

# ADAM-Plant

Program to simulate selective-breeding schemes for crop plants

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# 1. Program description

ADAM-Plant is a computer program that models selective breeding schemes for self-pollinated and cross-pollinated crop plants using stochastic simulation. The program simulates a population of plants and traces the genetic changes in the population under different selective-breeding scenarios. It caters to different population structures, genetic models, selection strategies, and mating designs. ADAM-plant can be used to evaluate breeding schemes and generate genetic data to test statistical tools. It is an important tool for comparing strategies for plant breeding and for estimating the effects of allocation of different resources to the breeding program. The program is written in FORTRAN.

## 2. Directories

There are three main directories associated with an ADAM-Plant simulation: submission, working, and output directories.

### ***Submission directory***

Directory from which a simulation is submitted.

### ***Working directory***

Temporary directory where a simulation is run. This directory is created by the Portable Batch System (PBS) on Foulum's Linux system.

### ***Output directory***

Directory to which output files from a simulation are written.

The submission and output directories can be the same directory.

## 3. Files

### **Script file**

*adam.script*, script file that submits a simulation. The directory in which *adam.script* is saved and from which a simulation is submitted becomes the submission directory.

The following files are located in the submission directory. All files, with the exception of input file, *input.prm*, are optional.

### **Input file**

*input.prm*, provides input parameters.

### **Seed files**

Files with random seeds when seeds are provided manually. File names are provided in namelist &RANDOMNUMBERSEEDS.

*seedsFile*, input file with seeds when *randomSeeds* 'file' in namelist &RANDOMNUMBERSEEDS.

*founderSeedsFile*, input file with seeds when *randomSeeds* 'manual' and *founderSeeds* 'file'.

*baseSeedsFile*, input file with seeds when *randomSeeds* 'manual' and *baseSeeds* 'file'.

*selectionSeedsFile*, input file with seeds when *randomSeeds* 'manual' and *selectionSeeds* 'file'.

These files contains two integer seeds per row (*seed1* and *seed2*), and one row per replicate. Each replicate is initiated with the seeds provided in the files.

### DMU files

Files required when DMU is used to estimate breeding values. The files required are determined by the breeding values that are to be estimated. For details of the files themselves, refer to the User's Manual for DMU.

(1) Polygenic breeding values (selection criterion 'polyblup' specified in namelists &SELECTION and &EVA of *input.prm*)

*dmu.polyblup.dir*, DMU-input parameters  
*dmu.polyblup.parm* (optional), (co)variance components

The files *dmudat* and *dmuped* (files with DMU-input data and polygenic-pedigree) must be specified in *dmu.polyblup.dir*. These files are created by ADAM.

The file *dmu.polyblup.parm* is optional. It can be used to provide (co)variance components, in which case, it must be specified in *dmu.polyblup.dir*. The alternative is to specify the (co)variance components in *dmu.polyblup.dir*.

(2) Genomic breeding values (selection criterion 'genomicblup')

*dmu.genomicblup.dir*, DMU-input parameters  
*dmu.genomicblup.parm* (optional), (co)variance components

The files *dmudat*, *dmuped*, *genotyped.dat*, and *gMatrix.prediction* (files with DMU-input data, polygenic-pedigree, genotyped plants, and genomic-relationships) must be specified in *dmu.genomicblup.dir*. These files are created by ADAM.

The file *dmu.genomicblup.parm* is optional. It can be used to provide (co)variance components, in which case, it must be specified in *dmu.genomicblup.dir*. The alternative is to specify the (co)variance components in *dmu.genomicblup.dir*.

### \$COMMENT ADAM-DMU interface

\$ANALYSE 12 2 0 0

\$DATA ASCII (6, 2, -9998. 0) dmudat

\$VARIABLE

id dam sex mn hys time trait wt

\$MODEL

1

0

1 0 2 5 1

1 1

0

0

\$VAR\_STR 1 PGMIX 1 ASCII dmuped genotyped. dat gmatrix. prediction 0. 25 G-ADJUST

\$PRIOR

1 1 1 1. 0000001

2 1 1 4. 0000000

Files used to estimate polygenic breeding values [*dmu.polyblup.dir* and *dmu.polyblup.parm* (optional)] are also required when polygenic breeding values are estimated instead of genomic breeding values.

(3) IBD breeding values (selection criterion 'ibdblup')

*dmu.ibdblup.dir*, DMU-input parameters  
*dmu.ibdblup.parm* (optional), (co)variance components

The files *dmudat*, *dmuped*, *genotyped.dat*, and *gMatrix.prediction* (files with DMU-input data, polygenic-pedigree, genotyped plants, and genomic-relationships) must be specified in *dmu.ibdblup.dir*. These files are created by ADAM.

The file *dmu.ibdblup.parm* is optional. It can be used to provide (co)variance components, in which case, it must be specified in *dmu.ibdblup.dir*. The alternative is to specify the (co)variance components in *dmu.ibdblup.dir*.

(4) GAS breeding values (selection criterion 'gas')

*dmu.gas.dir*, DMU-input parameters  
*dmu.gas.parm* (optional), (co)variance components

The files *dmudat* and *dmuped* must be specified in *dmu.gas.dir*. These files are created by ADAM.

The file *dmu.gas.parm* is optional. It can be used to provide (co)variance components, in which case, it must be specified in *dmu.gas.dir*. The alternative is to specify the (co)variance components in *dmu.gas.dir*.

Files used to estimate polygenic breeding values [*dmu.polyblup.dir* and *dmu.polyblup.parm* (optional)] are also required when polygenic breeding values are estimated instead of GAS breeding values.

NB. DMU and EVA files generated by ADAM, DMU, and EVA are copied to the output directory when debugOutput 'yes' in namelist &CONTROLPARAMETERS. These files are *dmu-script* file(s), G-matrix script and parameter files, *dmudat*, *dmuped*, *map.dat*, *marker.dat*, *gMatrix.dat*, *genotyped.dat*, *eva.dat*, *eva.log*, *eva-solution* file, and *dmu.lst*. These files are copied after they have been created; newly-created files overwrite older files.

## 4. Computer resource

ADAM must be run on 64-bit machine when genomic-breeding values are used as selection criterion in breeding schemes.

## 5. Script file

The following is an example of a script file, *adam.script*

```
#!/bin/bash
#PBS -N adam
#PBS -q gbi
#PBS -l walltime=1:00:00
#PBS -l nodes=1:ppn=2
#PBS -j eo

TMPDIR=/scratch/$USER/$PBS_JOBID      # Create temporary directory

export TMPDIR                          # Make TMPDIR accessible to subscripts
```

```

export MKL_NUM_THREADS=$(wc -l $PBS_NODEFILE | awk '{print $1}')
export OMP_NUM_THREADS=$MKL_NUM_THREADS # Limits number of cores ADAM and associated
                                         # programs, including DMU and G-Matrix, can use
                                         # Sets MKL_NUM_THREADS=OMP_NUM_THREADS=ppn.

cd $TMPDIR # Create TMPDIR working directory

ulimit -s unlimited # Unlimited file space

echo
echo Working directory: $TMPDIR
echo
echo Copying adam to working directory
echo

cp /hag/popgen/adam/trunk/adam adam # Copy ADAM to working directory

echo Running Adam
echo

./adam > $PBS_O_WORKDIR/adamlog.log # Run ADAM
                                     # Write information to log file

echo Adam simulation completed

```

## 6. Input file

Complete list of input parameters (namelists) in input file, input.prm:

```

&OUTPUTDIRECTORY
&CONTROLPARAMETERS
&CONTROL_GENOME
&LD
&RANDOMNUMBERSEEDS
&POPULATIONPARAMETERS
&BASEPOPULATION
&SELECTION
&PHENOTHRESHOLDS
&RULES
&EVA
&EVAPARAMETERS
&PHENOWEIGHTS
&GENOMICBLUPPARAMETERS
&IBDBLUPPARAMETERS
&IBSBLUPPARAMETERS
&EVAGENOMICRELATIONSHIPPARAMETERS
&EVAIBDRELATIONSHIPPARAMETERS
&EVAIBSRELATIONSHIPPARAMETERS
&DMUPARAMETERS
&BAYESPPARAMETERS
&MATINGPARAMETERS
&COMBINEDOBSERVATIONS
&OBSERVATIONCONSTRAINTS
&ECONOMICVALUES
&OBSERVATIONS
&CATEGORICALS
&MATRICES

```

&DESIGN\_MATRICES  
&MARKER\_NUMBERS  
&MARKER\_PARAMETERS  
&MARKER\_ALLELE\_FREQUENCIES  
&SAMPLE\_MARKER\_PARAMETERS  
&QTL\_PARAMETERS  
&QTL\_EFFECTS\_FREQUENCIES  
&SAMPLE\_QTL\_PARAMETERS  
&SAMPLE\_QTL\_NUMBERS  
&GAS\_PARAMETERS  
&TEMPLATE\_PARAMETERS  
&FOUNDER\_PARAMETERS  
&REPORT

## 7. Which namelists do I need?

All simulations require five namelists:

&OUTPUTDIRECTORY

&CONTROLPARAMETERS

&RANDOMNUMBERSEEDS

&ECONOMICVALUES

&REPORT

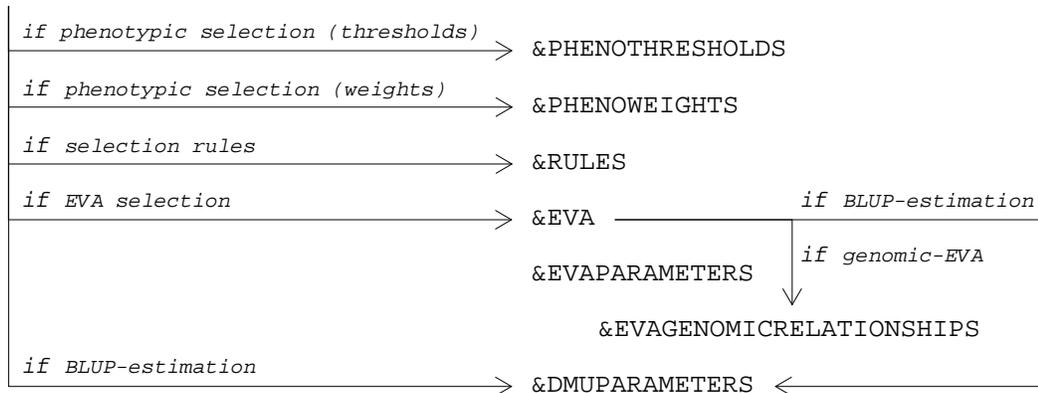
The remaining required namelists are determined by the variable *GeneticModel* in namelist &CONTROLPARAMETERS. *GeneticModel* can be 'polygenic', 'genomic', 'qtl', or 'ldonly'.

### polygenic, genomic, qtl

&POPULATIONPARAMETERS

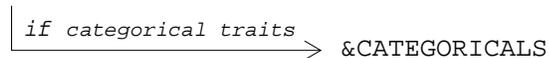
&BASEPOPULATION

&SELECTION



&MATINGPARAMETERS

&OBSERVATIONS

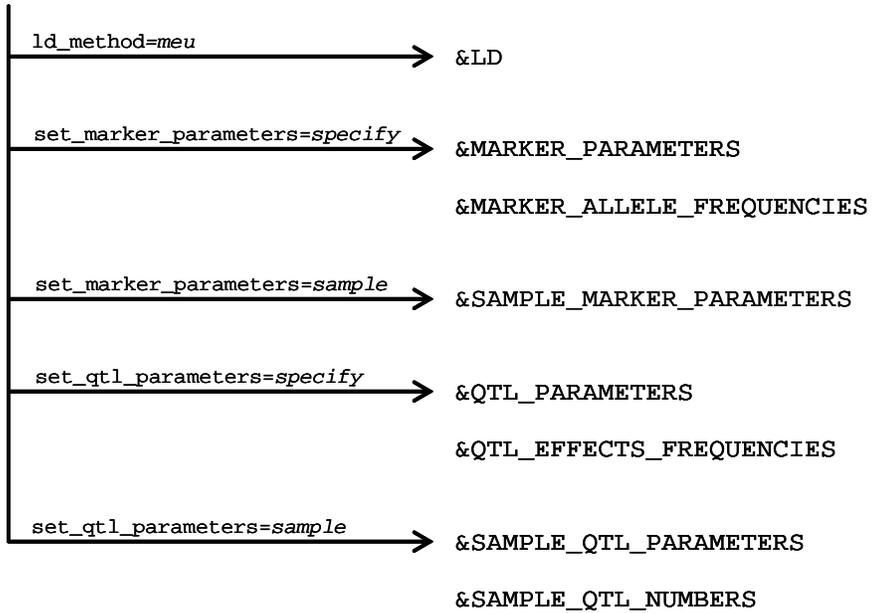


&MATRICES

&DESIGNMATRICES

**qtl**

&CONTROL\_GENOME



&MARKER\_NUMBERS

*if GAS-selection* (specified in &SELECTION)

