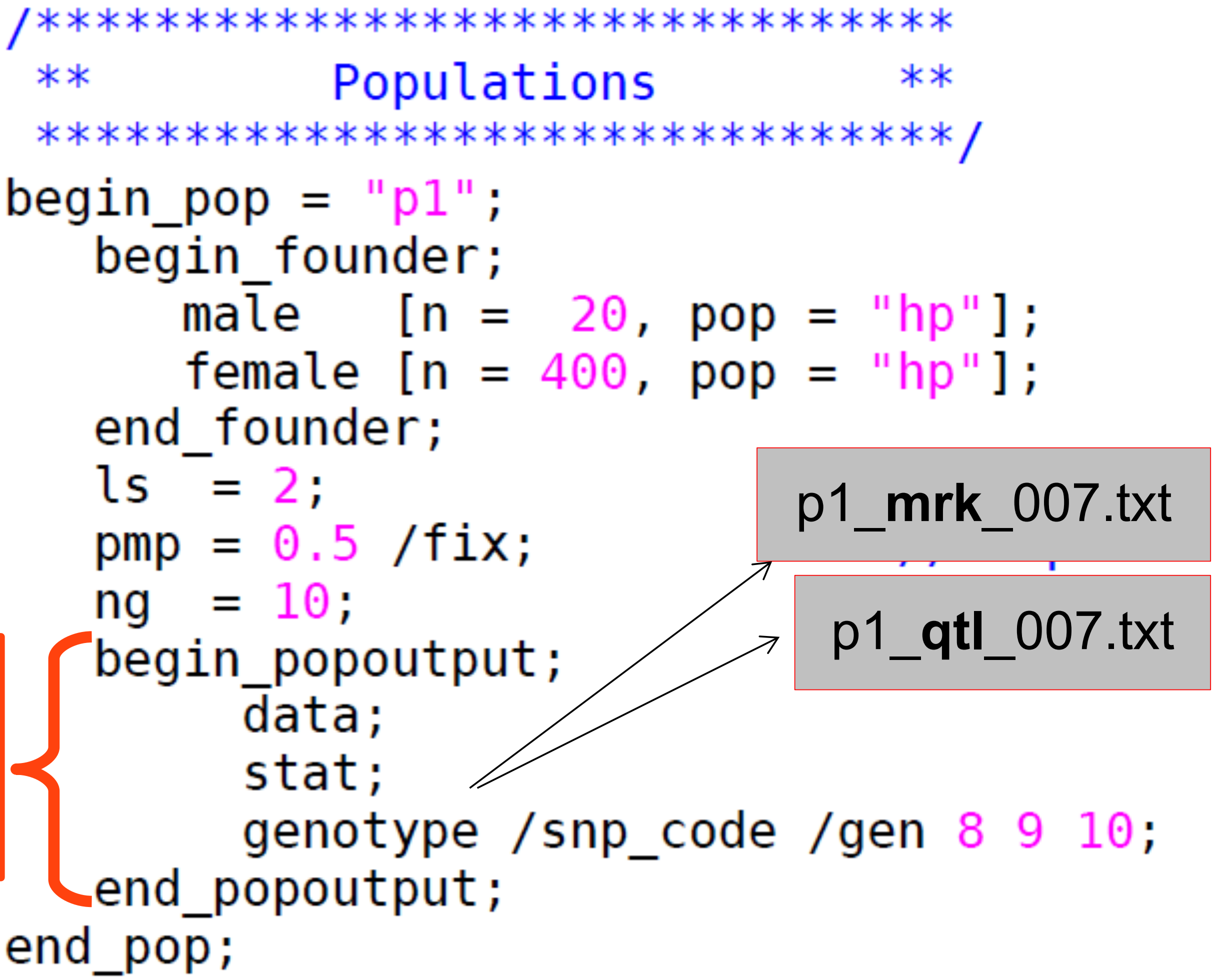


```
/*******************************
 **        Populations        **
 *******************************/
begin_pop = "p1";
   begin_founder;
      male   [n =   50, pop = "hp"];
      female [n = 2500, pop = "hp"];
   end_founder;
   ls  = 1 2 [0.2];        //Litter size
   pmp = 0.5;              //Proportion of male progeny
   ng  = 10;               //Number of generations
   md  = p_assort/ebv;     //Mating design
   sr  = 0.4;              //Replacement ratio for sires
   dr  = 0.2;              //Replacement ratio for dams
   sd  = ebv /h;           //Selection design
   cd  = phen/l;           //Culling design
   ebv_est = blup;
```

rnd, phen, tbv ebv and **age** (only for culling)

/l or **/h** to select low or high values

Breeding value estimation method



```
/********************************
 **          Populations       **
 ********************************/
begin_pop = "p1";
   begin_founder;
      male    [n =  20, pop = "hp"];
      female [n = 400, pop = "hp"];
   end_founder;
   ls   = 2;
   pmp = 0.5 /fix;
   ng   = 10;
   begin_popoutput;
        data;
        stat;
        genotype /snp_code /gen 8 9 10;
   end_popoutput;
end_pop;
```

p1_**mrk**_007.txt

p1_**qtl**_007.txt

Population specific parameters for saving outputs

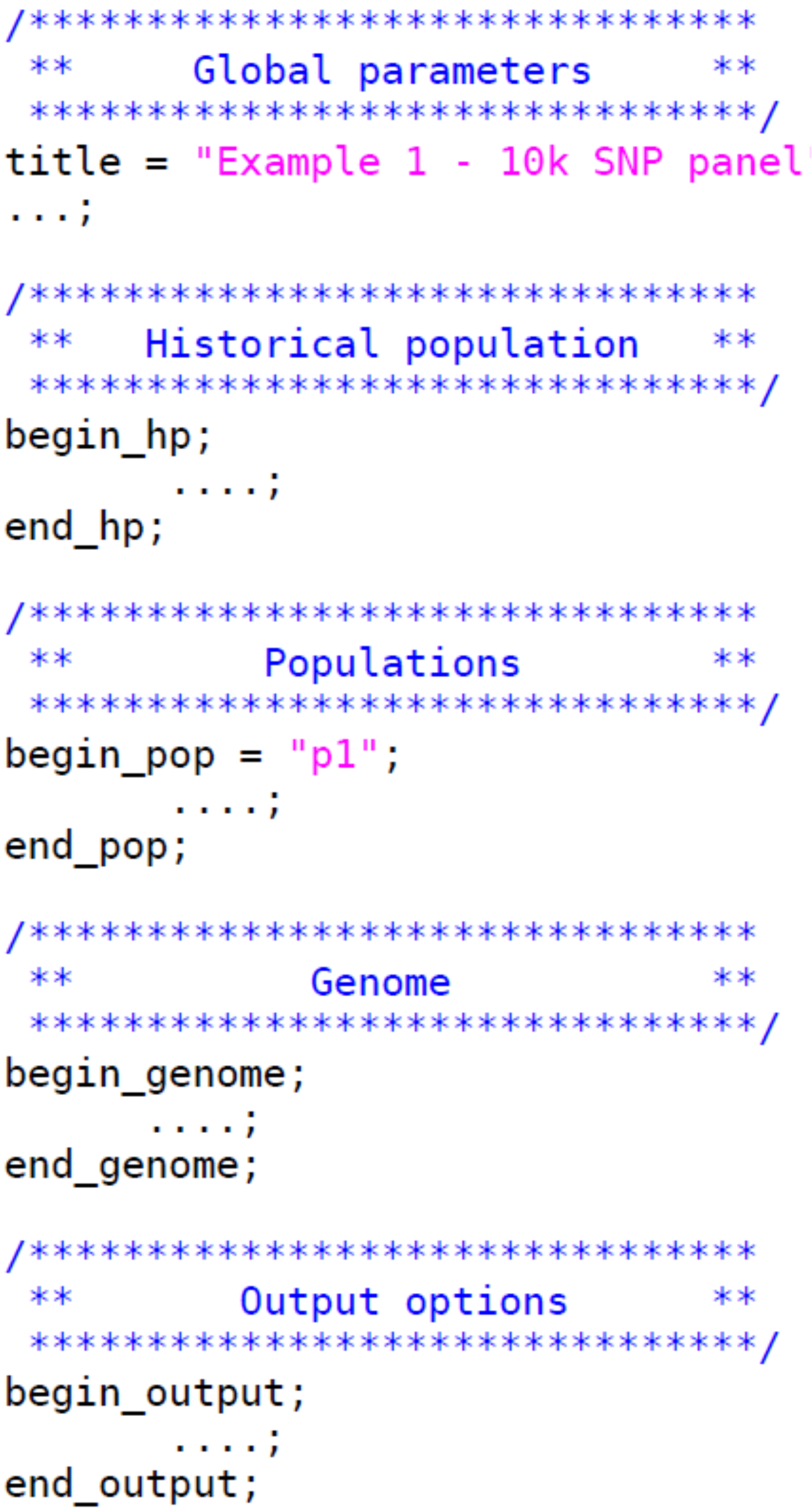
data: save individual's data except their genopype
(*File name:* 'population name'_**data**_'replicate number'.txt