&GAS\_PARAMETERS

**genomic, ldonly**

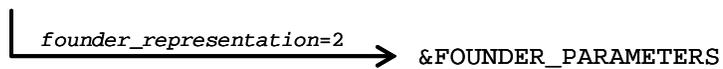
&CONTROL\_GENOME



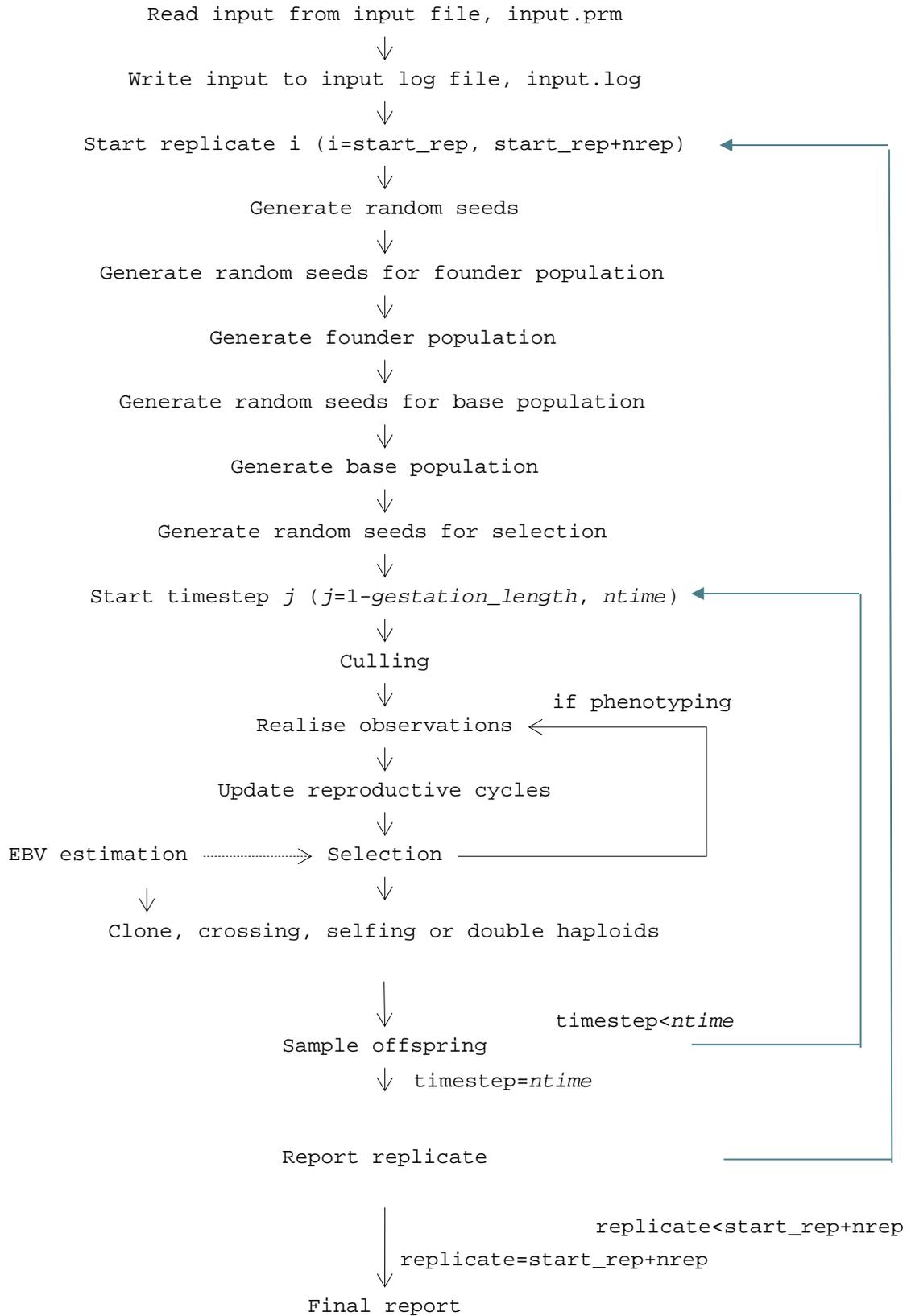
**genomic, qtl**

*if user\_marker\_template=yes* (specified in &CONTROL\_GENOME)

&TEMPLATE\_PARAMETERS



## 8. Working process



## 9. Genetic model and selection

Genetic model is the method used to generate breeding values. Selection involves the method used to select plants and the criterion by which plants are ranked. The selection criterion is often an estimated breeding value derived from a statistical analysis.

*Genetic models.* There are three genetic models available:

- (a) Polygenic model
- (b) Genomic model with linkage disequilibrium between QTL and markers
- (c) QTL model with or without linkage disequilibrium

An additional option, 'linkage disequilibrium only' (ldonly), is available to generate linkage disequilibrium with the genomic model. It is used to study linkage disequilibrium; a breeding scheme is not simulated.

*Selection methods.* There are three selection methods:

- (a) Threshold selection
- (b) Truncation selection
- (c) Optimum-contribution selection (EVA selection)

*Selection criteria.* There are eight selection criteria:

- (a) True breeding value
- (b) Random variable
- (c) Null variable
- (d) Phenotypic observation(s) with associated threshold(s)
- (e) Phenotypic observation(s) with associated weight(s)
- (f) Polygenic-BLUP breeding value
- (g) Genomic-BLUP breeding value
- (h) IBD-breeding value
- (i) GAS breeding value
- (j) BayesP

Genomic-BLUP and GAS breeding values cannot be used in the same breeding simulation

*Genetic model and selection method.* All three selection methods are available with each genetic model.

*Genetic model and selection criterion.* The genetic model determines the selection criteria that are available.

- (a) Polygenic:
  - (i) True breeding value
  - (ii) Random variable
  - (iii) Null variable
  - (iv) Phenotypic observation(s) with associated threshold(s)
  - (v) Phenotypic observation(s) with associated weight(s)
  - (vi) Polygenic-BLUP breeding value
- (b) Genomic:
  - (i) True breeding value
  - (ii) Random variable
  - (iii) Null variable
  - (iv) Phenotypic observation(s) with associated threshold(s)

- (v) Phenotypic observation(s) with associated weight(s)
- (vi) Polygenic-BLUP breeding value
- (vii) Genomic-BLUP breeding value
- (viii) IBD-BLUP breeding value
- (ix) GAS breeding value
- (x) BayesP

- (c) QTL:
- (i) True breeding value
  - (ii) Random variable
  - (iii) Null variable
  - (iv) Phenotypic observation(s) with associated threshold(s)
  - (v) Phenotypic observation(s) with associated weight(s)
  - (vi) Polygenic-BLUP breeding value
  - (vii) GAS breeding value

*Selection method and selection criterion.* The selection method determines the selection criteria that are available.

- (a) Threshold selection: Phenotypic observation(s) with associated threshold(s)
- (b) Truncation selection:
- (i) True breeding value
  - (ii) Random variable
  - (iii) Phenotypic observation(s) with associated weight(s)
  - (iv) Polygenic-BLUP breeding value
  - (v) Genomic-BLUP breeding value
  - (vi) IBD-breeding value
  - (vii) GAS breeding value
  - (viii) BayesP
- (c) EVA selection:
- (i) True breeding value
  - (ii) Null variable
  - (iii) Polygenic-BLUP breeding value
  - (iv) Genomic-BLUP breeding value
  - (v) IBD-breeding value
  - (vi) GAS breeding value
  - (vii) BayesP

*Selection criteria and phenotypic and genotypic observations.* Selection and the selection criterion used to rank plants can be influenced by the phenotypic and genotypic observations that are available.

- (a) True breeding value, random variable, and null variable

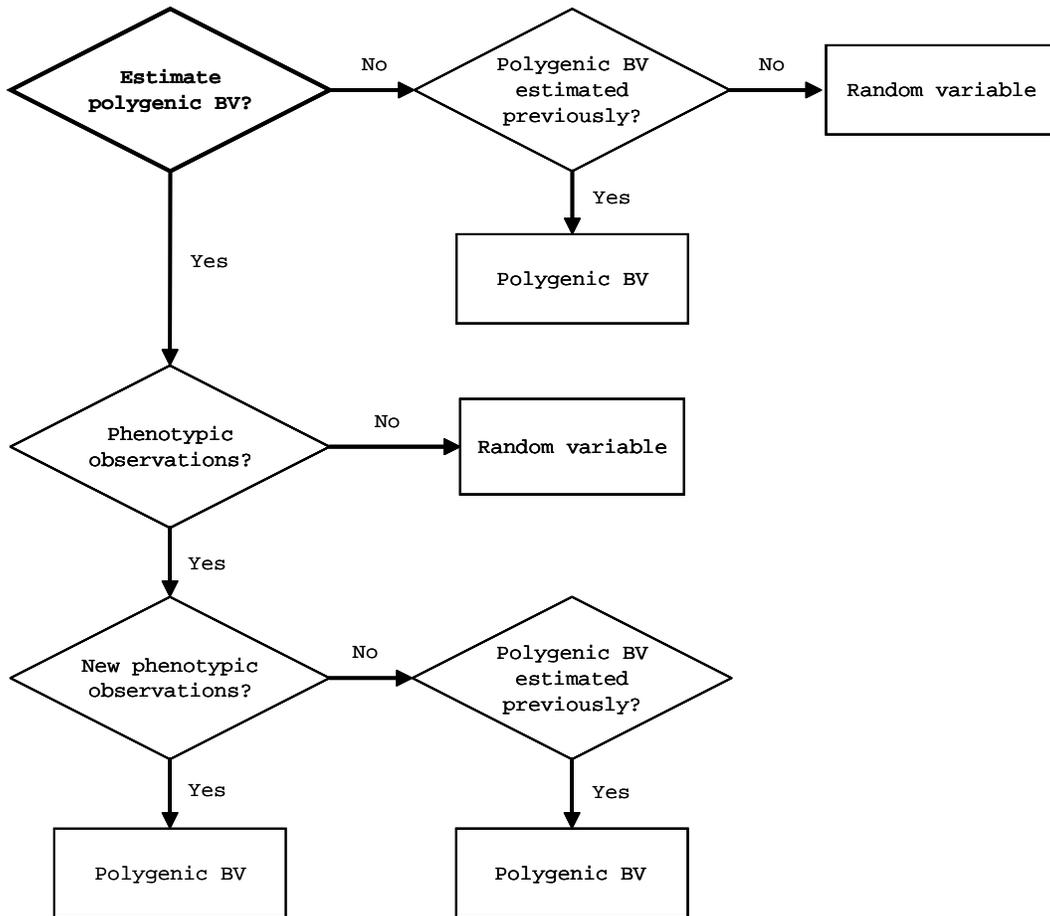
Selection candidates are always selected

- (b) Phenotypic observation(s) with associated threshold(s) or weight(s)

Selection candidates must have all specified phenotypes observed to be selected

(c) Polygenic breeding value

Polygenic breeding values requires that plants have phenotype(s) observed. When they are not, a random variable is used.

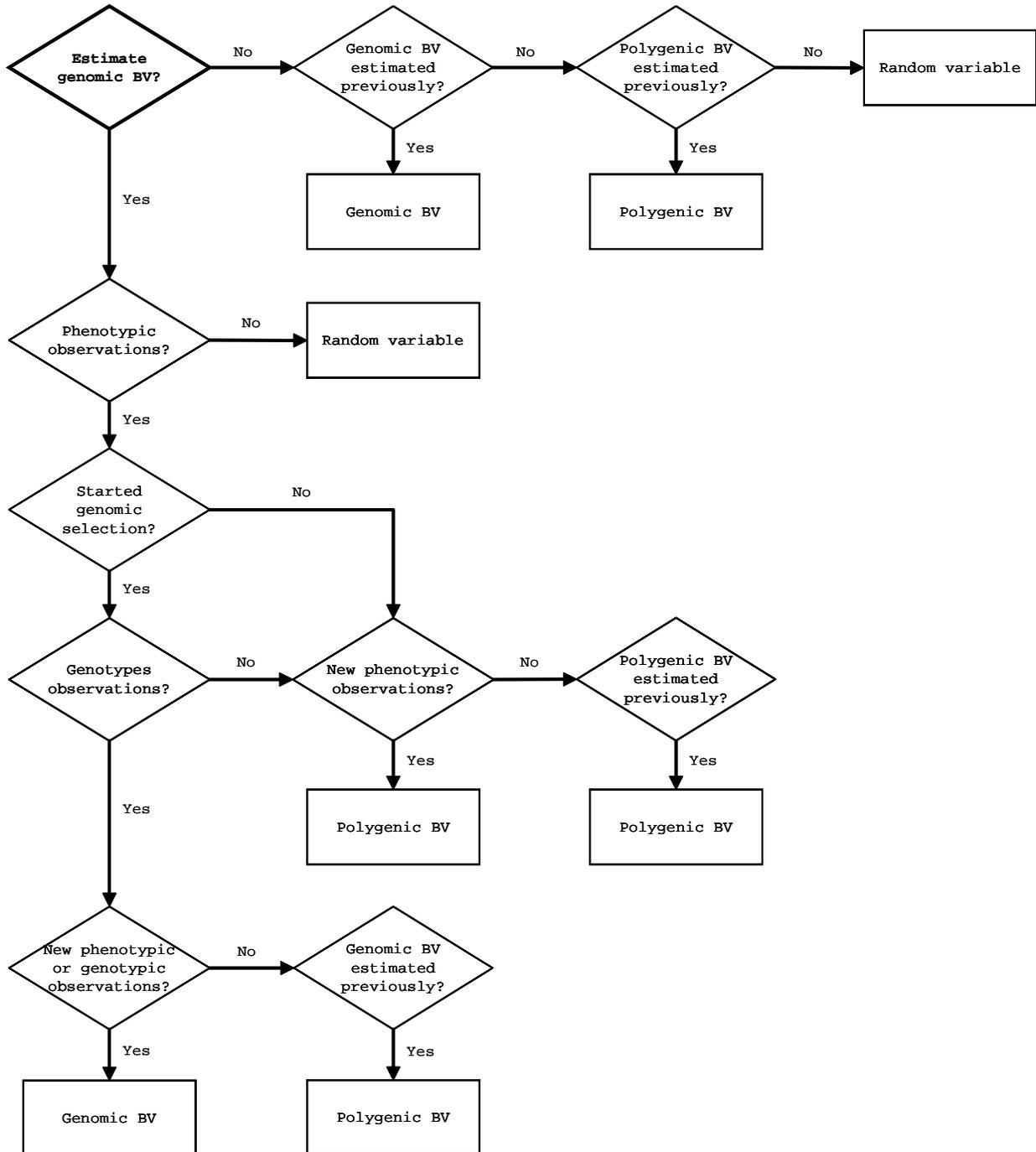


(d) IBD breeding value

IBD breeding values requires that plants have phenotype(s) observed. When they are not, a random variable is used.