stat: save brief statistic on simulated data

genotype: save genotype data

Parameter file

✓It consists of **five** main sections



```
/*******************************
 **     Global parameters     **
 *******************************/
title = "Example 1 - 10k SNP panel"
...;

/*******************************
 **   Historical population   **
 *******************************/
begin_hp;
       ....;
end_hp;

/*******************************
 **        Populations        **
 *******************************/
begin_pop = "p1";
       ....;
end_pop;

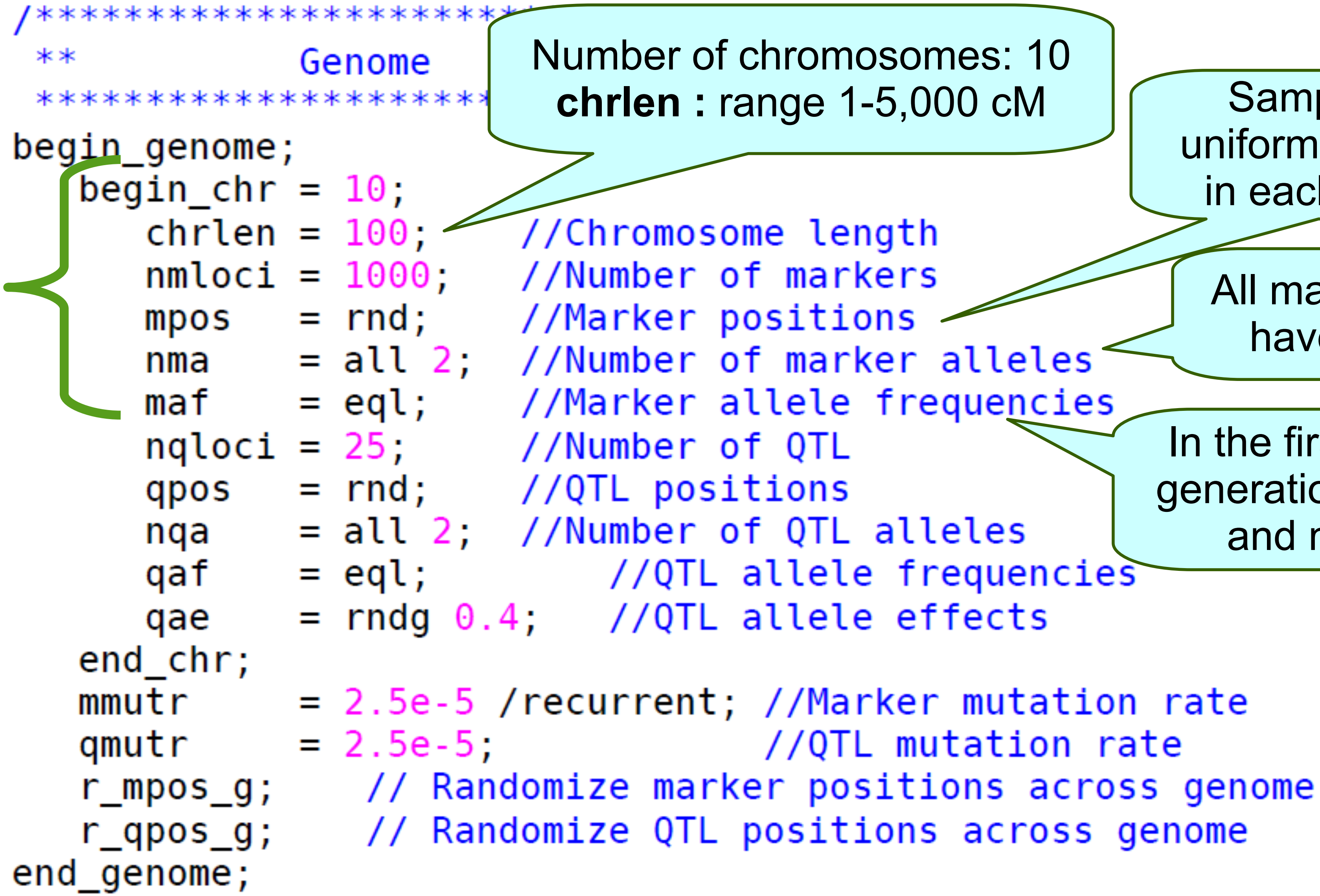
/*******************************
 **          Genome           **
 *******************************/
begin_genome;
      ....;
end_genome;

/*******************************
 **       Output options      **
 *******************************/
begin_output;
       ....;
end_output;
```

4. Genome section

Marker information

Example – 10k SNP panel



```
/***********************
 **          Genome
 *********************
begin_genome;
   begin_chr = 10;
      chrlen = 100;     //Chromosome length
      nmloci = 1000;    //Number of markers
      mpos   = rnd;     //Marker positions
      nma    = all 2;   //Number of marker alleles
      maf    = eql;     //Marker allele frequencies
      nqloci = 25;      //Number of QTL
      qpos   = rnd;     //QTL positions
      nqa    = all 2;   //Number of QTL alleles
      qaf    = eql;         //QTL allele frequencies
      qae    = rndg 0.4;    //QTL allele effects
   end_chr;
   mmutr     = 2.5e-5 /recurrent; //Marker mutation rate
   qmutr     = 2.5e-5;            //QTL mutation rate
   r_mpos_g;     // Randomize marker positions across genome
   r_qpos_g;     // Randomize QTL positions across genome
end_genome;
```