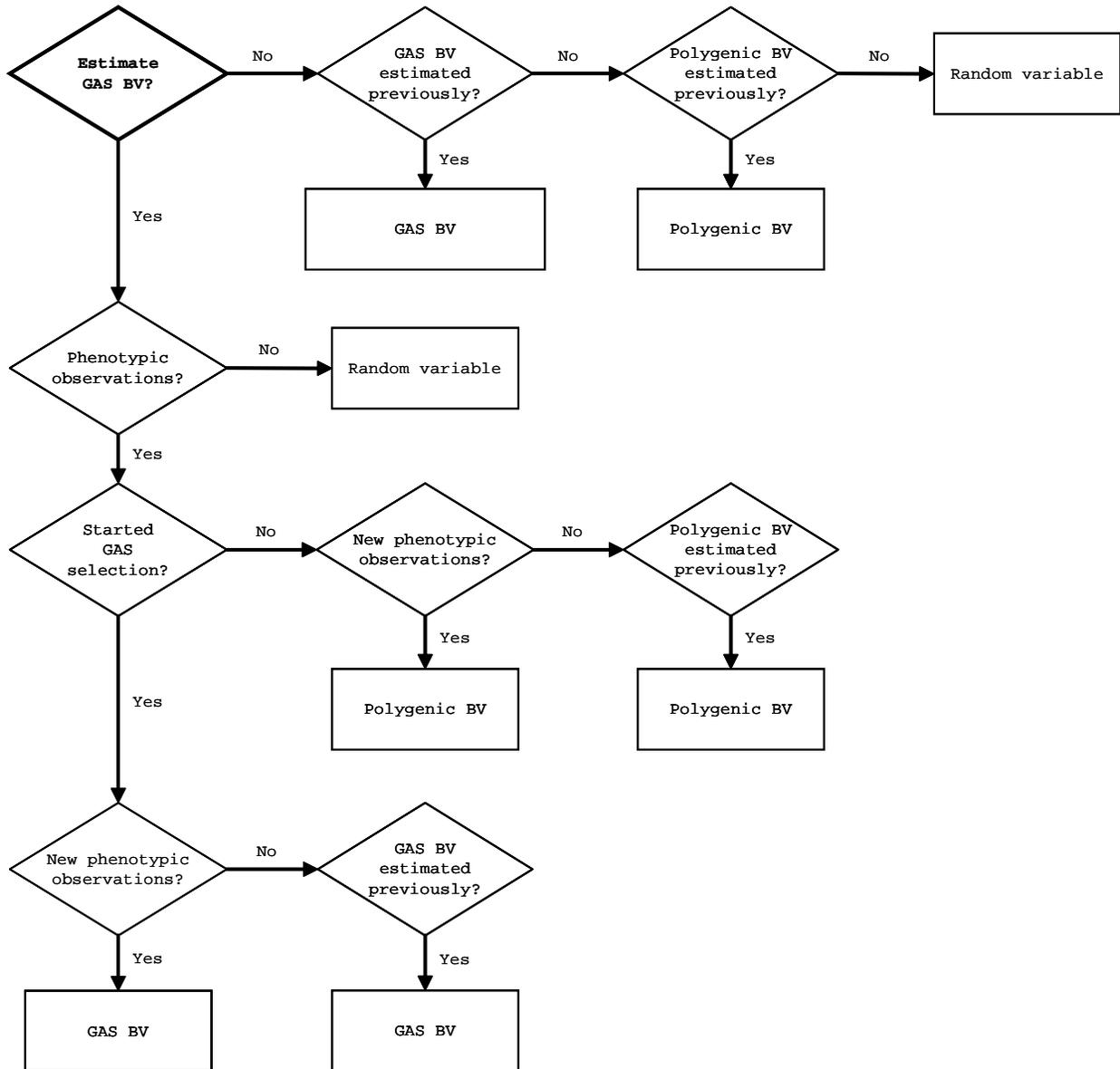
(d) Genomic breeding value

Genomic breeding values requires that plants have phenotypes and genotypes observed. When they are not observed, polygenic breeding value or random variable is used.



(e) GAS breeding value

GAS breeding value requires that plants have phenotypes observed (all plants are presumed genotyped). When they are not observed, random variable is used.



If relationship used to constrain rate of in breeding in EVA specified as 'genomic', but not plants are genotyped, 'pedigree' is used.

(e) BayesP

BayesP breeding value requires that plants have phenotypes observed (all plants are presumed genotyped). When they are not observed, random variable is used.

*GeneticModel* must be 'genomic', *nebv*==1, and *genotyped\_at\_birth*=='yes'

SUBROUTINE *blupSelectionCriteria* to see which *selection\_criteria* are compatible in the same breeding scheme

## 10. Realising traits

Phenotypic observations can be realised in three ways:

- 1) At the start of each time step; specified in namelist &OBSERVATIONS
- 2) At selection; specified in namelists &SELECTION, &EVA, and &OBSERVATIONS
- 3) As maternal traits; specified in namelist &OBSERVATIONS

There is a variable *RealiseBaseObservations* in namelist &BASEPOPULATIONS that enables phenotyping of base plants that fulfil the criteria specified in namelist &OBSERVATIONS.

## 11. Founder population and base with genomic information

With genomic information, *GeneticModel* 'genomic'

*Founder population.*

*Genomic-base population.* Genomic-base plants/population are/is generated by sampling from *nchrom* x 2 pools of chromosome haplotypes generated in the *LD\_npat* and *LD\_nmat* founder population. When we generate a founder population with *LD\_npat* and *LD\_nmat* founder males and females. This generates *LD\_npat* x 2 (paternal and maternal) and *LD\_nmat* x 2 haplotypes for male and female founder plants for the *nchrom* chromosomes.

We sample QTL effects so that the QTL/genomic (co)variances equal those specified by the user.

For each genomic-base plant, we sample paternal and maternal haplotypes/chromosome arms for each chromosome pair by sampling haplotypes/chromosome arms from the *nchrom* x 2 pools, size *LD\_npat* x 2 and *LD\_nmat* x 2. So, for genomic-base plant *i*, the paternal haplotype for chromosome *j* is sampled from the *LD\_npat* x 2 pool of male founder haplotypes from chromosome *j*; the maternal haplotype for chromosome *j* is sampled from the *LD\_nmat* x 2 pool of female founder haplotypes from chromosome *j*.

For base plant id ...

**iloc=0**

**! Sample founder chromosomes ignoring sex of founder plants**

```

do i chr=1, nchrom
do-loop out and replace with do-loop at 1460 to test non-positive G
offspring
    i hp=ceiling((random_standard_uniform())*real(LD_npat+LD_nmat))
    kp=1
    if (random_standard_uniform())>.5d0) kp=2
    i hm=ceiling((random_standard_uniform())*real(LD_npat+LD_nmat))
    km=1
    if (random_standard_uniform())>.5d0) km=2
    if (i hm==i hp) km=3- kp
    do i=1, (chrom(i chr)%nmarker+chrom(i chr)%nqt1)
        i loc=i loc+1
        if (i hp<=LD_npat) then
            temp_pat(i loc)=hap_pat(i chr, i hp, kp, i)
        else
            temp_pat(i loc)=hap_mat(i chr, i hp-LD_npat, kp, i)
        end if
        if (i hm<=LD_npat) then
            temp_mat(i loc)=hap_pat(i chr, i hm, km, i)
        else
            temp_mat(i loc)=hap_mat(i chr, i hm-LD_npat, km, i)
        end if
    end do
end do

```

! Comment this  
! Also for

## 12. Sampling and ebv\_obs

(i) Observations

Vector of *nobs* observations,  $\mathbf{y}_{nobs,i,j}$ , realised for plant *i* with sex *j* (*j* = 1 for males, 2 females), sire(*i*), and dam(*i*):

$$\begin{aligned}
\mathbf{y}_{nobs,i,j} = & \text{geneticMeans}_{ntbv} + \\
& \mathbf{XFemales}_{nobs \times ntbv} \cdot \text{femaleDeviations}_{ntbv} \cdot (j-1) + \\
& \mathbf{ZDirect}_{nobs \times ntbv} \cdot (\mathbf{a}_{p,ntbv,i} + \mathbf{a}_{G,ntbv,i}) + \\
& \mathbf{ZPaternal}_{nobs \times ntbv} \cdot (\mathbf{a}_{p,ntbv,sire(i)} + \mathbf{a}_{G,ntbv,sire(i)}) + \\
& \mathbf{ZMaternal}_{nobs \times ntbv} \cdot (\mathbf{a}_{p,ntbv,dam(i)} + \mathbf{a}_{G,ntbv,dam(i)}) + \\
& \mathbf{RDirect}_{nobs \times nres} \cdot \mathbf{e}_{nres,i} + \\
& \mathbf{RPaternal}_{nobs \times nres} \cdot \mathbf{e}_{nres,sire(i)} + \\
& \mathbf{RMaternal}_{nobs \times nres} \cdot \mathbf{e}_{nres,dam(i)}
\end{aligned}$$

where

**(ii) *ebv\_observation***

The  $nobs+nCombinedObs \times nebv$  matrix *ebv\_observation*, specified in namelist DMUPARAMETERS, variable *ebv\_observation*, is used to create DMU-input data (*dmudat*) and retrieve BLUP-breeding values estimated by DMU. [Translation/Transition matrix between ADAM and DMU] Elements of *ebv\_observation* associate observations with BLUP-breeding values. Elements can be '0' or '1'.

```

ebv_observation
  ( 1  0  0  0 ) 1
  ( 0  1  1  0 ) 2      Observation
  ( 0  0  0  1 ) 3      1:nobs+nCombinedObs
  ( 0  0  0  1 ) 4
  1  2  3  4
BLUP-breeding value
  1:nebv

```

DMU-input data. Element *ebv\_observation(i,j)* ( $i = 1 \dots nobs+nCombinedObs$ ,  $j = 1 \dots nebv$ ) set to '1' results in the *i*th observation for the *k*th plant being written to DMU-input data under *ebv j*, where a trait is a characteristic for which a BLUP-breeding value is estimated. The structure of the input data for the *k*th plant with *ebv\_observation* (above) is:

```

ebv1    ebv2    ebv3    ebv4
obs1    obs2    obs2    obs3
-        -        -        obs4

```

The general structure for DMU-input data is:

<b>ebv<sub>1</sub></b>	<b>ebv<sub>2</sub></b>	...	<b>ebv<sub>nebv</sub></b>
obs <sub>1</sub>	obs <sub>1</sub>		obs <sub>1</sub>
obs <sub>2</sub>	obs <sub>2</sub>		obs <sub>2</sub>
.	.		.
.	.		.
.	.		.
<small>obs<sub>nobst+nCombinedObs</sub></small>	<small>obs<sub>nobst+nCombinedObs</sub></small>		<small>obs<sub>nobst+nCombinedObs</sub></small>

where the columns of the input data correspond to the columns of *ebv\_observation* and the observations written to each column correspond to rows within each column of *ebv\_observation* set to '1'.

Columns of *ebv\_observation* with 'all-zeros' (i.e., no elements set to '1') result in the associated estimated breeding value not being written to the input data. Rows of *ebv\_observation* with 'all-zeros' result in the associated observations not being written.

If the *i*th row has multiple elements set to '1', the *i*th observation for the *k*th plant is written to DMU-input data under multiple traits; traits with columns in row *i* of *ebv\_observation(i,j)* set to '1'. If the *j*th column has multiple elements set to '1', observations *n* for the *k*th plant are written under the *j*th trait, where the *n* observations are a subset of rows in column *j* with *ebv\_observation(i,j)* set to '1'.

*BLUP-breeding values*. Columns containing a '1' requires the *j*th BLUP-breeding values to be estimated by DMU.

*ebv\_observation* and the model fitted to the DMU-input data by DMU must be aligned. The model fitted by DMU must be aligned with the DMU-input data and the *nebv* BLUP-breeding values expected to be estimated.

**Example 1: Typical DMU-input data and DMU model. Includes genetic-maternal effect.**

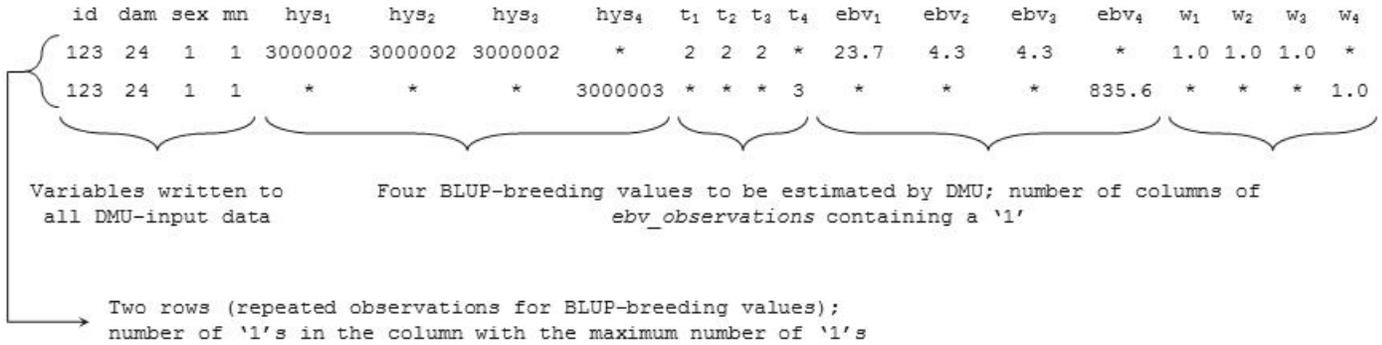
*ebv\_observation*

$$\begin{pmatrix} 1 & 0 & 0 & 0 \\ 0 & 1 & 1 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 0 & 1 \end{pmatrix}$$

Phenotypic observations generated and realised for an plant during a simulation

id	observation	phenotype	time	hys	weight	realised
123	1	23.7	2	3000002	1.0	true
123	2	4.3	2	3000002	1.0	true
123	3	941.0	*	*	*	false
123	4	835.6	3	3000003	1.0	true

DMU-input data

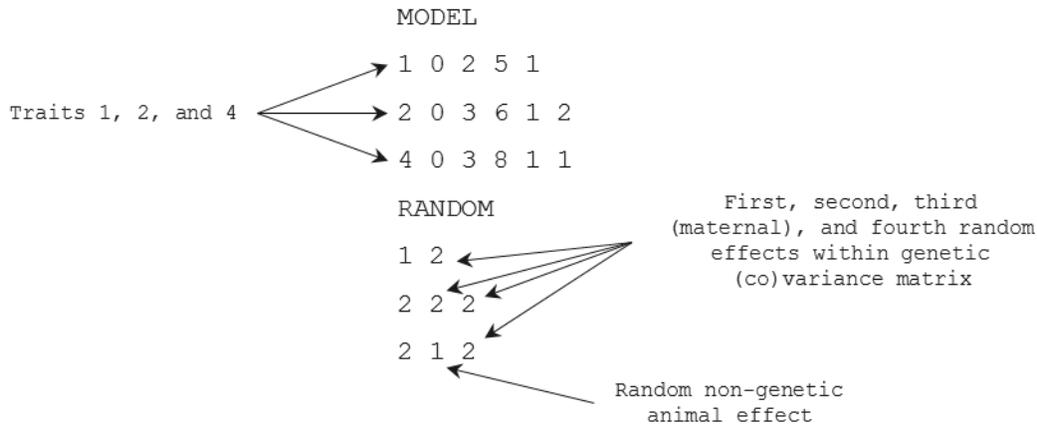


where  $trait_i$  is the  $i$ th characteristic for which a BLUP-breeding value is estimated,  $hys_i$  and  $t_i$  are herd-year-season and time associated with the  $i$ th trait, and \* is the largest representable integer for  $hys_i$  and  $t_i$  and -9999.0 for  $obs_i$  and  $w_i$ .

Note that observation 2, associated with BLUP-breeding values 2 and 3, is written twice.

Observation must be realised and, if specified, realised within *PreviousObsTimeSteps*, otherwise observation set to -9999.0. Fixed variables set to huge(1).

DMU model



The prior variances and covariances must be specified in random factor number sequence i.e. priors for random factor 1 must be specified before priors for random factor 2 and so

on. Each line consists of 3 integers a real number (free format). The first integer is the  
20

random factor number followed by row-column (trait) combination and finally the prior  
(co)variance.

Model must be specified with the order of the BLUP-breeding values to be estimated  
(random effect within genetic (co)variance matrix) 1:nebv.

Solution (SOL) file generated by DMU

Effect type	Trait number	Random-effect number	Effect number	Class code	Consecutive class number	Prediction	SE(Prediction)
4	1	1	1	123	6	-2.3	0.10
4	2	2	1	123	6	0.93	0.14
4	3	3	1	123	6	0.11	0.09
4	4	4	1	123	6	27.1	3.43

4: Random genetic      Random-effects within genetic (co)variance matrix      Animal id      BLUP-breeding value  
Maternal effect

BLUP-breeding values transferred from solution file

id	BLUP-BV number (ebv_observation)	Random-effect number (DMU)	BLUP-breeding value
123	1	1	-2.3
123	2	2	0.93
123	3	3	0.11 ← Maternal effect
123	4	4	27.2

**Example 2: Phenotypic observation not written to DMU-input data**

ebv\_observation

$$\begin{pmatrix} 1 & 0 \\ 0 & 0 \\ 0 & 1 \\ 0 & 1 \end{pmatrix}$$

Phenotypic observations

id	observation	phenotype	time	hys	weight	realised
123	1	23.7	2	3000002	1.0	true
123	2	4.3	2	3000002	1.0	true
123	3	941.0	2	3000002	1.0	true
123	4	835.6	3	3000003	1.0	true

DMU-input data

id	dam	sex	mn	hys <sub>1</sub>	hys <sub>2</sub>	t <sub>1</sub>	t <sub>2</sub>	ebv <sub>1</sub>	ebv <sub>2</sub>	w <sub>1</sub>	w <sub>2</sub>
123	24	1	1	3000002	3000002	2	2	23.7	941.0	1.0	1.0
123	24	1	1	*	3000003	*	3	*	835.6	*	1.0

DMU model

```

MODEL
1 0 2 5 1
2 0 3 6 1 1
RANDOM
1 2
2 1 2

```

Solution (SOL) file generated by DMU

Effect type	Trait number	Random-effect number	Effect number	Class code	Consecutive class number	Prediction	SE(Prediction)
4	1	1	1	123	6	-2.3	0.10
4	2	2	1	123	6	27.1	3.43

BLUP-breeding values transferred from solution file

id	BLUP-BV number ( <i>ebv_observation</i> )	Random-effect number (DMU)	BLUP-breeding value
123	1	1	-2.3
123	2	2	27.1

**Example 3: BLUP-breeding value not estimated by DMU**

*ebv\_observation*

$$\begin{pmatrix} 1 & 0 & 0 \\ 0 & 0 & 1 \end{pmatrix}$$

Phenotypic observations

id	observation	phenotype	time	hys	weight	realised
123	1	23.7	2	3000002	1.0	true
123	2	4.3	2	3000002	1.0	true

DMU-input data

id	dam	sex	mn	hys <sub>1</sub>	hys <sub>3</sub>	t <sub>1</sub>	t <sub>3</sub>	ebv <sub>1</sub>	ebv <sub>3</sub>	w <sub>1</sub>	w <sub>3</sub>
123	24	1	1	3000002	3000002	2	2	23.7	4.3	1.0	1.0

DMU model

```
MODEL
1 0 2 5 1
2 0 2 6 1
RANDOM
1 1
1 1
```

Solution (SOL) file generated by DMU

Effect type	Trait number	Random-effect number	Effect number	Class code	Consecutive class number	Prediction	SE(Prediction)
4	1	1	1	123	6	-2.3	0.10
4	2	2	1	123	6	0.93	0.14

BLUP-breeding values transferred from solution file

id	BLUP-BV number ( <i>ebv_observation</i> )	Random-effect number (DMU)	BLUP-breeding value
123	1	1	-2.3
123	2	-	0.0
123	3	2	0.93

NB. BLUP-breeding value 2 was not estimated by DMU. It was set to 0.0.

**Example 4: Unusual order of *ebv\_observation***

ebv\_observation

$$\begin{pmatrix} 0 & 0 & 1 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \end{pmatrix}$$

Phenotypic observations

id	observation	phenotype	time	hys	weight	realised
123	1	23.7	2	3000002	1.0	true
123	2	4.3	2	3000002	1.0	true
123	3	941.0	2	3000002	1.0	true

DMU-input data

id	dam	sex	mn	hys <sub>1</sub>	hys <sub>2</sub>	hys <sub>3</sub>	t <sub>1</sub>	t <sub>2</sub>	t <sub>3</sub>	ebv <sub>1</sub>	ebv <sub>2</sub>	ebv <sub>3</sub>	w <sub>1</sub>	w <sub>2</sub>	w <sub>3</sub>
123	24	1	1	3000002	3000002	3000002	2	2	2	4.3	941.0	23.7	1.0	1.0	1.0

DMU model

MODEL

3 0 2 7 1

1 0 2 5 1

2 0 2 6 1

RANDOM

1 1

1 1

1 1

Solution (SOL) file generated by DMU

Effect type	Trait number	Random-effect number	Effect number	Class code	Consecutive class number	Prediction	SE(Prediction)
4	1	1	1	123	6	-2.3	0.10
4	2	2	1	123	6	0.93	0.14
4	3	3	1	123	6	27.1	3.43

BLUP-breeding values transferred from solution file

id	BLUP-BV number ( <i>ebv_observation</i> )	Random-effect number (DMU)	BLUP-breeding value
123	1	1	-2.3
123	2	2	0.93
123	3	3	27.2

**Example 5: Excessive parameterisation; impractical example**

*ebv\_observation*

$$\begin{pmatrix} 1 & 1 \\ 1 & 1 \end{pmatrix}$$

Phenotypic observations

id	observation	phenotype	time	hys	weight	realised
123	1	23.7	2	3000002	1.0	true
123	2	4.3	2	3000002	1.0	true

DMU-input data

id	dam	sex	mn	hys <sub>1</sub>	hys <sub>2</sub>	t <sub>1</sub>	t <sub>2</sub>	ebv <sub>1</sub>	ebv <sub>2</sub>	w <sub>1</sub>	w <sub>2</sub>
123	24	1	1	3000002	3000002	2	2	23.7	23.7	1.0	1.0
123	24	1	1	3000002	3000002	2	2	4.3	4.3	1.0	1.0

DMU model

MODEL

1 0 3 5 1 1

2 0 3 6 1 1

RANDOM

2 1 2

2 1 2

Solution (SOL) file generated by DMU

Effect type	Trait number	Random-effect number	Effect number	Class code	Consecutive class number	Prediction	SE(Prediction)
4	1	1	1	123	6	-2.3	0.10
4	2	2	1	123	6	0.93	0.14

BLUP-breeding values transferred from solution file

id	BLUP-BV number ( <i>ebv_observation</i> )	Random-effect number (DMU)	BLUP-breeding value
123	1	1	-2.3
123	2	2	0.93

Phenotypic observations can be realised in three ways:

Hvis du har en fænotype, som både har direkte og maternelle effekter, og de maternelle effekter både er genetiske og miljømæssige, så skal du bruge to *tbv*'er og to *res*'er pr. obs.

[10:31:44] Anders Christian Sørensen: Det samme hvis du har en fællse kuldeffekt, så vil det modelleres som en ekstra residual hos moderen.

[10:32:05] Anders Christian Sørensen: *nres* kan altså sagtens tænkes at være forskellig fra *nobs*

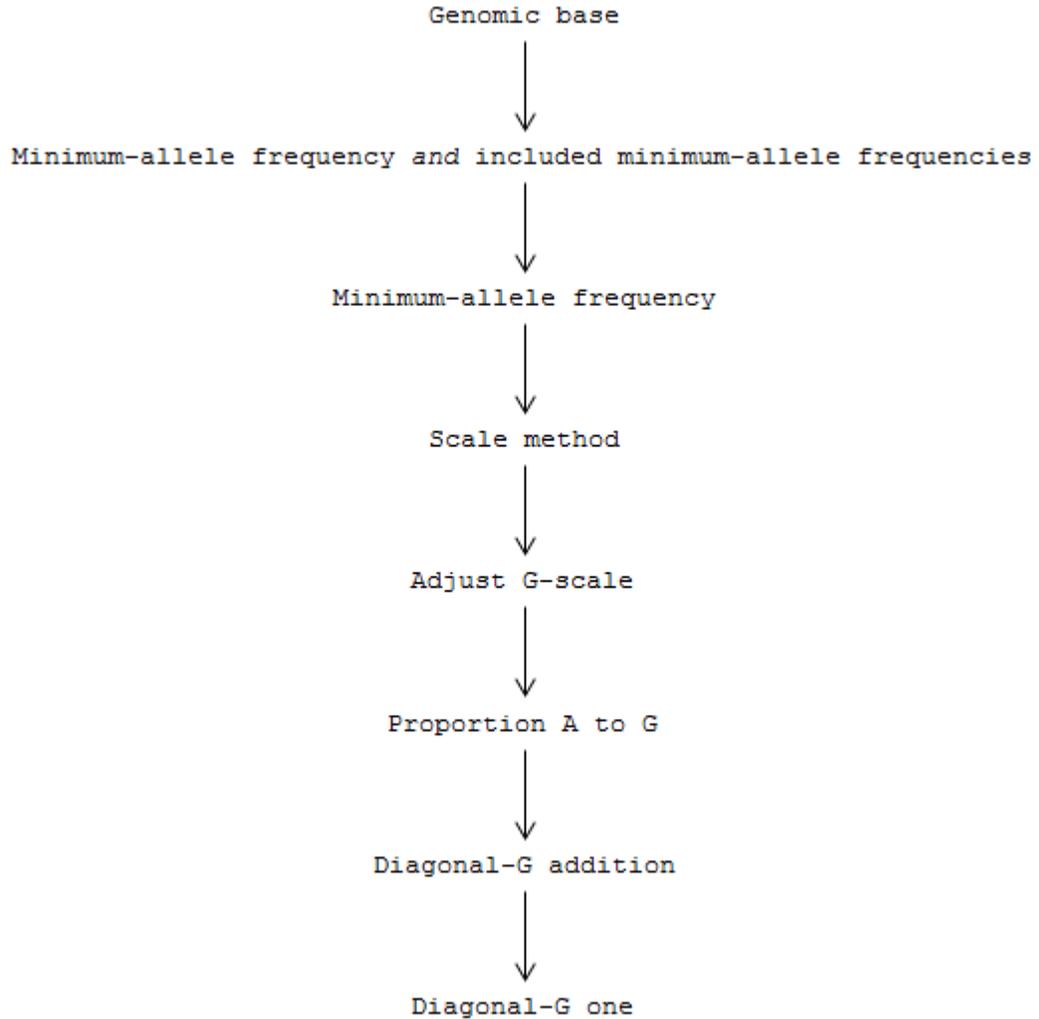
```
obs(:)=MATMUL(REAL(Zbv, sp), pop(i d)%tbv_poly) + MATMUL(REAL(Wres, sp), pop(i d)%res) !  
Add bv+resi dual
```

```
if (pop(i d)%sex==2) obs(:) = obs(:) + MATMUL(REAL(xmean, sp), sexdi f)
```

```
dam=pop(i d)%dam  
if (dam/=0) then  
  obs(:) = obs(:) + MATMUL(REAL(Zmatbv, sp), pop(dam)%tbv_poly) +  
MATMUL(REAL(Wmres, sp), pop(dam)%res)  
  ! add maternal genetic and environmental effects  
end if
```

### 13. Genomic-relationship matrices

The following flow diagram outlines the sequence used to generate genomic-relationship matrices used to predict genomic-breeding values, control rates of inbreeding using genomic information and EVA, and monitor rates of inbreeding:



Let  $\mathbf{X}_{m,n}$  be a  $m \times n$  matrix of marker genotypes for  $n$  individuals at  $m$  loci. The marker genotype for individual  $j$  at locus  $i$  is denoted  $x_{i,j} = 0, 1, \text{ or } 2$  when the genotype is 11, 12, or 22 and marker alleles are denoted 1 and 2.

**Alternative:**  $\mathbf{X}_{n,m}$  *USE ALTERNATIVE, more conventional*

, where ...

genomic base define the plants included in the genomic-base population that are used to calculate marker-allele frequencies,  $p_i$  and  $1-p_i$ , used to 'centre' and 'scale' genotypes at locus  $i$ ,

all	All genotyped plants in the population, <included in dmudat>
base	All plants in the base population ignoring genotyping
genotypedbase	All genotyped plants in the base population
tracedbase	All plants in the base population <included in dmudat> ignoring genotyping

tracedgenotypedbase All genotyped plants in the base population <included in dmudat>

*loci*, *maf*, and *mafInclude* defines the loci used to construct genomic matrices. *loci* defines the loci used as genetic markers (QTL and markers, QTL, or markers), *maf* Threshold for minimum-allele frequency *mafInclude* Minimum-allele frequency of loci included.