Number of chromosomes: 10
chrlen : range 1-5,000 cM

Samples from uniform distribution in each replicate

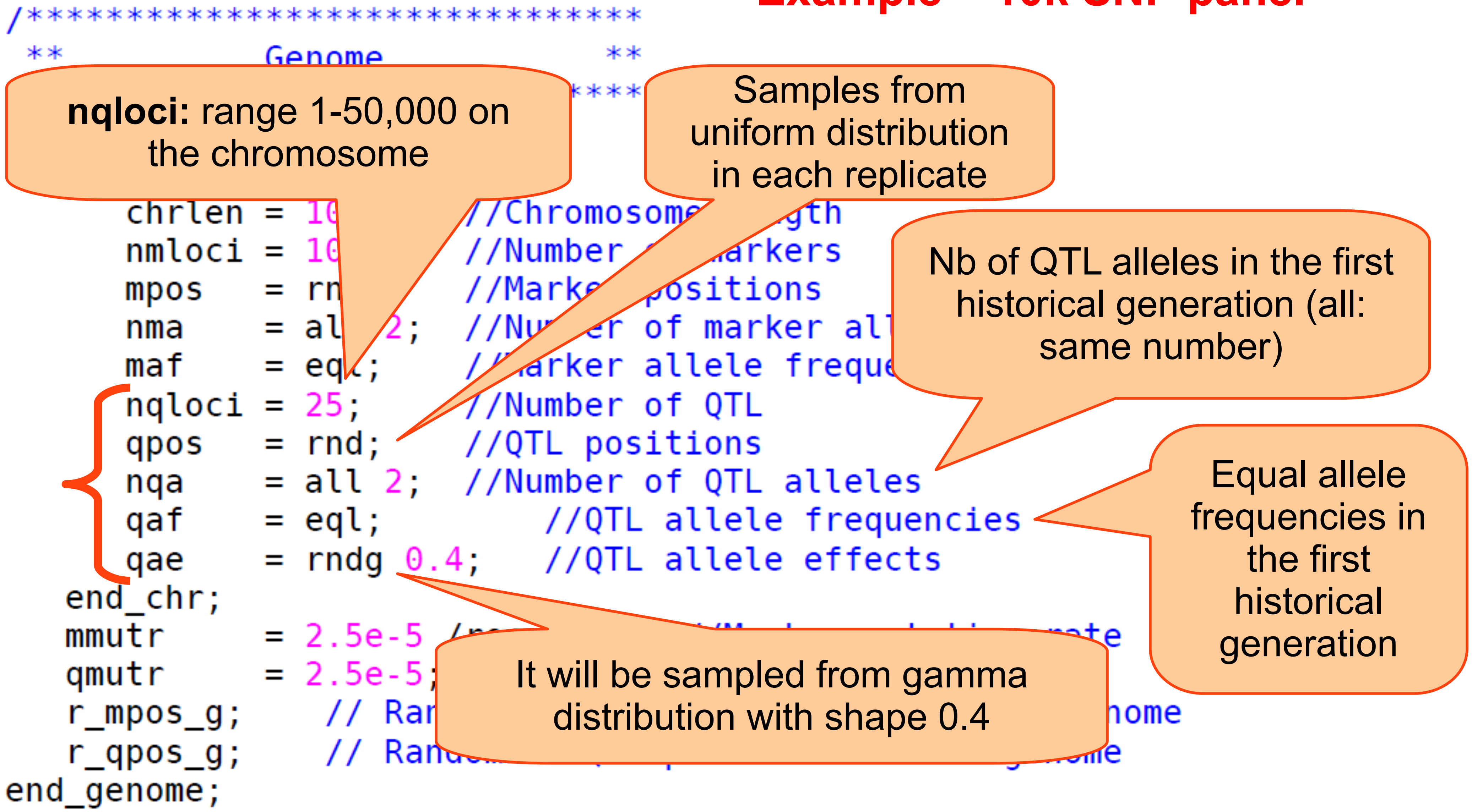
All marker loci will have 2 alleles

In the first historical generation, then drift and mutation

4. Genome section

QTL information

Example – 10k SNP panel



```
/******************************
 **           Genome             **
                              ****
    chrlen = 10      //Chromosome   gth
    nmloci = 10      //Number     arkers
    mpos   = rn      //Marke   positions
    nma    = al  2;  //Nu   er of marker al
    maf    = eq ;    //  arker allele freque
    nqloci = 25;     //Number of QTL
    qpos   = rnd;    //QTL positions
    nqa    = all 2;  //Number of QTL alleles
    qaf    = eql;        //QTL allele frequencies
    qae    = rndg 0.4;   //QTL allele effects
  end_chr;
  mmutr      = 2.5e-5 /                     ate
  qmutr      = 2.5e-5;
  r_mpos_g;     // Ran                       nome
  r_qpos_g;     // Rand                      nome
end_genome;
```

nqloci: range 1-50,000 on the chromosome

Samples from uniform distribution in each replicate

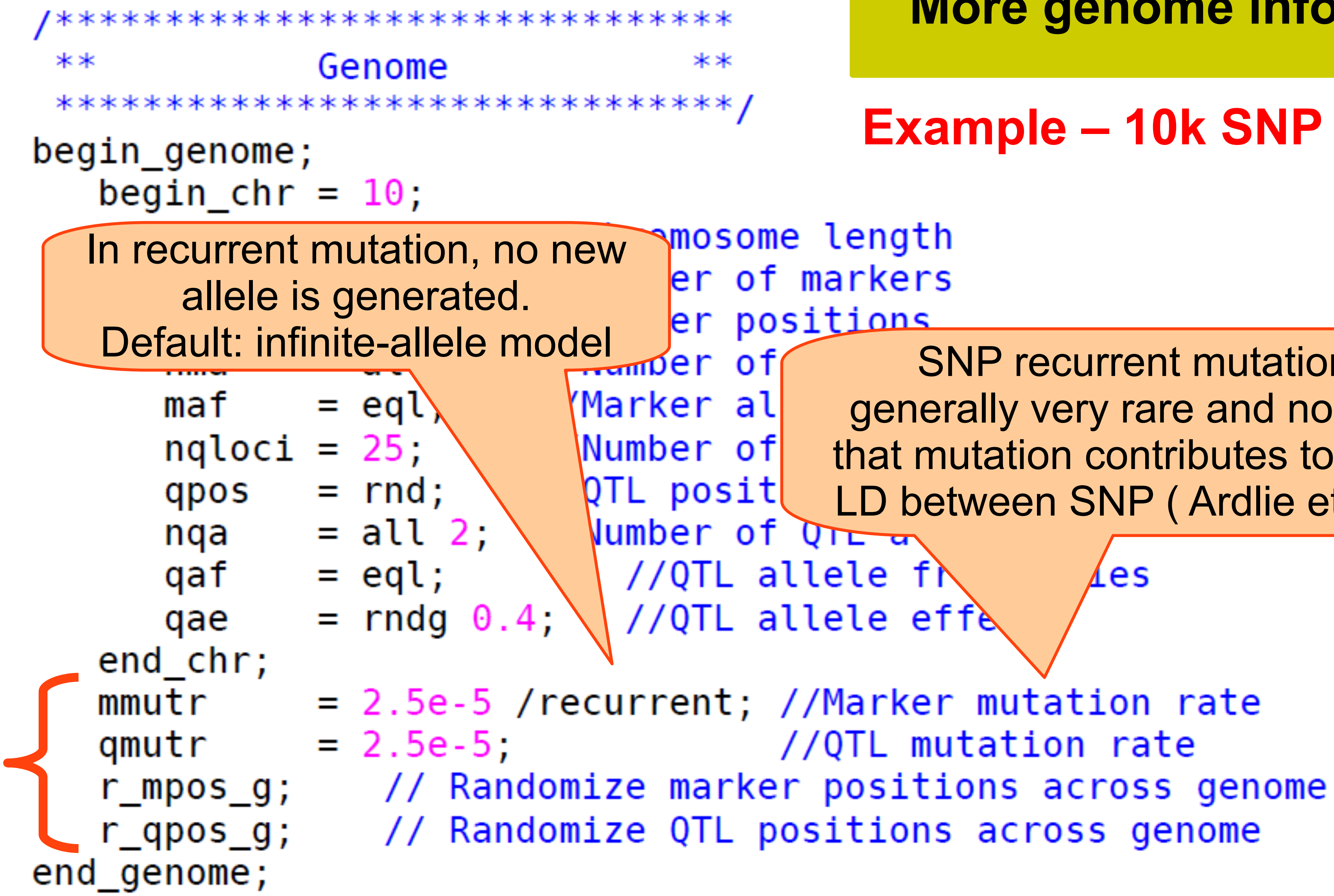
Nb of QTL alleles in the first historical generation (all: same number)

Equal allele frequencies in the first historical generation

It will be sampled from gamma distribution with shape 0.4

More genome information

Example – 10k SNP panel



```
/********************************
 **          Genome          **
 ********************************/
begin_genome;
   begin_chr = 10;
                           omosome length
                           er of markers
                           er positions
                           umber of
      maf    = eql;       /Marker al
      nqloci = 25;        Number of
      qpos   = rnd;       QTL posit
      nqa    = all 2;     Number of QTL a
      qaf    = eql;         //QTL allele fr        ies
      qae    = rndg 0.4;    //QTL allele effe
   end_chr;
   mmutr     = 2.5e-5 /recurrent; //Marker mutation rate
   qmutr     = 2.5e-5;            //QTL mutation rate
   r_mpos_g;     // Randomize marker positions across genome
   r_qpos_g;     // Randomize QTL positions across genome
end_genome;
```

In recurrent mutation, no new allele is generated.
Default: infinite-allele model