*loci* all QTL and markers  
qtl QTL  
markers Markers

*maf* Definition: Threshold for minimum-allele frequency

*mafInclude* Definition: Minimum-allele frequency of loci included  
above Include loci with minimum-allele frequency greater than or equal to *maf*  
below Include loci with minimum-allele frequency less than or equal to *maf*

### Centring

Marker genotypes are centred by subtracting the mean of the marker genotypes:  $x_{ij} = x_{ij} - 2p_i$ , where  $p_i$  is frequency of allele 2 at locus  $i$  (and  $2p_i$  is the mean of the marker genotype at locus  $i$ , which is the same as averaging marker genotypes at locus  $i$  across  $n$  individuals). In matrix notation, this is  $\mathbf{X}_{m,n} = \mathbf{X}_{m,n} - (2\mathbf{p})\mathbf{1}_n^T$ , where  $\mathbf{p}$  is a column vector  $\mathbf{p} = (p_1, p_2 \dots p_m)$  and  $\mathbf{1}_n^T$  is a  $1 \times n$  sum vector transposed column sum vector having all of its elements equal to one. [IS  $p$  FREQUENCY AT ALLELE 2 OR MAF? WHAT DOES SU'S PROGRAM DO?]

Alternative:  $\mathbf{X}_{n,m} - \mathbf{1}_n(2\mathbf{p})^T$

Equivalent is  $\mathbf{X}_{n,m}$  be a  $n \times m$  matrix of marker genotypes for  $n$  individuals at  $m$  loci. The marker genotype for individual  $j$  at locus  $i$  is denoted  $x_{i,j} = -1, 0, \text{ or } 1$  when the genotype is 11, 12, or 22 and marker alleles at locus  $i$  are denoted 1 and 2. Marker genotypes are centred by subtracting the mean of the marker genotypes:  $x_{ij} = x_{ij} - (2p_i - 1)$ . In matrix notation, this is  $\mathbf{X}_{n,m} = \mathbf{X}_{n,m} - \mathbf{1}_n (2\mathbf{p} - 1)^T$ .

Either way, end up with deviations from the respective means that that are the same. Centering sets mean values of the allele effects [genotypes?] to 0.

*locusWeight* is the weight applied to each locus. How? [Order!]

one Weight 1.0 applied to each locus; each locus has equal weight  
goddard Weight applied to each locus as a function of allele frequency,  $1.0/(p_i(1-p_i))$ , where  $p_i$  is the minimum-allele frequency at locus  $i$  (after Goddard 2009)  
jannink Weight applied to each locus as a function of allele frequency,  $(\arcsin(1)-\arcsin(\sqrt{p_i}))/p_i(1-p_i)$  (after Jannink 2010)  
Default: *locusWeight* must be specified

*scaleMethod*

Definition: Method to scale  $\mathbf{G}$ -matrix  
Type: Integer  
Options:  
1 Divide  $\mathbf{G}$  by sum of  $2p(1-p)$   
2 Divide each locus genotype by  $\sqrt{2p_i(1-p_i)}$ , where  $p_i$  is frequency of an allele at locus  $i$

Default: *scaleMethod* must be specified

*Scaling (locusWeight and scaleMethod)*

Marker genotypes are standardised to a unit variance

*scaleMethod* 1:  $\mathbf{X}_{n,m} \cdot \mathbf{X}_{n,m}^T$  s

$x_{ij} = x_{ij}/s$  (*scaleMethod* 1), where  $s = v_i / \sum_{i=1}^m 2p_i(1-p_i)$ , or  $x_{ij} = x_{ij} / \sqrt{2p_i(1-p_i)}$

(*scaleMethod* 2. In matrix notation, this is  $\mathbf{x}_{m,n} = \mathbf{x}_{m,n}/s$  and  $\mathbf{x}_{m,n} = \mathbf{x}_{m,n} / (\sqrt{2\mathbf{p}(\mathbf{1}_n - \mathbf{p})} \mathbf{1}_n^T)$ . Note: s is a constant, there is no rescaling of markers relative to each other. Or is

it:  $\mathbf{x}_{m,n} = \mathbf{x}_{m,n} / \left( \sqrt{2\text{dia}(\mathbf{p}(\mathbf{1}_n - \mathbf{p})^T)} \mathbf{1}_n^T \right)$ , where  $v_i$  is the weight applied to locus  $i$ .

Alternative:  $\mathbf{X}_{n,m} = \mathbf{X}_{n,m}/s$  and  $\mathbf{X}_{n,m} = \mathbf{X}_{n,m} / (\mathbf{1}_n \sqrt{2\mathbf{p}(\mathbf{1}_n - \mathbf{p})})$

$G = \mathbf{X}_{m,n}^T \mathbf{X}_{m,n}$

Alternative:  $G = \mathbf{X}_{n,m} \mathbf{X}_{n,m}^T$

**If weighting** then

$(\{0,1,2\} - 2p) * \text{SQRT}(\text{weight} / (2p(1-p)))$

Then  $XX^T$

But

*adjustGScale*

Definition: Adjust G to same scale as A

Type: Integer

Options:

0 **G**-matrix not adjusted

1 **G**-matrix is adjusted, where  $\alpha$  and  $\beta$  are estimated from all genotyped plants

2 **G**-matrix is adjusted, where  $\alpha$  and  $\beta$  are estimated from all genotyped plants in the genomic-base population

Default: *adjustGScale* must be specified

*Adjusting marker-based relationship matrix*

Parameters  $\alpha$  and  $\beta$  are estimated by fitting **G** to **A** and solving two equations:

$\overline{\mathbf{G}}\beta + \alpha = \overline{\mathbf{A}}$  and  $d\mathbf{G}\beta + \alpha = d\mathbf{A}$ ,  $\overline{\mathbf{G}}$  and  $\overline{\mathbf{A}}$  are means of all elements in the two matrices, and  $d\mathbf{G}$  and  $d\mathbf{A}$  are means of diagonal elements in the two matrices.

*propAToG*

Definition: Proportion of A-matrix to modify G-matrix

Type: Real

Options:  $0.0 \leq \text{propAToG} \leq 1.0$

Default: *percentAToG* must be specified

*addDiagG*

Definition: Value added to diagonal elements of G-matrix <to make the matrix positive-definite>

Type: Real

Options: *addDiagG*  $\geq 0.0$  [Set to 0.0 if A-matrix used]

Default: *addDiagG* must be specified

*diagGOne*

Definition: Scale mean of diagonal elements of G-matrix so the mean of the diagonal equals *diagGOne*

Type: Real

Options: *diagGOne* ≥ 0.0, where 0.0 does not bring about scaling

Default: *diagGOne* must be specified

Genomic-matrix **G**: The genomic-inbreeding coefficient for individual *i* is  $\mathbf{G}_{ii} - 1$ . Genomic relationships between individuals *i* and *j*, which are analogous to the relationship coefficients of Wright (1922), are obtained by dividing elements  $\mathbf{G}_{ij} / \sqrt{\mathbf{G}_{ii}\mathbf{G}_{jj}}$  ... Wright's formulae is  $A_{ij} = 2f_{ij} / \sqrt{(1+F_i)(1+F_j)}$ , which means that off-diagonal elements are equal to  $2f_{ij}$ ?

Questions

Do we account for inbreeding coefficient of parents when using off-diagonal elements of **G** (parents) to calculate inbreeding coefficients of offspring or is the inbreeding coefficient of offspring simply equal to  $f_{ij}$  (i.e., `pop(iid)%genomicFParent(i)=0.5*r`)?

Is it better to work with **G** accounting for inbreeding, that is,  $A_{ij} = 2f_{ij} / \sqrt{(1+F_i)(1+F_j)}$ ?

What if several markers that have correlation 1?

**IBD and IBS**

IBD and IBS between two individuals:  $\frac{1}{2} \frac{\sum_{k=1}^n \sum_{i=1}^2 \sum_{j=2}^2 \delta_{kij}}{n}$ , where  $\delta_{kij}$  is the allele sharing status at locus *k*, which is equal to 1 if allele *i* from the first individual is identical to the allele *j* from the second individual, and 0 otherwise.

Use  $\frac{1}{2}$  to realise relationship ( $\frac{1}{4}$  realises coancestry)

## 14. Description of namelists

**&OUTPUTDIRECTORY**

`OutDirectory=OutDirectory /`

**\*\*Task\*\***

Destination for output files

**\*\*Properties of name\*\***

`OutDirectory` Definition: Directory for output

Type: Character

Options: Any existing and accessible directory

Default: An existing and accessible directory must be provided

**\*\*Additional information\*\***

`OutDirectory` must be enclosed in quotation marks (" or ') and end with a forward slash (/). For example, `OutDirectory='/bob/adam/test/'`

## &CONTROLPARAMETERS

```
GeneticModel=GeneticModel  
nrep=nrep  
ntime=ntime  
start_rep=start_rep  
time_steps_season=time_steps_season  
PreviousObsTimeSteps=PreviousObsTimeSteps  
constant_mendelian_variance=constant_mendelian_variance /
```

### \*\*Task\*\*

Input that controls the physical aspects of the simulation

### \*\*Properties of names\*\*

<i>GeneticModel</i>	Definition: Genetic model used to generate breeding values Type: Integer Options: polygenic Polygenic model genomic Genomic model with linkage disequilibrium between QTL and markers qtl QTL model with or without linkage disequilibrium ldonly Genomic LD used to generate linkage disquilibrium; breeding scheme is not simulated Default: polygenic
<i>nrep</i>	Definition: Number of replicates simulated. Also applies to the number of replicates in the LD-generating routine when <i>GeneticModel</i> 'ldonly'. Type: Integer Options: ≥1 Default: 1
<i>ntime</i>	Definition: Number of time steps Type: Integer Options: ≥1 Default: 1
<i>start_rep</i>	Definition: Starting replicate number Type: Integer Options: ≥1 Default: 1
<i>time_steps_season</i>	Definition: Number of time steps per season; used to simulate HYS effects Type: Real Options: ≥0.0 Default: 1.0
<i>PreviousObsTimeSteps</i>	Definition: Number of prior time steps within which realised observations are included when estimating polygenic, genomic, and GAS breeding values. Observations realised within the specified number of time steps are included in the

estimation. Observations realised beyond the specified number of time steps are excluded.

Type: Integer

Options:  $\geq 1$

Default: HUGE(1), largest possible integer

*constant\_mendelian\_variance*

Definition: Determines whether inbreeding of parents reduces the variance of the Mendelian sampling term of the offspring

Type: Character

Options:

no Uses inbreeding of parents to determine the variance of the Mendelian sampling term of the offspring

yes Uses 0.5 for variance [half of the additive genetic (co)variance(s)] of the Mendelian sampling term of the offspring independent of the inbreeding of the parents [Mendelian-sampling terms for offspring are independent of the inbreeding of the parents; Mendelian-sampling variance is half genetic variances, specified for **G**]

Default: no

**\*\*Relation to subsequent namelists\*\***

*GeneticModel* is a control parameter; it largely determines the subsequent namelists required

polygenic	Required	&POPULATIONPARAMETERS, &BASEPOPULATION, &SELECTION, &MATINGPARAMETERS, &OBSERVATIONS, &MATRICES, and &DESIGN_MATRICES
	Optional	&RULES, &EVA, &DMUPARAMETERS, &PHENOTHRESHOLDS, &PHENOWEIGHTS, and &CATEGORICALS
qtl	Required	&POPULATIONPARAMETERS, &BASEPOPULATION, &SELECTION, &MATINGPARAMETERS, &OBSERVATIONS, &MATRICES, &DESIGN_MATRICES, &CONTROL_GENOME, &MARKER_PARAMETERS/&MARKER_ALLELE_FREQUENCIES or &SAMPLE_MARKER_PARAMETERS, &QTL_PARAMETERS/&QTL_EFFECTS_FREQUENCIES or &SAMPLE_QTL_PARAMETERS/&SAMPLE_QTL_NUMBERS, and &MARKER_NUMBERS
	Optional	&RULES, &EVA, &DMUPARAMETERS, &PHENOTHRESHOLDS, &PHENOWEIGHTS, &CATEGORICALS, &LD, &GAS_PARAMETERS, and &REPORT
genomic	Required	&POPULATIONPARAMETERS, &BASEPOPULATION, &SELECTION, &MATINGPARAMETERS, &OBSERVATIONS, &MATRICES, and &DESIGN_MATRICES, &CONTROL_GENOME, and &LD
	Optional	&RULES, &EVA, &DMUPARAMETERS, &PHENOTHRESHOLDS, &PHENOWEIGHTS, and &CATEGORICALS
ldonly	Required	&CONTROL_GENOME and &LD

**\*\*Additional information\*\***

When *GeneticModel* 'ldonly', *GeneticModel* and *nrep* are the only parameters required in namelist &CONTROL\_GENOME.

## &CONTROL\_GENOME

```
nchrom=nchrom
ChromLengths=ChromLengths
genotyped_at_birth=genotyped_at_birth
LD_method=LD_method
set_marker_parameters=set_marker_parameters
set_qtl_parameters=set_qtl_parameters
templateDensity=templateDensity
```

### \*\*Task\*\*

Chromosome information and methods used to simulate QTL and genetic markers. Specify first time step at which non-polygenic breeding values are used as selection criterion.

### \*\*Properties of names\*\*

```
nchrom          Definition: Number of chromosomes in the genome. A
                  chromosome is defined as a single segment of
                  DNA, whose inheritance is completely
                  independent of any other chromosomes.
                  Type: Integer
                  Options: ≥1
                  Default: 0

ChromLengths   Definition: Length (cM) of each chromosome
                  Type: Integer
                  Dimension: nchrom*1; a length required for each chromosome
                  Options: ≥0
                  Default: -1

genotyped_at_birth Definition: Plants genotyped at birth
                  Type: character
                  Options:
                    yes Plants are genotyped at birth
                    no Plants are not genotyped at birth
                  Default: no

LD_method      Definition: Method to establish linkage disequilibrium (LD)
                  between QTL and marker alleles
                  Options:
                    no      LD is not established; QTL and marker
                           alleles are in linkage equilibrium
                    meu     LD established using the method of
                           Meuwissen (2000, 2001)
                    genomicld LD established using the method of genomic LD
                  Type: Character
                  Default: genomicld

set_marker_parameters Definition: Specify if marker parameters are provided or
                  sampled
                  Type: Integer
                  Options
                    specify Marker parameters are provided
                    sample  Marker parameters are sampled
                  Default: set_marker_parameters must be specified when
                           GeneticModel 'qtl'
```

*set\_qtl\_parameters*      Definition: Specify if QTL parameters are provided or sampled  
Type: Integer  
Options:  
    specify QTL parameters are provided  
    sample QTL parameters are sampled  
Default: *set\_qtl\_parameter* must be specified when *GeneticModel* 'qtl'

*templateDensity*      Definition: Density of markers on marker template; number of markers per cM. *templateDensity*>0.0 generates marker and QTL templates.