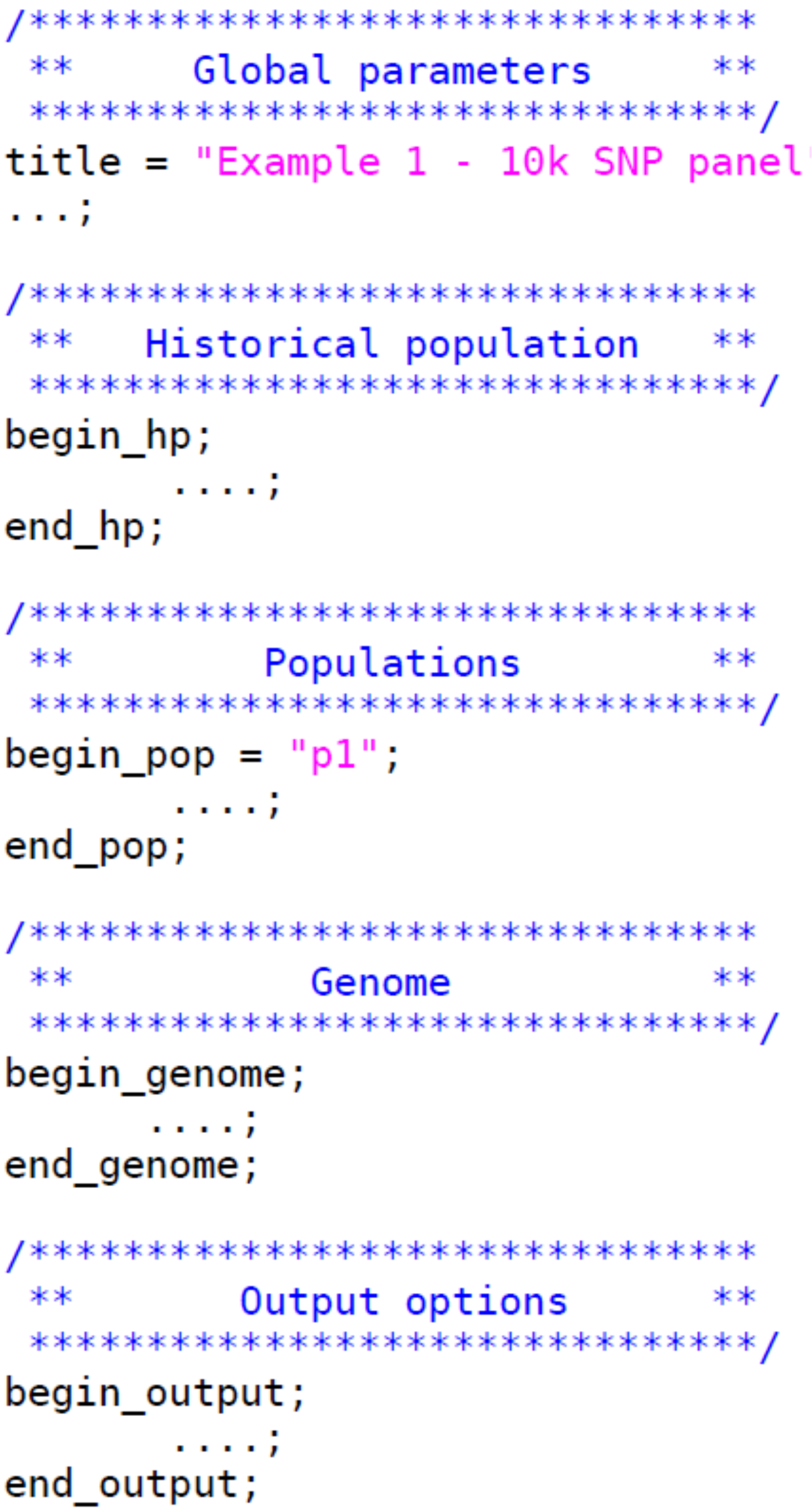
SNP recurrent mutations are generally very rare and no evidence that mutation contributes to erosion of LD between SNP (Ardlie et al., 2002)

Other possibilities :

- Missing marker/QTL genotypes
- Genotyping errors can be simulated (marker/QTL)

Parameter file

✓It consists of **five** main sections



```
/******************************
 **      Global parameters     **
 ******************************/
title = "Example 1 - 10k SNP panel
...;

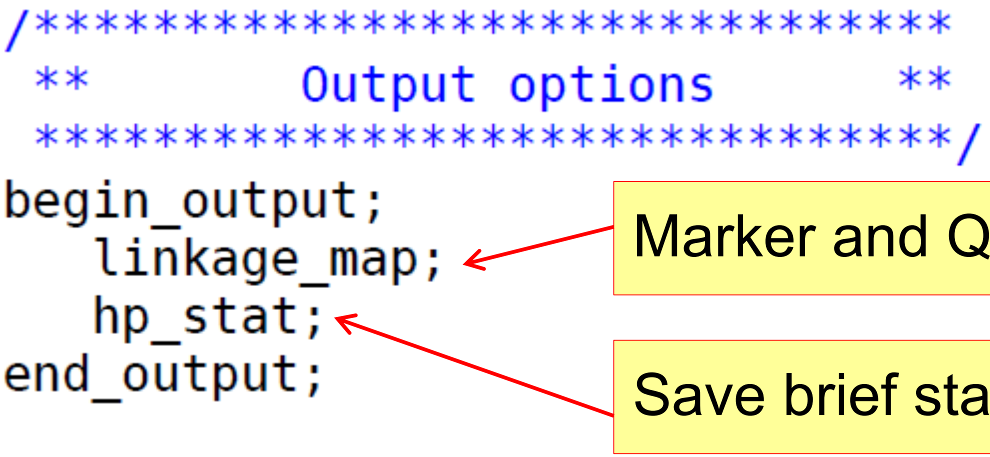
/******************************
 **    Historical population   **
 ******************************/
begin_hp;
       ....;
end_hp;

/******************************
 **        Populations         **
 ******************************/
begin_pop = "p1";
       ....;
end_pop;

/******************************
 **          Genome            **
 ******************************/
begin_genome;
      ....;
end_genome;

/******************************
 **       Output options       **
 ******************************/
begin_output;
       ....;
end_output;
```

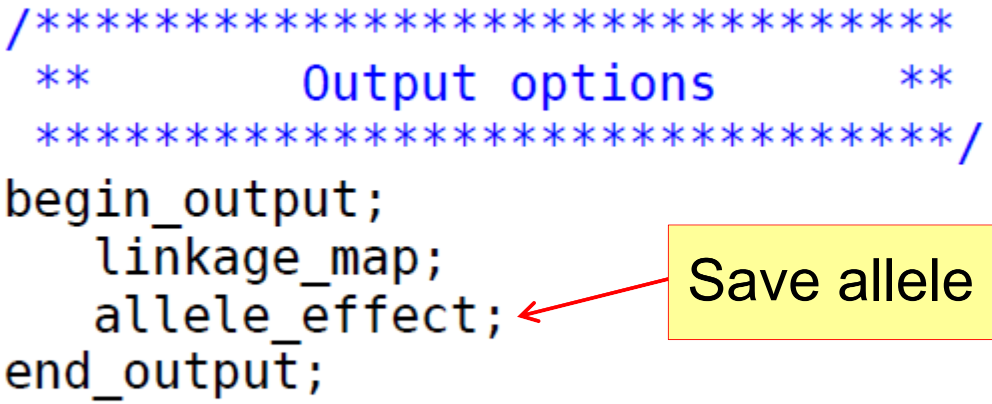
5. Output section



```
/*******************************
 **       Output options      **
 *******************************/
begin_output;
   linkage_map;
   hp_stat;
end_output;
```

Marker and QTL linkage map (GWAS)

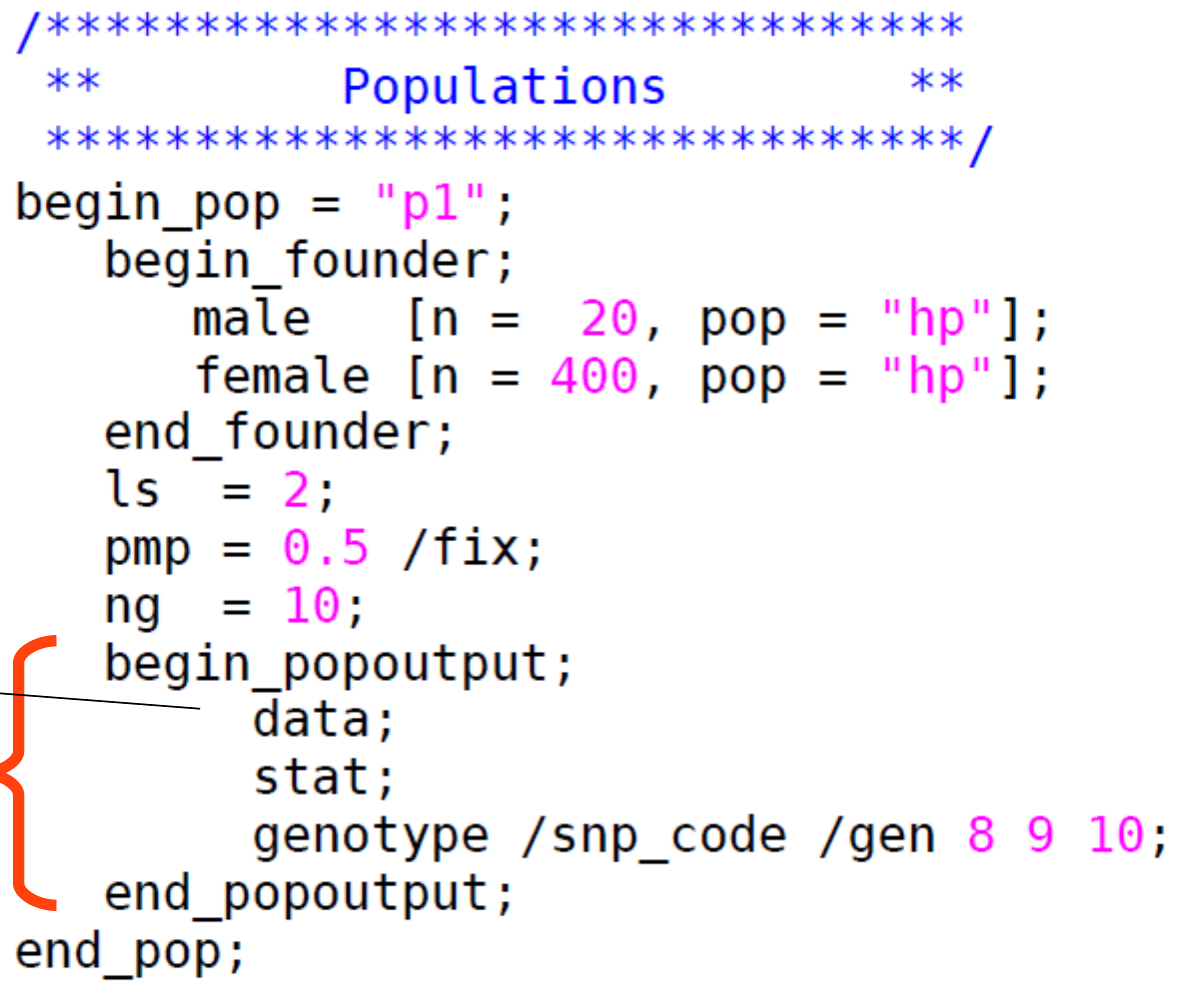
Save brief statistics on historical population



```
/*******************************
 **       Output options      **
 *******************************/
begin_output;
   linkage_map;
   allele_effect;
end_output;
```