Marker template

is a dense marker map that provides unique genotypes for all base individuals. It is sampled for all offspring according to Mendelian sampling terms allowing for recombination. The markers are not available for selection purposes but only serve to monitor inbreeding.

Type: Real  
Options:  
    0.0 Marker template is not created  
    >0.0 Marker template is created with marker density *templateDensity*  
Default: 0.0

**\*\*Relation to subsequent namelists\*\***

Subsequent namelists required is largely determined by *GeneticModel* in namelist &CONTROLPARAMETERS. The relevant options for *GeneticModel* are 'genomic', 'qtl', and 'ldOnly'.

- qtl            (a) Namelist &LD is required when *LD\_method* 'meu'
- (b) (i) Namelists &MARKER\_PARAMETERS and &MARKER\_ALLELE\_FREQUENCIES are required when *set\_marker\_parameters* 'specify'
- (ii) Namelist &SAMPLE\_MARKER\_PARAMETERS is required when *set\_marker\_parameters* 'sample'
- (c) (i) Namelists &QTL\_PARAMETERS and &QTL\_EFFECTS\_FREQUENCIES are required when *set\_qtl\_parameters* 'specify'
- (ii) Namelists &SAMPLE\_QTL\_PARAMETERS and &SAMPLE\_QTL\_NUMBERS are required when *set\_qtl\_parameters* 'sample'
- (d) Namelist &MARKER\_NUMBERS is required
- (e) Namelist &GAS\_PARAMETERS is required when *selection\_criterion* 'gas' in any selection stage of namelist &SELECTION, variable *selection\_scheme*, or *MaleSelCrit* and/or *FemaleSelCrit* 'gas' in any EVA-selection stage of namelist &EVA, variable *EvaSelection*
- (f) Namelist &TEMPLATE\_PARAMETERS is required when *use\_marker\_template* 'yes'

- genomic      (a) Namelist &LD is required when *LD\_method* 'genomicld'
- (b) Namelist &TEMPLATE\_PARAMETERS is required when *use\_marker\_template* 'yes'

ldonly        Namelist &LD is required when *LD\_method* 'genomicld'

**\*\*Additional information\*\***

- 1) *templateDensity* can only be greater than 0.0 when *GeneticModel* 'qtl' or 'genomic'.
- 2) *templateDensity*>0.0 generates marker and QTL templates.

*templateDensity*>0.0 is the trigger to generate marker and QTL templates. IBD-inbreeding coefficients are reported in output file(s). Selection method 'ibdBlup' can be used for prediction and 'ibd' relationship matrix can be used to restrict average relationship with EVA.

If *templateDensity* 0.0, the templates are not generated and selection method 'ibdBlup' and 'ibd' relationship matrix are not valid.

**\*\*Example\*\***

The following illustrates how the input for this namelist is provided. In the example, there are two chromosomes. The lengths of the chromosomes are 110 and 97 cM. Only variables *nchrom* and *ChromLength* are illustrated.

```
&CONTROL_GENOME
nchrom=2
ChromLength=
  110
   97
genotyped_at_birth=no
LD_method=genomicLD /
```

**\*\*Additional information\*\***

- 1) *genotyped\_at\_birth* is only used when *GeneticModel* 'qtl' or 'genomic'. When *GeneticModel* 'ldOnly', *genotyped\_at\_birth* is set to 'no'.
- 2) *genotyped\_at\_birth* must be 'yes' when *GeneticModel* 'qtl' and selection criterion 'gas'
- 3) (a) *LD\_method* must be 'no' or 'meu' when *GeneticModel* 'qtl'  
(b) *LD\_method* must be 'genomicld' when *GeneticModel* 'genomic' or 'ldOnly'
- 4) *set\_marker\_parameters* and *set\_qtl\_parameters* must be specified when *GeneticModel* 'qtl'. Otherwise, *set\_marker\_parameters* and *set\_qtl\_parameters* are not used.
- 5) *startGenomicSelectionTime* is only used when *GeneticModel* 'genomic' and genomic-breeding values are used as selection criterion. When *startGenomicSelectionTime*>1, polygenic breeding values or random variables are used as the selection criterion up to time step *startGenomicSelectionTime* (see section Genetic model and selection; ADAM's motor).
- 6) *startGasTime* is only used when *GeneticModel* 'qtl' and GAS-breeding values are used as selection criterion. When *startGasTime*>1, polygenic breeding values or random variables are used as the selection criterion up to time step *startGasTime* (see section Genetic model and selection; ADAM's motor).

**&LD**

```
LD_ngen=LD_ngen
LD_npat=LD_npat
LD_nmat=LD_nmat
cri_val_qtl=cri_val_qtl
nPotentialLoci=nPotentialLoci
nmarker_per_qtl=nmarker_per_qtl
mutation_rate=mutation_rate
CullingProportion=CullingProportion
ProportionPositiveMutations=ProportionPositiveMutations
```

```

population_history=population_history
nmale_start=nmale_start
nfemale_start=nfemale_start
nmale_end=nmale_end
nfemale_end=nfemale_end
nmale_bottleneck=nmale_bottleneck
nfemale_bottleneck=nfemale_bottleneck
gen_bottle=gen_bottle
nmale_mean=nmale_mean
nfemale_mean=nfemale_mean
nmale_std=nmale_std
nfemale_std=nfemale_std
ldStructure=ldStructure
qtlDistribution=qtlDistribution
StoreHaplotypes=StoreHaplotypes
StoreHaplotypesDirectory=StoreHaplotypesDirectory
UseStoredHaplotypes=UseStoredHaplotypes
UseStoredHaplotypesDirectory=UseStoredHaplotypesDirectory
ldInterval=ldInterval
maxNQtls=maxNQtls,
markersMaf=markersMaf,
maxNMarkers=maxNMarkers,
nMarkersMaxMaf=nMarkersMaxMaf
resampleQtlMarkers=resampleQtlMarkers /

```

**\*\*Task\*\***

Parameters to generate linkage disequilibrium between QTL and marker alleles

**\*\*Properties of names\*\***

<i>LD_ngen</i>	Definition: Number of generations simulated to generate LD Type: Integer Options: $\geq 1$ Default: 1000
<i>LD_npat</i>	Definition: Number of paternal founders in each generation Type: Integer Options: $\geq 1$ Default: 100 <i>GeneticModel 'qtl', LD_method 'meu' only</i>
<i>LD_nmat</i>	Definition: Number of maternal founders in each generation Type: Integer Options: $\geq 1$ Default: 100 <i>GeneticModel 'qtl', LD_method 'meu' only</i>
<i>cri_val_qtl</i>	Definition: Proportional sensitivity when determining QTL frequency. A <i>cri_val_qtl</i> of, for example, 0.2 means a 20% difference is accepted between the sampled and the specified QTL frequency. Type: Real Options: $0.0 < cri\_val\_qtl \leq 1.0$ Default: 0.20 <i>GeneticModel 'qtl', LD_method 'meu' only</i>
<i>nPotentialLoci</i>	Definition: Number of (homozygotic) loci on the genome; QTL and markers Type: Integer Options: $\geq 1$

Default: 1

*nmarker\_per\_qtl* Definition: Ratio of marker to QTL loci  
Type: Integer  
Options: 7, 15, 31  
Default: 7

*mutation\_rate* Definition: Mutation rate; probability of mutation occurring at each locus of diploid genotype. Mutation occurs on recombinant haploid genotypes. Probability of a mutation occurring at each locus of a recombinant haploid genotype is  $0.5 \cdot \text{mutation\_rate}$ .  
Type: Real  
Options:  $0.0 \leq \text{mutation\_rate} \leq 1.0$   
Default: 0.0

*CullingProportion* Definition: Desired proportion of sampled plants culled before becoming founders  
Type: Real  
Options:  $0.0 \leq \text{CullingProportion} \leq 0.5$   
Default: 0.0

ProportionPositiveMutations  
Definition: Proportion of mutations that generate a positive effect at QTL loci  
Type: Real  
Options:  $0.0 < \text{ProportionPositiveMutations} < 1.0$   
Default: 0.0

*population\_history* Definition: Defines change in population size over generations  
Type: Character  
Options:  
constant Constant population size  
expanding Population size increases  
decreasing Population size decreases  
bottlenecked Population size goes through a bottleneck  
fluctuating Random population size at each generation  
Default: constant

*nmale\_start* Definition: Number of male parents; number in first generation  
Type: Integer  
Options:  $\geq 1$   
Default: 100

*nfemale\_start* Definition: Number of female parents; number in first generation  
Type: Integer  
Options:  $\geq 1$   
Default: 100

*nmale\_end* Definition: Number of male parents at in the final generation  
Type: Integer

Options:  $\geq 1$   
Default: 100

*nfemale\_end* Definition: Number of female parents in the final generation  
Type: Integer  
Options:  $\geq 1$   
Default: 100

*nmale\_bottleneck* Definition: Number of male parents at peak of population  
bottleneck; when population size is lowest  
Type: Integer  
Options:  $\geq 1$   
Default: 100

*nfemale\_bottleneck* Definition: Number of female parents at peak of population  
bottleneck  
Type: Integer  
Options:  $\geq 1$   
Default: 100

*gen\_bottle* Definition: Generation in which population bottleneck peaks  
Type: Integer  
Options:  $1 \leq \text{gen\_bottle} \leq \text{LD\_ngen}$   
Default: 500

*nmale\_mean* Definition: Mean number of male parents in each generation  
Type: Integer  
Options:  $\geq 1$   
Default: 100

*nmale\_std* Definition: Standard deviation of number of male parents in  
each generation  
Type: Integer  
Options:  $\geq 1$   
Default: 10

*nfemale\_mean* Definition: Mean number of female parents in each generation  
Type: Integer  
Options:  $\geq 1$   
Default: 100

*nfemale\_std* Definition: Standard deviation of number of female parents  
in each generation  
Type: Integer  
Options:  $\geq 1$   
Default: 10

*ldStructure* Definition: Generation of linkage disequilibrium (founder  
populations) across replicate breeding schemes.  
Applies when *GeneticModel* 'genomic' and 'qtl'; not  
'ldonly'.  
Type: Character  
Options:  
    same      Same generation of linkage disequilibrium across  
                replicates

unique Unique generation of linkage disequilibrium  
across replicates  
Default: same

*qtlDistribution*

Definition: Distribution of QTL-effects

Type: Character

Options:

exponential Exponential distribution (only for *ntbv*=1)  
with scale parameter (1/rate) of the  
exponential set to 0.01  
normal Normal distribution with mean 0

Default: exponential

Only applies with GeneticModel 'genomic' and LD\_method 'genomicld' as sampling after LD

*StoreHaplotypes*

Definition: Controls whether sampled genetic architecture  
and haplotypes are stored in files:  
geneticarchitecture.dat and basehaplotypes.dat

Type: Character

Options:

yes Files are generated  
no No files are generated

Default: no

GeneticModel 'genomic' in namelist &CONTROLPARAMETERS, LD\_method 'genomicld' in  
namelist &LD, and StoreHaplotypes 'yes' in namelist &LD

*StoreHaplotypesDirectory*

Definition: Directory to store haplotype files,  
geneticarchitecture.dat and basehaplotypes.dat

Type: Character

Options:

Existing directory or directory that can be created

Default: *OutDirectory*

Only applies with GeneticModel 'genomic' and LD\_method 'genomicld' as sampling after  
LD; Only used if StoreHaplotypes 'yes'; end with '/'

! Initialise StoreHaplotypesDirectory and UseStoredHaplotypesDirectory

StoreHaplotypesDirectory=trim(adjustl(OutDirectory))

UseStoredHaplotypesDirectory=trim(adjustl(OutDirectory))

*UseStoredHaplotypes*

Definition: Controls whether sampled genetic architecture  
and haplotypes are read from files,  
geneticarchitecture.dat and basehaplotypes.dat

Type: Character

Options:

yes No founder population is sampled and genetic  
architecture and haplotypes are read from files  
no Founder population is sampled

Default: no

Only applies with GeneticModel 'genomic' and LD\_method 'genomicld' as sampling after LD

*UseStoredHaplotypesDirectory*

Definition: Directory from which haplotype files,  
geneticarchitecture.dat and basehaplotypes.dat,  
are read

Type: Character

Options:

Existing directory

Default: *OutDirectory*

Only applies with GeneticModel 'genomic' and LD\_method 'genomicld' as sampling after LD; only used if *UseStoredHaplotypes* 'yes'; end with '/'

*ldInterval* Definition: length of genomic-distance intervals (cM) used when generating files (data and pdf) of LD versus genomic distance

Type: Real

Options:  $0.0125 \leq ldInterval \leq \text{sum}(ChromLengths)/40$

Default: 0.25 (0-10cM)

Only applies with GeneticModel 'genomic' or 'ldonly' and LD\_method 'genomicld' as sampling after LD

*maxNQtls* Definition: Maximum number of QTL sampled for each chromosome. QTL are randomly sampled from segregating QTL-loci generated by linkage disequilibrium. Sampled QTL are used in subsequent simulations.

Type: Integer

Dimension: *nchrom*, where *nchrom* is the number of chromosomes in the genome provided in namelist &CONTROL\_GENOME

Options:  $\geq 0$ ; sum of *maxNQtls*  $\geq 1$ ; or nothing provided

Default: huge(1)

If provided, sum of *maxNQtls* must be  $\geq 1$

*maxNQtls* for a chromosome is not realised when the *maxNQtls* is greater than the number of segregating QTL-loci generated by linkage disequilibrium. In these cases, all segregating QTL are used. When the maximum number is less than the number of segregating QTL-loci, all segregating QTL are sampled/used.

If *maxNQtls* is provided for one chromosome, it must be provided for all *nchrom* chromosomes. If *maxNQtls* is not provided, all segregating QTL are sampled/used in subsequent simulations.

*markersMaf* Definition: Threshold for marker minimum-allele frequency on each chromosome;

segregating markers generated by linkage disequilibrium with minimum-allele frequency larger than *markersMaf* sampled and used in simulations, where minimum-allele frequency is calculated using founder plants

Type: Real

Dimension: *nchrom*, where *nchrom* is the number of chromosomes in the genome provided in namelist &CONTROL\_GENOME

Options:  $0.0 \leq markersMaf \leq 0.5$ ; or nothing provided

Default: 0.0

If *markersMaf* is provided for one chromosome, it must be provided for all *nchrom* chromosomes. If *markersMaf* is not provided, all segregating markers are sampled/used in subsequent simulations.