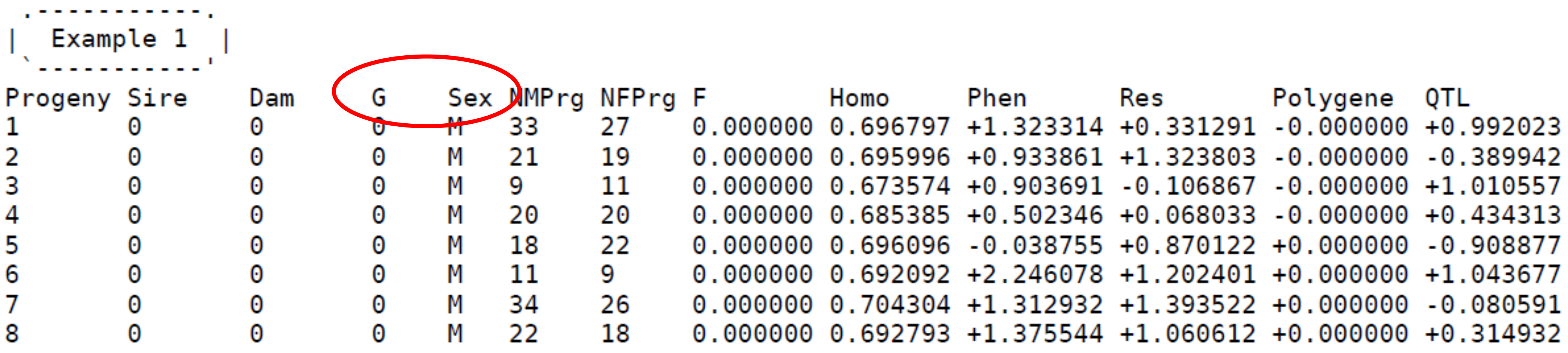
Save allele effects

QMSim outputs



```
/*******************************
 **         Populations       **
 *******************************/
begin_pop = "p1";
   begin_founder;
      male   [n =  20, pop = "hp"];
      female [n = 400, pop = "hp"];
   end_founder;
   ls  = 2;
   pmp = 0.5 /fix;
   ng  = 10;
   begin_popoutput;
        data;
        stat;
        genotype /snp_code /gen 8 9 10;
   end_popoutput;
end_pop;
```

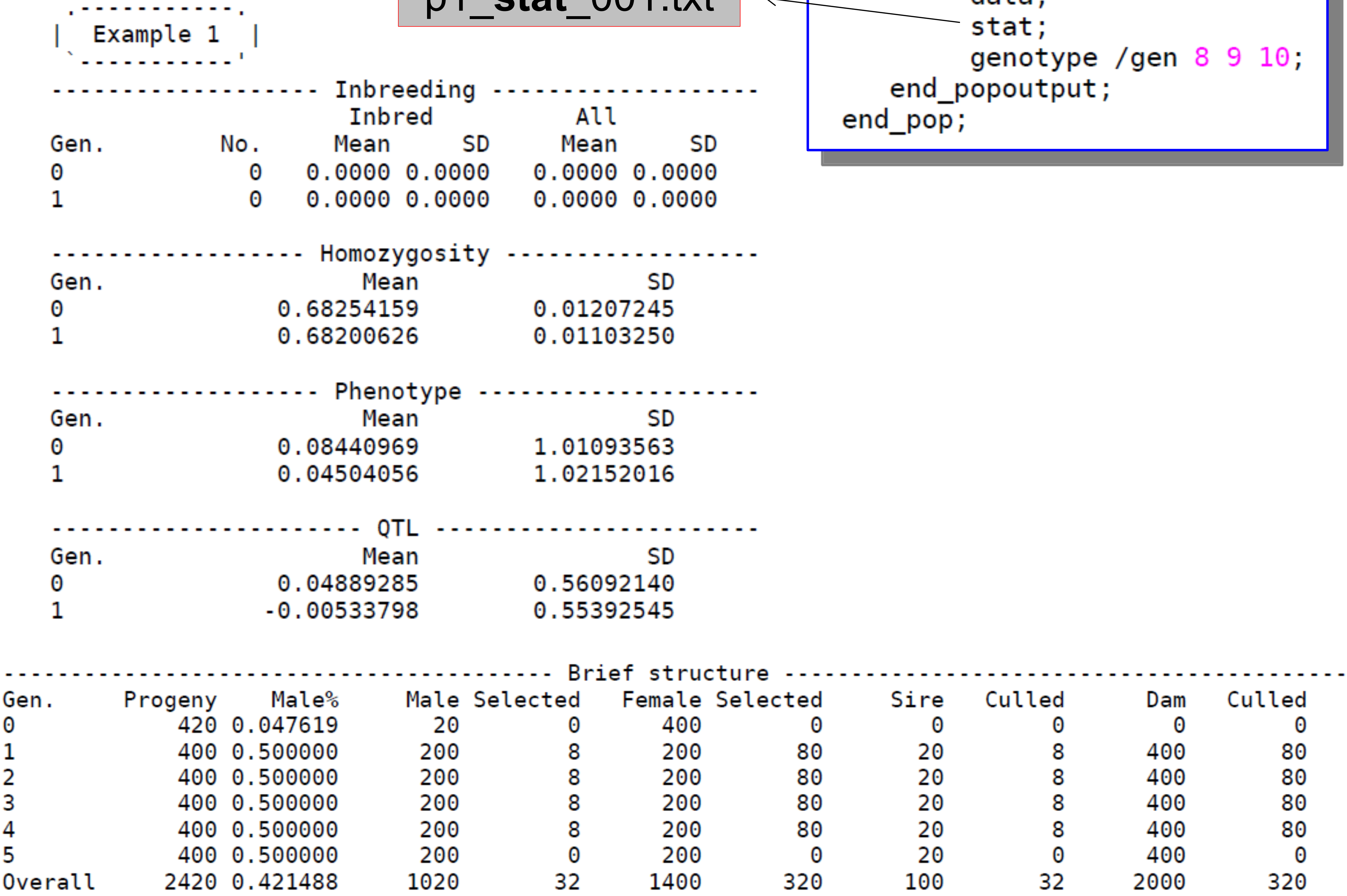
p1_**data**_001.txt



```
 .-----------.
|  Example 1  |
 `-----------'
Progeny Sire    Dam     G    Sex NMPrg NFPrg F        Homo     Phen      Res       Polygene  QTL
1       0       0       0    M   33    27    0.000000 0.696797 +1.323314 +0.331291 -0.000000 +0.992023
2       0       0       0    M   21    19    0.000000 0.695996 +0.933861 +1.323803 -0.000000 -0.389942
3       0       0       0    M   9     11    0.000000 0.673574 +0.903691 -0.106867 -0.000000 +1.010557
4       0       0       0    M   20    20    0.000000 0.685385 +0.502346 +0.068033 -0.000000 +0.434313
5       0       0       0    M   18    22    0.000000 0.696096 -0.038755 +0.870122 +0.000000 -0.908877
6       0       0       0    M   11    9     0.000000 0.692092 +2.246078 +1.202401 +0.000000 +1.043677
7       0       0       0    M   34    26    0.000000 0.704304 +1.312932 +1.393522 +0.000000 -0.080591
8       0       0       0    M   22    18    0.000000 0.692793 +1.375544 +1.060612 +0.000000 +0.314932
```