*maxNMarkers* Definition: Maximum number of markers sampled for each chromosome. Markers are randomly sampled from segregating marker-loci generated by linkage disequilibrium. Sampled markers are used in subsequent simulations.

Type: Integer  
Dimension: *nchrom*, where *nchrom* is the number of chromosomes in the genome provided in namelist &CONTROL\_GENOME  
Options:  $\geq 0$ ; sum of *maxNMarkers*  $\geq 1$ ; or nothing provided  
Default: huge(1)

If provided, sum of *maxNMarkers* must be  $\geq 1$

*maxNMarkers* for a chromosome is not realised when the *maxNMarkers* is greater than the number of segregating marker-loci generated by linkage disequilibrium. In these cases, all segregating markers are used. When the maximum number is less than the number of segregating marker-loci, all segregating markers are sampled/used.

If *maxNMarkers* is provided for one chromosome, it must be provided for all *nchrom* chromosomes. If *maxNMarkers* is not provided, all segregating markers are sampled/used in subsequent simulations.

*nMarkersMaxMaf* chromosome, Definition: Maximum number of markers sampled on each chromosome, where the *nMarkersMaxMaf* segregating markers generated by linkage disequilibrium with the highest minimum-allele frequencies are used and minimum-allele frequency is calculated using founder plants. Maximum number of markers sampled for each chromosome. Markers are randomly sampled from segregating marker-loci generated by linkage disequilibrium. Sampled markers are used in subsequent simulations.

Type: Integer  
Dimension: *nchrom*, where *nchrom* is the number of chromosomes in the genome provided in namelist &CONTROL\_GENOME  
Options:  $\geq 0$ ; sum of *nMarkersMaxMaf*  $\geq 1$ ; or nothing provided  
Default: huge(1)

If provided, sum of *nMarkersMaxMaf* must be  $\geq 1$

*nMarkersMaxMaf* for a chromosome is not realised when the *nMarkersMaxMaf* is greater than the number of segregating marker-loci generated by linkage disequilibrium. In these cases, all segregating markers are used. When the maximum number is less than the number of segregating marker-loci, all segregating markers are sampled/used.

If *nMarkersMaxMaf* is provided for one chromosome, it must be provided for all *nchrom* chromosomes. If *nMarkersMaxMaf* is not provided, all segregating markers are sampled/used in subsequent simulations.

Markers are sampled for *markerMaf* before *maxNMarkers* [higher precedence]. *markerMaf* and *maxNMarkers* can be used together; they cannot be used with *nMarkersMaxMaf*.

*resampleQtlMarkers* Definition: QTL and markers are resampled for each replicate from the segregating QTL and marker loci generated by linkage disequilibrium  
Type: Character  
Options:  
yes QTL and markers are resampled

no QTL and markers are not resampled  
Default: no

**\*\*Additional information\*\***

1) The parameters required is determined by *GeneticModel*, *LD\_method*, and *population\_history*

(a) *GeneticModel* 'genomic', *LD\_method* 'genomicLD'

- (i) *LD\_ngen*
- (ii) *nPotentialLoci*
- (iii) *nmarker\_per\_qtl*
- (iv) *mutation\_rate*
- (v) *CullingProportion*
- (vi) *ProportionPositiveMutations*
- (vii) *population\_history*

*population\_history* 'constant', 'expanding', 'decreasing', 'bottlenecked'

- (viii) *nmale\_start*
- (ix) *nfemale\_start*

*population\_history* 'expanding', 'decreasing', 'bottlenecked'

- (x) *nmale\_end*
- (xi) *nfemale\_end*

*population\_history* 'bottlenecked'

- (xii) *nmale\_bottleneck*
- (xiii) *nfemale\_bottleneck*
- (xiv) *gen\_bottle*

*population\_history* 'fluctuating'

- (xv) *nmale\_mean*
- (xvi) *nmale\_std*
- (xvii) *nfemale\_mean*
- (xviii) *nfemale\_std*
- (xix) *ldStructure*
- (xx) *qtlDistribution*
- (xxi) *StoreHaplotypes*
- (xxii) *StoreHaplotypesDirectory*
- (xxiii) *UseStoredHaplotypes*
- (xxiv) *UseStoredHaplotypesDirectory*
- (xxv) *ldInterval*

(b) *GeneticModel* 'ldOnly', *LD\_method* 'genomicLD'

- (i) *LD\_ngen*
- (ii) *nPotentialLoci*
- (iii) *nmarker\_per\_qtl*
- (iv) *mutation\_rate*
- (v) *CullingProportion*
- (vi) *ProportionPositiveMutations*
- (vii) *population\_history*

*population\_history* 'constant', 'expanding', 'decreasing', 'bottlenecked'

- (viii) *nmale\_start*
- (ix) *nfemale\_start*

*population\_history* 'expanding', 'decreasing', 'bottlenecked'

(xi) *nmale\_end*  
 (xii) *nfemale\_end*

*population\_history* 'bottlenecked'  
 (xiii) *nmale\_bottleneck*  
 (xiv) *nfemale\_bottleneck*  
 (xv) *gen\_bottle*

*population\_history* 'fluctuating'  
 (xvi) *nmale\_mean*  
 (xvii) *nmale\_std*  
 (xviii) *nfemale\_mean*  
 (xix) *nfemale\_std*

(xixi) *ldInterval*

(c) *GeneticModel* 'qtl', *LD\_method* 'meu'  
 (i) *LD\_ngen*  
 (ii) *LD\_npat*  
 (iii) *LD\_nmat*  
 (vi) *cri\_val\_qtl*  
 (vii) *ldStructure*

*ld\_hayes* only run when *LD\_method* 'genomicld'

- 2) (a) When *GeneticModel* 'genomic' and *LD\_method* 'genomicLD' or *GeneticModel* 'qtl' and *LD\_method* 'meu', a population of plants with QTL and markers in linkage disequilibrium is generated. The pool of genotypes for these plants is sampled with replacement to generate the base population used in a subsequent breeding scheme.
- (b) When *GeneticModel* 'ldOnly' and *LD\_method* 'genomicLD', LD is generated to study linkage disequilibrium. A subsequent breeding scheme is not simulated and, therefore, the pool of genotypes is not used to generate the base population.

How are the genotypes actually sampled?

- 3) Low *cri\_val\_qtl* values will cause the program to run slowly
- 4) (a) The number of replicates of the LD-generating routine when *GeneticModel* 'ldOnly' and *LD\_method* 'genomicLD' is *nrep* provided in *namelist* &CONTROLPARAMETERS.
- (b) When *GeneticModel* 'genomic' and *LD\_method* 'genomicLD', *nrep* applies to the number of replicate breeding schemes. The LD-generating routine is only run once.
- 5) *nmarker\_per\_qtl*<nBits
- 6) *ExponentialScale* ...  
 ) *CullingProportion* ... (Expected) number of offspring that are culled by 'natural' selection.
- 7) When *population\_history* 'constant', only *nmale\_start* and *nfemale\_start* are used
- 8) When *population\_history* 'expanding' or 'decreasing', *nmale\_start*,

*nfemale\_start*, *nmale\_end*, and *nfemale\_end* are used

- 9) When *population\_history* 'bottlenecked', *nmale\_start*, *nfemale\_start*, *nmale\_end*, *nfemale\_end*, *nmale\_bottleneck*, *nfemale\_bottleneck*, and *gen\_bottle* are used
- 10) When *population\_history* 'fluctuating', *nmale\_mean*, *nmale\_std*, *nfemale\_mean*, and *nfemale\_std* are used
- 11) When *randomSeeds* 'manual', *founderSeeds* 'file', and *GeneticModel* 'genomic' or 'qtl', *ldStructure* in *namelist* &LD cannot be 'same'. It must be 'unique'. When *genetic Model* 'qtl', *nrep*>1, and *ldStructure* 'same', then cannot have *randomSeeds* 'manual', *founderSeeds* 'file'. When *genetic Model* 'genomic', *nrep*>1, *ldStructure* 'same', and *UseStoredHaplotypes* 'no', cannot have *randomSeeds* 'manual', *founderSeeds* 'file'.
- 12) When *GeneticModel* 'genomic' or 'qtl' and *ldStructure* 'same', seeds provided in the first replicate are used to generate the founder population used across all replicates.
- 13) *qtlDistribution*. Exponential (single trait) or normal (single or multiple traits). QTL (co)variance scaled so that equal to pre-defined (co)variance.

What QTL effects presented when LD-only?

QTL effects sampled from exponential distribution when generating LD. QTL-effects for breeding scheme can be these exponential effects (single trait only) or normal (resampled).

- 14) *StoreHaplotypes* and *UseStoredHaplotypes* cannot both take a value of 'yes'.

*StoreHaplotypesDirectory*, existing directory or ADAM creates new directory. Must be valid directory.

*UseStoredHaplotypesDirectory*, existing directory containing haplotype files

When use *UseStoreHaplotypesDirectory*, &CONTROL\_GENOME *nchrom* and *ChromLengths* are used. They must be provided. *nchrom* and the number of lengths in *ChromLengths* defined in *input.prm* must conform with the number in stored haplotypes. Beware! The lengths of the chromosomes in *ChromLengths* need not be the same as the lengths saved in stored haplotypes [MH: Do we change this?].

- 15) *ldInterval* only used when *printLdHayesFiles* 'yes'. Otherwise, file with LD versus genomic distance are not generated and *ldInterval* not required.

ACS: I've replaced the variable *SelectionCoefficient* used in sampling genomic LD by the variables *CullingProportion*, which gives the desired proportion of plants culled in each generation of the founder population, and *ExponentialScale*, which gives the scale parameter for the exponential distribution for sampling QTL effects. Notice the parametrisation of the exponential distribution here. It is the scale parameter (1/lambda), which is the inverse of the rate parameter, lambda. *ExponentialScale* is only used [to sample QTL effects when generating LD. ~~if~~ If the exponential distribution is chosen for sampling QTL effects in breeding scheme, these effects are maintained. If normal distribution is used instead, normal deviates are sampled for segregating alleles.](#)

How sample genotypes of base plants from pool of founder genomes?

Store/Use haplotypes: Det er kun haplotyper og qtl indikator, men ikke effekter. Det eneste der skal matche med input er antal Chromosomer. Så vidt jeg kan se/huske, gemmer du alle haplotyper og qtl indikatorer ved slutningen af DoGenomicLD. Hvis man vælger at bruge "stored haplotypes", springer man over DoGenomicLD. Derefter "vælger/fjerner" du qtl'er og markører samt tilføjer qtl-effekter.

Jeg regner med, at du gemmer "seg\_locus(i)%effect" i ...

```

DO i=1,SUM(nSegLoci(:,:))

    WRITE (UNIT=io_genarch,FMT=*,IOSTAT=ier) seg_locus(i)%al_freq,
seg_locus(i)%link_group, &
                                seg_locus(i)%position, seg_locus(i)%qtl,
seg_locus(i)%effect
    IF (ier/=0) THEN
        WRITE (string,'(angel)') &
            'Error in MODULE ld_hayes, SUBROUTINE
WriteGeneticArchitecture(puke)
            & Data was not written to output file geneticArchitecture.dat
correctly.'
        CALL handle_error(string,ier)
    END IF

END DO

```

... for at kunne bruge effekterne, når qtlDistribution=='exponential' og ntbv==1? Ja, men de kan sagtens bruges med en anden fordeling af effekter og en anden ntbv

) If *nMarkersMaxMaf* < huge(1)/is provided, neither *markerMaf* nor *maxNMarkers* can be provided. That is, *markerMaf* cannot be >0.0 and *maxNMarkers* cannot be <huge(1).

) When *maxNQtl*, *markerMaf*, *maxNMarkers*, and *nMarkersMaxMaf* not provided, all segregating QTL are sampled/used in subsequent simulations.

) *resampleQtlMarkers* can only be 'yes' when (i) *ldStructure* 'same', and (ii) *maxNQtl*, *maxNMarkers*, or *nMarkersMaxMaf* are less than huge(1) or *markerMaf* >0.0.

#### &RANDOMNUMBERSEEDS

```

randomSeeds=randomSeeds
seed1=seed1
seed2=seed2
seedsFile=seedsFile
founderSeeds=founderSeeds
founderSeed1=founderSeed1
founderSeed2=founderSeed2
founderSeedsFile=founderSeedsFile
baseSeeds=baseSeeds
baseSeed1=baseSeed1
baseSeed2=baseSeed2
baseSeedsFile=baseSeedsFile
selectionSeeds=selectionSeeds
selectionSeedsFile=selectionSeedsFile /

```

**\*\*Task\*\***

Input seed for random-number generators in Randlib

**\*\*Properties of names\*\***

*randomSeeds* Definition: Method used to generate seeds that initialise Randlib's random-number generator  
Type: Character  
Options:  
    computer Seeds randomly generated from /dev/urandom  
    user Seeds provided by user, *seed1* and *seed2*  
    file Seeds provided by user; *seed1* and *seed2* for each replicate specified in file, *seedsFile*  
    manual User specifies methods that generate seeds used to generate founder population, base population, and carry out selection  
Default: *randomSeeds* must be specified

*seed1* Definition: First integer seed of current random-number generator  
Type: Integer\*4  
Options:  $0 \leq \textit{seed1} \leq \textit{huge}(1)$   
Default: 123456789

*seed2* Definition: Second integer seed of current random-number generator  
Type: Integer\*4  
Options:  $0 \leq \textit{seed2} \leq \textit{huge}(1)$   
Default: 987654321

*seedsFile* Definition: Input file with seeds when *randomSeeds* file; two integer seeds per row (*seed1* and *seed2*), one row per replicate. Each replicate is initiated with specified seeds.  
When *randomSeeds* 'computer' or 'user', *seed1* and *seed2* used by RandLib in each replicate are written to *seedsFile*. This file can be used as input in subsequent simulations when the same seeds are required.  
Type: Character  
Options: Valid filename with  $0 \leq \textit{seed1} \leq \textit{huge}(1)$ ,  $0 \leq \textit{seed2} \leq \textit{huge}(1)$   
Default: seeds.in

*founderSeeds* Definition: Method used to provide seeds to generate founder population(s) when *randomSeeds* manual  
Type: Character  
Options:  
    computer Seeds randomly generated from /dev/urandom  
    user Seeds provided by user; *founderSeed1* and *founderSeed2*  
    file Seeds provided by user; *seed1* and *seed2* for each replicate specified in file, *founderSeedsFile*  
Default: user

*founderSeed1* Definition: First seed provided when *founderSeeds* user; *seed1* is set to *founderSeed1*  
Type: Integer\*4  
Options:  $0 \leq \textit{founderSeed1} \leq \textit{huge}(1)$   
Default: 123456789

*founderSeed2* Definition: Second seed provided when *founderSeeds* user;

*seed2* is set to *founderSeed2*

Type: Integer\*4  
Options:  $0 \leq \textit{founderSeed2} \leq \textit{huge}(1)$   
Default: 987654321

*founderSeedsFile*      Definition: Input file with seeds when *randomSeeds* manual and *founderSeeds* file; two integer seeds per row (*seed1* and *seed2*), one row per replicate. Founder populations in each replicate are generated with specified seeds. When *randomSeeds* 'manual' and *founderSeeds* 'computer' or 'user', *seed1* and *seed2* used by RandLib to generate the founder population in each replicate are written to *founderSeedsFile*. This file can be used as input in subsequent simulations when the same seeds are required.