p1_**stat**_001.txt

```
    begin_popoutput;
        data;
        stat;
        genotype /gen 8 9 10;
    end_popoutput;
end_pop;
```



```
   .-----------.
  |  Example 1  |
   `-----------'
  ------------------- Inbreeding -------------------
                          Inbred              All
  Gen.          No.     Mean      SD      Mean      SD
  0               0    0.0000 0.0000    0.0000 0.0000
  1               0    0.0000 0.0000    0.0000 0.0000

  ------------------ Homozygosity ------------------
  Gen.                     Mean                  SD
  0                  0.68254159          0.01207245
  1                  0.68200626          0.01103250

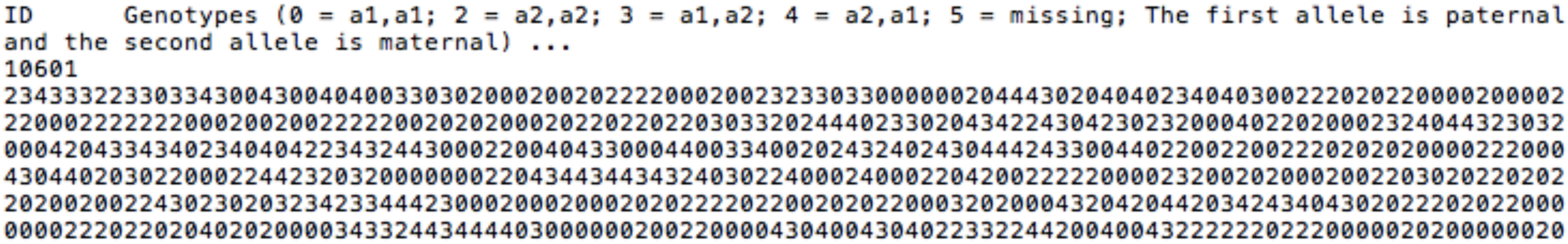
  ------------------- Phenotype -------------------
  Gen.                     Mean                  SD
  0                  0.08440969          1.01093563
  1                  0.04504056          1.02152016

  ---------------------- QTL ----------------------
  Gen.                     Mean                  SD
  0                  0.04889285          0.56092140
  1                 -0.00533798          0.55392545

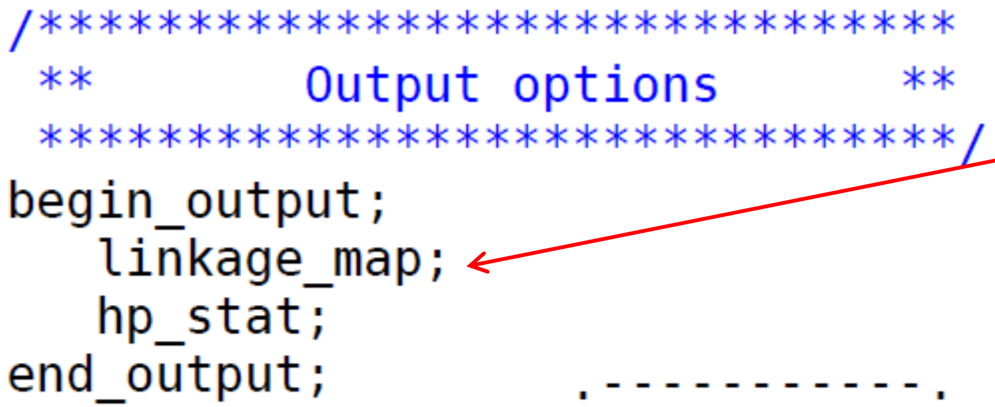
---------------------------------------- Brief structure ----------------------------------------
Gen.      Progeny    Male%     Male Selected   Female Selected      Sire   Culled       Dam   Culled
0             420 0.047619       20        0       400        0        0        0         0        0
1             400 0.500000      200        8       200       80       20        8       400       80
2             400 0.500000      200        8       200       80       20        8       400       80
3             400 0.500000      200        8       200       80       20        8       400       80
4             400 0.500000      200        8       200       80       20        8       400       80
5             400 0.500000      200        0       200        0       20        0       400        0
Overall      2420 0.421488     1020       32      1400      320      100       32      2000      320
```

p1_**mrk**_001.txt

```
   begin_popoutput;
        data;
        stat;
        genotype /snp_code /gen 4 5;
   end_popoutput;
end_pop;
```

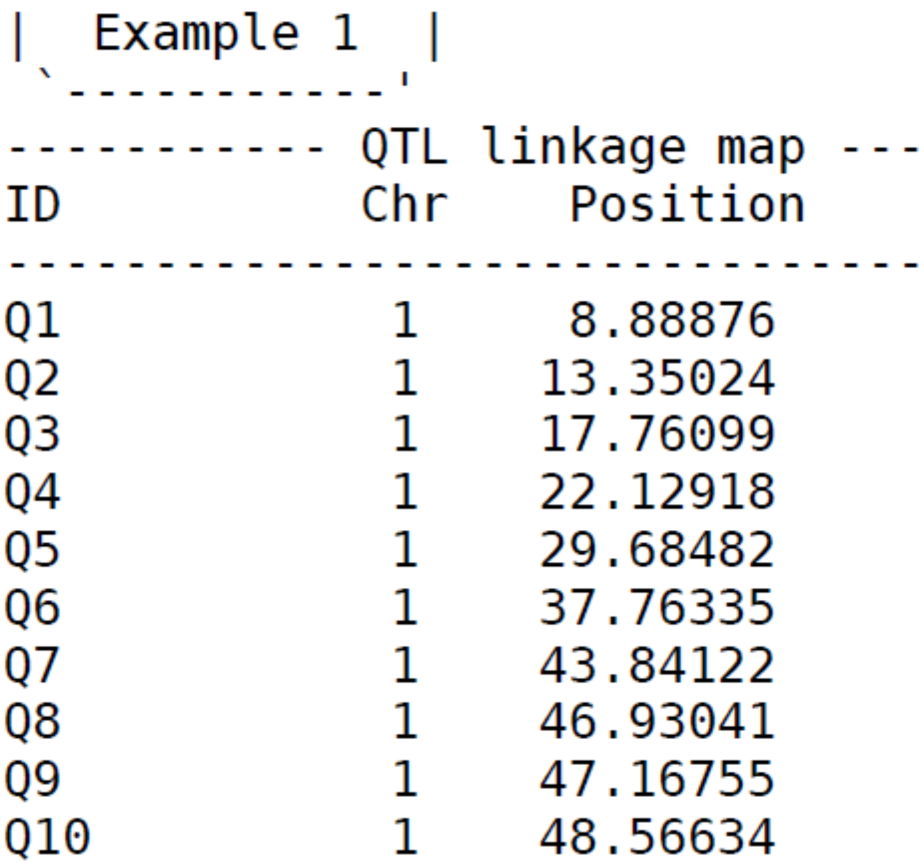


```
ID      Genotypes (0 = a1,a1; 2 = a2,a2; 3 = a1,a2; 4 = a2,a1; 5 = missing; The first allele is paternal
and the second allele is maternal) ...
10601
23433322330334300430040400330302000200202222000200232330330000002044430204040234040300222020220000200002
22000222222200020020022222002020200020220220220303320244402330204342243042302320004022020002324044323032
00042043343402340404223432443000220040433000440033400202432402430444243300440220022002220202020000222000
43044020302200022442320320000000220434434434324030224000240002204200222220000232002020002002203020220202
20200200224302302032342334442300020002000202022220220020202200032020004320420442034243404302022202022000
00002220220204020200003433244344440300000002002200000430400430402233224420040043222220222000002020000020
```

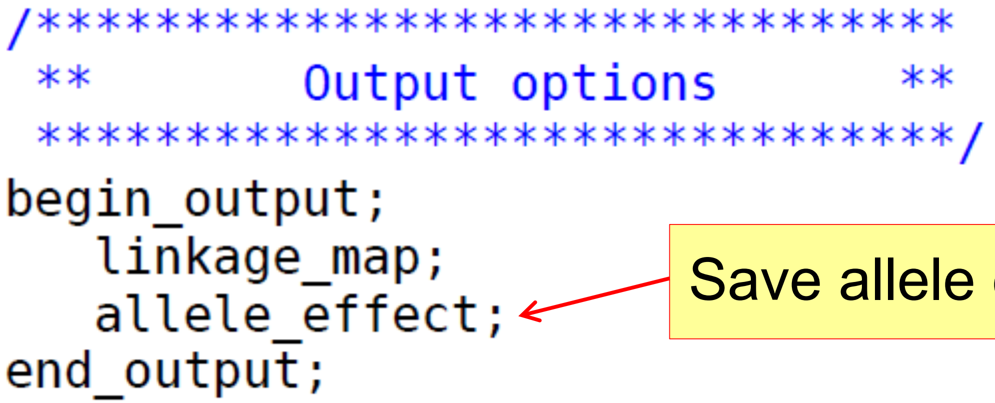


```
/*******************************
 **       Output options      **
 *******************************/
begin_output;
   linkage_map;
   hp_stat;
end_output;
```

Marker and QTL linkage map

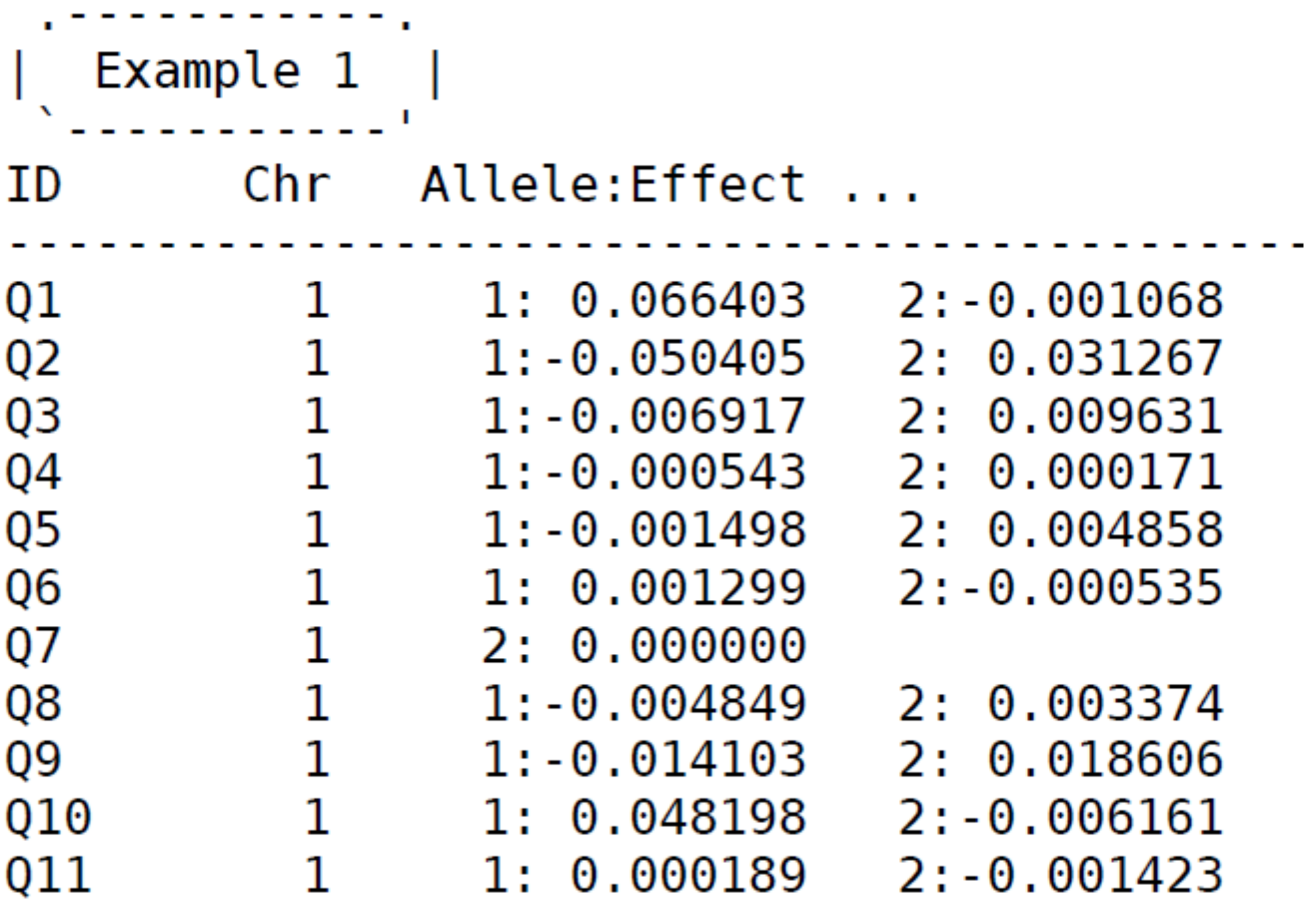


```
 .------------.
|  Example 1   |
 `------------'
----------- QTL linkage map ---
ID          Chr     Position
------------------------------
Q1            1      8.88876
Q2            1     13.35024
Q3            1     17.76099
Q4            1     22.12918
Q5            1     29.68482
Q6            1     37.76335
Q7            1     43.84122
Q8            1     46.93041
Q9            1     47.16755
Q10           1     48.56634
```



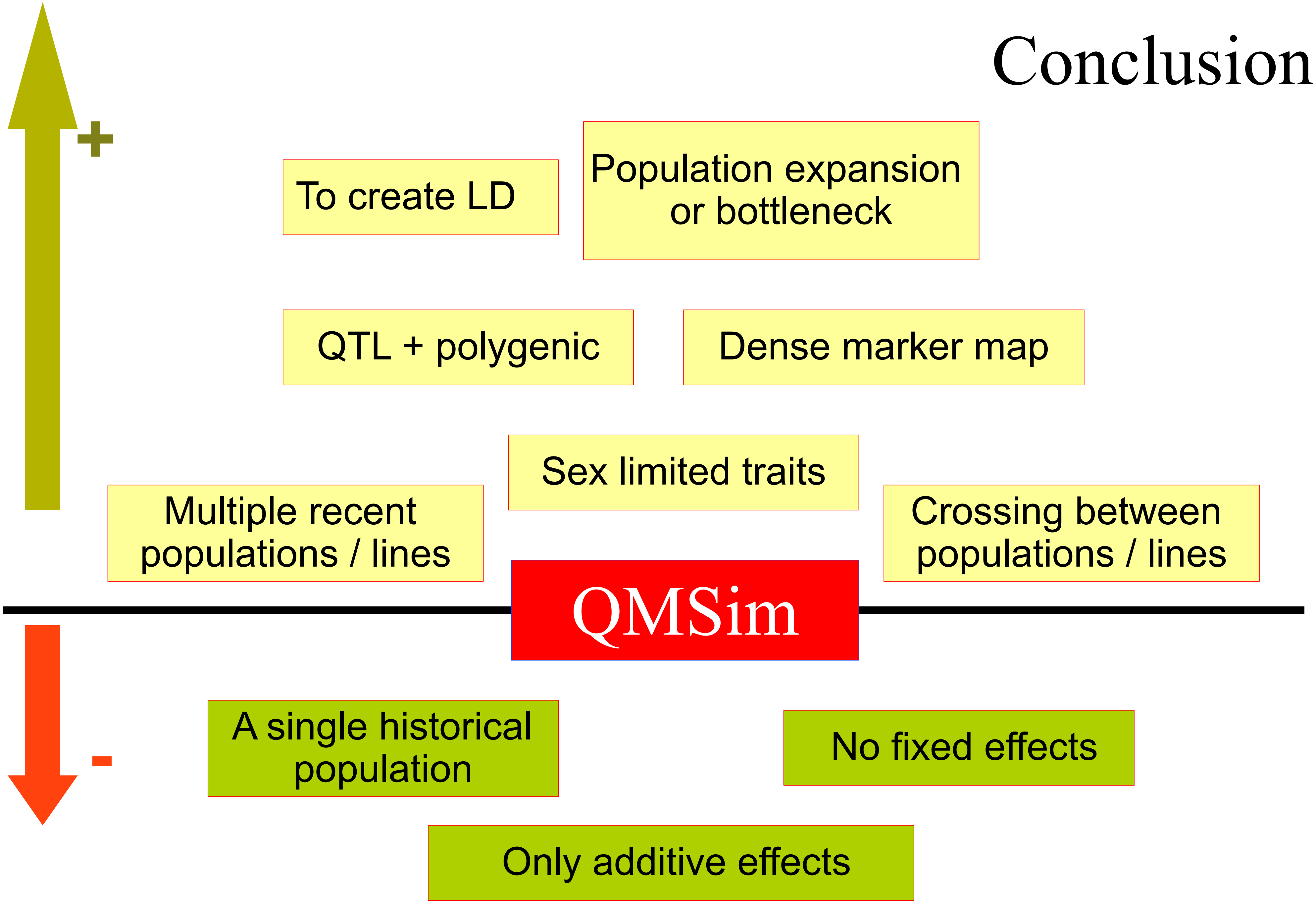
```
/******************************
 **        Output options      **
 ******************************/
begin_output;
   linkage_map;
   allele_effect;
end_output;
```

Save allele effects



```
 .-----------.
|  Example 1  |
 `-----------'
ID      Chr   Allele:Effect ...
-------------------------------------------
Q1        1     1: 0.066403   2:-0.001068
Q2        1     1:-0.050405   2: 0.031267
Q3        1     1:-0.006917   2: 0.009631
Q4        1     1:-0.000543   2: 0.000171
Q5        1     1:-0.001498   2: 0.004858
Q6        1     1: 0.001299   2:-0.000535
Q7        1     2: 0.000000
Q8        1     1:-0.004849   2: 0.003374
Q9        1     1:-0.014103   2: 0.018606
Q10       1     1: 0.048198   2:-0.006161
Q11       1     1: 0.000189   2:-0.001423
```

Conclusion



+

To create LD

Population expansion or bottleneck

QTL + polygenic

Dense marker map

Sex limited traits

Multiple recent populations / lines

Crossing between populations / lines

QMSim

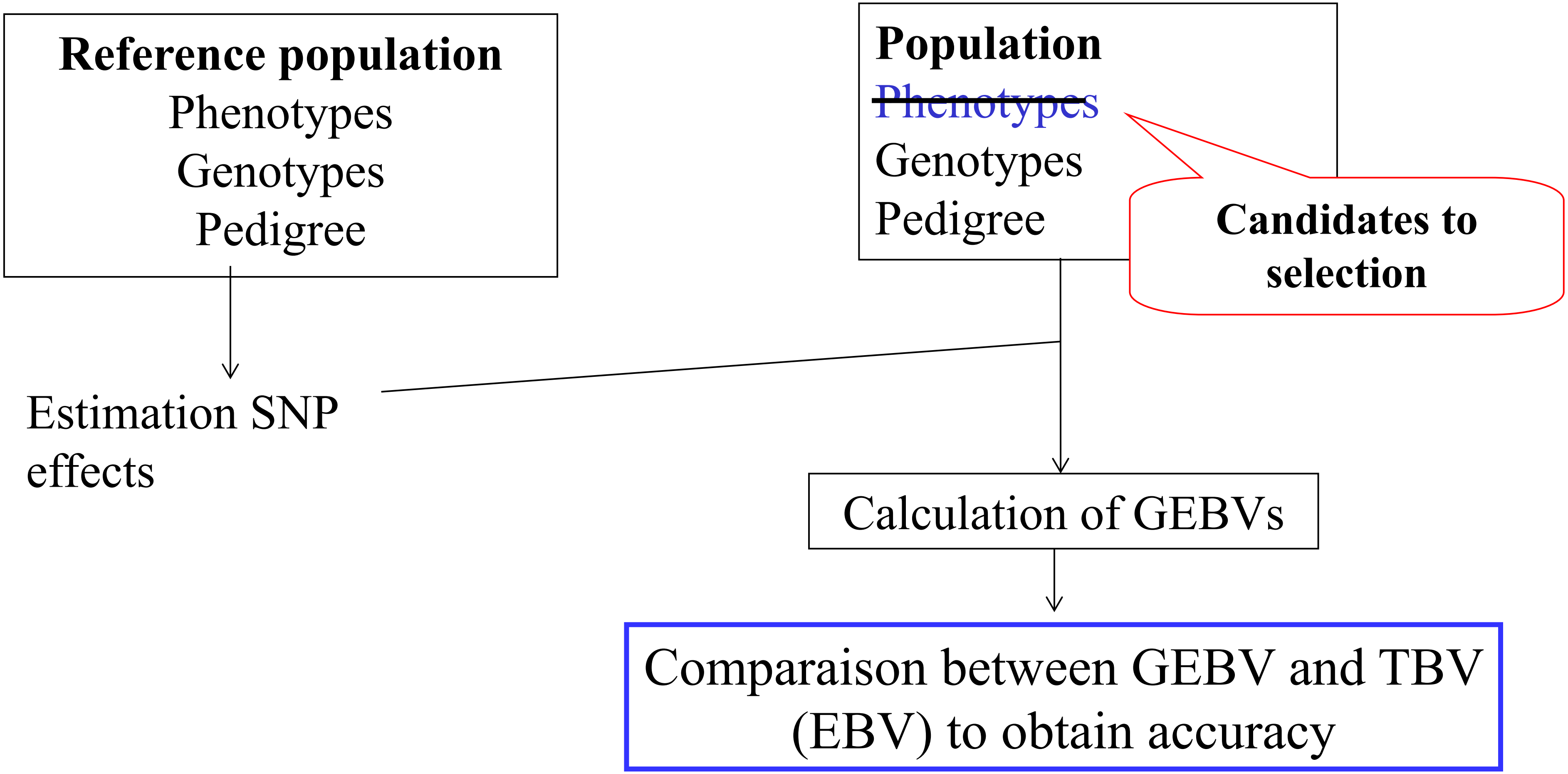
-

A single historical population

No fixed effects

Only additive effects

Genomic selection : validation



Reference population

Phenotypes

Genotypes

Pedigree

Estimation SNP effects

Population

~~Phenotypes~~

Genotypes

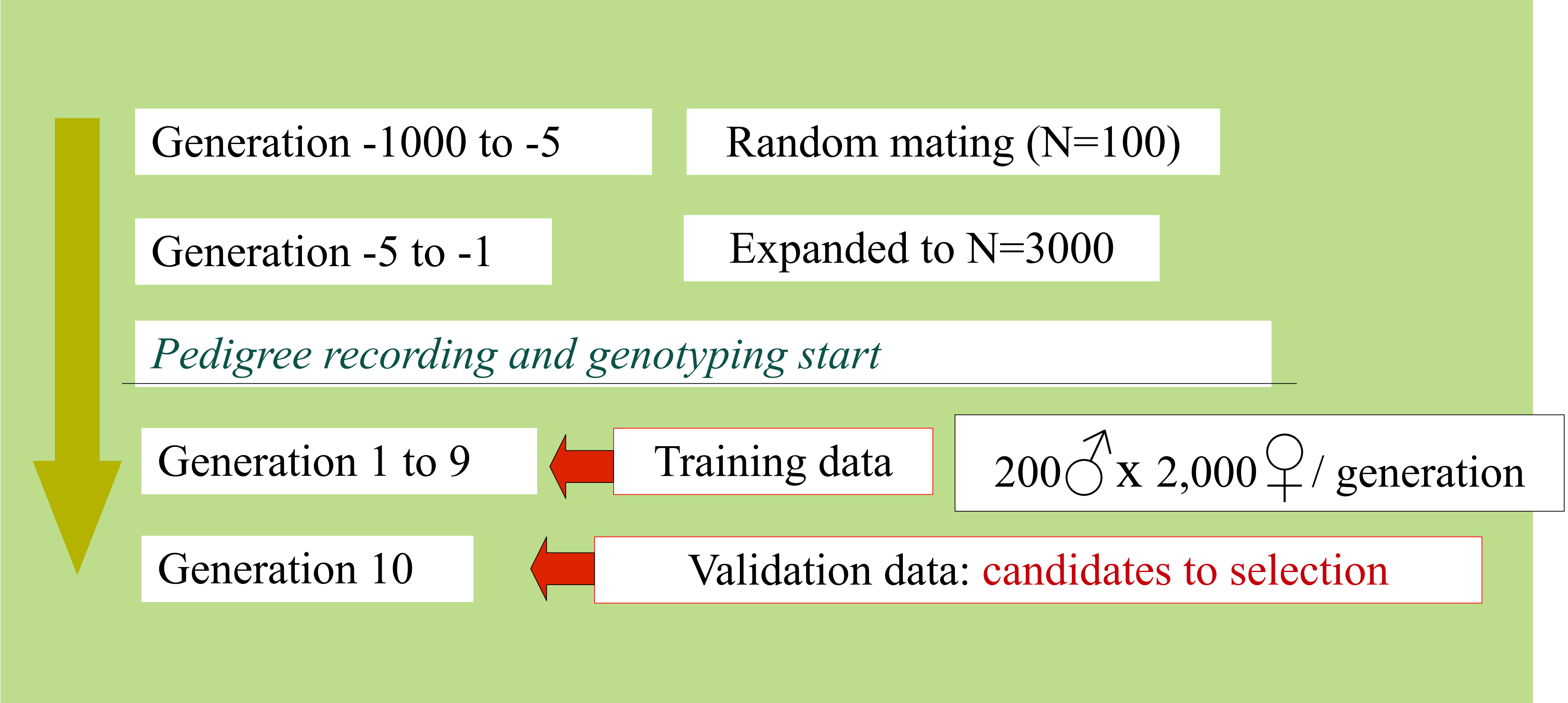
Pedigree

Candidates to selection

Calculation of GEBVs

Comparaison between GEBV and TBV (EBV) to obtain accuracy

Example of simulation



Generation -1000 to -5 — Random mating (N=100)

Generation -5 to -1 — Expanded to N=3000

Pedigree recording and genotyping start

Generation 1 to 9 ← Training data — 200♂x 2,000♀/ generation

Generation 10 ← Validation data: candidates to selection