Type: Character  
Options: Valid filename with  $0 \leq \textit{seed1} \leq \textit{huge}(1)$ ,  $0 \leq \textit{seed2} \leq \textit{huge}(1)$   
Default: *founderSeeds.in*

*baseSeeds*      Definition: Method used to provide seeds to generate base population(s) when *randomSeeds* manual

Type: Character  
Options:

- computer Seeds randomly generated from /dev/urandom
- user      Seeds provided by user; *baseSeed1* and *baseSeed2*
- file      Seeds provided by user; *seed1* and *seed2* for each replicate specified in file, *baseSeedsFile*

Default: user

*baseSeed1*      Definition: First seed provided when *baseSeeds* user; *seed1* is set to *baseSeed1*

Type: Integer\*4  
Options:  $0 \leq \textit{baseSeed1} \leq \textit{huge}(1)$   
Default: 123456789

*baseSeed2*      Definition: Second seed provided when *baseSeeds* user; *seed2* is set to *baseSeed2*

Type: Integer\*4  
Options:  $0 \leq \textit{baseSeed2} \leq \textit{huge}(1)$   
Default: 987654321

*baseSeedsFile*      Definition: Input file with seeds when *randomSeeds* manual and *baseSeeds* file; two integer seeds per row (*seed1* and *seed2*), one row per replicate. Base populations in each replicate are generated with specified seeds. When *randomSeeds* 'manual' and *baseSeeds* 'computer' or 'user', *seed1* and *seed2* used by RandLib to generate the base population in each replicate are written to *baseSeedsFile*. This file can be used as input in subsequent simulations when the same seeds are required.

Type: Character

Options: Valid filename with  $0 \leq \text{seed1} \leq \text{huge}(1)$ ,  $0 \leq \text{seed2} \leq \text{huge}(1)$   
Default: baseSeeds.in

*selectionSeeds*

Definition: Method used to provide seeds to carry out selection when *randomSeeds* manual

Type: Character

Options:

computer Seeds randomly generated from /dev/urandom  
file Seeds provided by user; *seed1* and *seed2* for each replicate specified in file, *selectionSeedsFile*

Default: computer

*selectionSeedsFile*

Definition: Input file with seeds when *randomSeeds* manual and *selectionSeeds* file; two integer seeds per row (*seed1* and *seed2*), one row per replicate. Selection process in each replicate is initiated with specified seeds. When *randomSeeds* 'manual' and *selectionSeeds* 'computer', *seed1* and *seed2* used by RandLib to carry out selection in each replicate are written to *selectionSeedsFile*. This file can be used as input in subsequent simulations when the same seeds are required.

Type: Character

Options: Valid filename with  $0 \leq \text{seed1} \leq \text{huge}(1)$ ,  $0 \leq \text{seed2} \leq \text{huge}(1)$

Default: selectionSeeds.in

**\*\*Additional information\*\***

- 1) (a) *seed1* and *seed2* are only used when *randomSeeds* 'user'  
(b) *seedsFile* is only used as input when *randomSeeds* 'file'  
(c) *founderSeeds*, *baseSeeds*, and *selectionSeeds* are only used when *randomSeeds* 'manual'
- 2) (a) *founderSeed1* and *founderSeed2* are only used when *randomSeeds* 'manual' and *founderSeeds* 'user'  
(b) *founderSeedsFile* is only used as input when *randomSeeds* 'manual' and *founderSeeds* 'file'
- 3) (a) *baseSeed1* and *baseSeed2* are only used when *randomSeeds* 'manual' and *baseSeeds* 'user'  
(b) *baseSeedsFile* is only used as input when *randomSeeds* 'manual' and *baseSeeds* 'file'
- 4) *selectionSeedsFile* is only used as input when *randomSeeds* 'manual' and *selectionSeeds* 'file'.
- 5) When *GeneticModel* 'ldonly', *randomSeeds* must be 'computer', 'user', or 'file'. It cannot be 'manual'.
- 6) *seed1* and *seed2* remain the seeds of Randlib's random-number generator throughout simulations. They are updated using the information provided the namelist.
- 7) When *randomSeeds* 'manual', *founderSeeds* 'file', and *GeneticModel* 'genomic' or 'qtl', *ldStructure* in namelist &LD cannot be 'same'. It must be 'unique'.

8) The format of input files `seedsFile`, `founderSeedsFile`, `baseSeedsFile`, `selectionSeedsFile` is:

```
<seed1 for replicate 1> <seed2 for replicate 1>
<seed1 for replicate 2> <seed2 for replicate 2>
.
.
.
<seed1 for replicate n> <seed2 for replicate n>
```

where  $0 \leq \text{seed1} \leq \text{huge}(1)$  and  $0 \leq \text{seed2} \leq \text{huge}(1)$ .

This is also the format when `seed1` and `seed2` used by `RandLib` are written to these files

9) When `GeneticModel` 'genomic' or 'qtl' and `ldStructure` 'same', seeds provided in the first replicate are used to generate the founder population used across all replicates.

## &POPULATIONPARAMETERS

```
npop=npop
nherd=nherd
ntbv=ntbv
nobs=nobs
nres=nres
nCombinedObs=nCombinedObs
nObsConstraints=nObsConstraints
nebv=nebv
nF=nF
SpeedBreeding=SpeedBreeding
NewCycleInterval=NewCycleInterval
OldAgePlants=OldAgePlants
```

### \*\*Task\*\*

Basic input to generate population(s)

### \*\*Properties of names\*\*

```
npop          Definition: Number of populations
              Type: Integer
              Options: 1
              Default: 1
```

```
nherd        Definition: Number of herds in each population
              Type: Integer
              Options: ≥1
              Default: 1
```

```
ntbv         Definition: Number of traits, where a trait is a characteristic
              for which a true breeding value is sampled and an
              estimated breeding value can be predicted
              Type: Integer
              Options: ≥1
```

Default: 1

*nobs* Definition: Number of observations, where an observation is the phenotype of a *ntbv* trait. Not all observations are necessarily realised for each plant.  
Type: Integer  
Options: ≥1  
Default: 1

*nres* Definition: Number of residuals, where a residual is an environmental deviation sampled for a *nobs* observation. Environmental deviation includes all non-additive genetic effects.  
Type: Integer  
Options: ≥1  
Default: 1

*nCombinedObs* Definition: Number of combined observations, where a combined observation is a phenotype generated by combining *nobs* observations. Not all combined observations are necessarily realised for each plant.  
Type: Integer  
Options: ≥0  
Default: 0

*nObsConstraints* Definition: Number of constraints applied to *nobs* and *nCombinedObs* observations, where a constraint is a restriction by which observations must comply  
Type: Integer  
Options: ≥0  
Default: 0

*nebv* Definition: Number of selection criteria used to calculate estimated aggregate-breeding value  
Type: Integer  
Options: ≥0  
Default: 0

*nF* Definition: The last generation of a breeding cycle  
Type: Integer  
Options: ≥1  
Default: 1

*SpeedBreeding* Definition: Determines whether speed breeding is applied.  
Type: Character  
Options:  
no Speed breeding is not used  
yes Uses Speed breeding  
Default: no

*NewCycleInterval* Definition: The number of time steps after which a new cycle starts  
Type: Integer



population are reproductive; measured in time steps. Used when *age\_class\_base* 'input'.

Type: Integer

Options: ≥1

Default: 1

#### *RealiseBaseObservations*

Definition: Observations realised for base plants that fulfil the criteria specified in namelist &OBSERVATIONS

Type: Character

Options:

yes Observations are realised

no Observations are not realised

Default: yes

#### \*\*Additional information\*\*

- 1) Information provided in namelists &POPULATIONPARAMETERS, &SELECTION, and &EVA is used to generate the base population when *age\_class\_base* 'no\_structure' and 'create\_structure'
- 2) *age\_class\_base* 'no\_structure'
  - (a) Variables *max\_age\_base\_plantss*
  - (b) All base males and females have the same age. They are all born at time 0. The consequence of this is that, when the minimum reproductive age of the base plants is greater than 0, there will be time steps with no selection candidates available for reproduction. This does not cause the program to stop.
  - (c) When germ plasm is used for reproduction,
    - (i) Germ plasm is stored for all base males if male germ plasm is used for reproduction. The number of germ plasm stored is the sum of all germ plasm stored for males during a time step. That is, the sum of germ plasm stored at each stage of &NAMELIST selection, variable *selection\_scheme* with *sex\_code* 1, 3, or 5 and *destiny\_sel* 2, 12, 26, or 126 and &NAMELIST EVA, variable *EvaSelection* with *MaleDestinySel* 2, 12, 26, or 126.
    - (ii) Germ plasm is stored for all base females if female germ plasm is used for reproduction. The number of germ plasm stored is the sum of all germ plasm stored for females during a time step. That is, the sum of germ plasm stored at each stage of &NAMELIST selection, variable *selection\_scheme* with *sex\_code* 2, 4, or 6 and *destiny\_sel* 2, 12, 127, or 147 and &NAMELIST EVA, variable *EvaSelection* with *FemaleDestinySel* 2, 12, 127, or 147.

#### &SELECTION

```
selection_groups=selection_groups
selection_scheme=
FirstTime LastTime Treproductive generation sex_code
live_status population_id selection_unit age(1)
age(2) selection_method selection_criterion
MendelianIndexWeight RunBlup numbers related_stage tag
destiny_sel destiny_unsel repro_capacity litter_size sex_ratio
n_germplasm SelectionRule /
```

NB! Number of lines in *selection\_scheme* must equal *selection\_groups*

When *sex\_code* 7 (EVA selection), all remaining variables in *selection\_scheme* are read, but not used. See 1) of 'Additional information'.

**\*\*Task\*\***

Input for selection

**\*\*Properties of names\*\***

*selection\_groups*      Definition: Number of selection stages  
Type: Integer  
Options:  $\geq 1$   
Default: 1

*FirstTime*              Definition: First time step where the selection group is  
used  
Type: Integer  
Options:  
     $1 - \text{gestation\_length} \leq \text{FirstTime} \leq \text{LastTime}$   
Default: *FirstTime* must be specified

*LastTime*                Definition: Last time step where the selection group is  
used  
Type: Integer  
Options:  $\text{FirstTime} \leq \text{LastTime} \leq \text{ntime}$   
Default: *LastTime* must be specified

*Treproductive*         Definition: time steps fro mating to birth  
Type: Integer  
Options:  $\geq 0$   
Default: 0

*Generation*             Definition: generation in a breeding cycle  
Type: Integer  
Options:  $\geq 0$   
Default: must be specified

*sex\_code*                Definition: Type of selection  
Type: Integer  
Options:  
    0 Truncation or select-all selection  
    7 EVA-selection among plants tagged for  
    EVA-selection  
Default: *sex\_code* must be specified

*live\_status*            Definition: Live status of selection candidates  
Type: Integer  
Options:  
    0 Plant is candidate for selection if it is alive  
    or it is not alive and has germplasm stored  
    1 Only live plants are candidates for selection  
    2 Only plants not alive and with germplasm stored are  
    candidates for selection  
Default: *live\_status* must be specified

*population\_id* Definition: Specifies which population is selected  
Type: Integer  
Options:  $1 \leq \text{population\_id} \leq \text{npop}$   
Default: *population\_id* must be specified

*selection\_unit* Definition: Unit on which selection operates  
Type: Character  
Options:  
    *across\_pop* Across all populations  
    *population* Across all herds within the specified population  
  
    *entire\_fam* Entire full-sib families  
  
    *entire\_gpfam* Entire families defined based on the common grandparent  
  
    *entire\_ggpfam* Entire families defined based on the common grand grandparent  
  
    *within\_fam* Within full-sibs families  
  
    *wihtin\_gpfam* Within families defined based on the common grandparent  
  
    *within\_ggpfam* Within families defined based on the common grand grandparent  
  
Default: *selection\_unit* must be specified

*age(1)* Definition: Youngest age at which plants are considered for selection  
Type: Integer  
Options:  
    *age(1)* ≥ 1 when *Treproductive* = 0  
    *age(1)* ≥ 0 when *Treproductive* > 0  
Default: *age(1)* must be specified

*age(2)* Definition: Oldest age at which plants are considered for selection  
Type: Integer  
Options: *age(2)* ≥ *age(1)*  
Default: *age(2)* must be specified

*selection\_method* Definition: Method of selection  
Type: Character  
Options:  
    *select\_all* Select all plants  
    *threshold* Threshold selection  
    *truncation* Truncation selection  
Default: *selection\_method* must be specified

*selection\_criterion* Definition: Criterion on which plants are selected  
Type: Character  
Options:

tbv	True breeding value
random	Random variable
phenothreshold	Phenotypic observation(s) with associated threshold(s)
phenoweight	Phenotypic selection with observations weighted
polyblup	Polygenic-BLUP breeding value
genomicblup	Genomic-BLUP breeding value
ibdblup	IBD-BLUP breeding value
gas	GAS-breeding value
bayesp	BayesP-breeding values

Default: *selection\_criterion* must be specified

When bayesP, *GeneticModel* must be 'genomic', nebv==1, and genotyped\_at\_birth)/='yes'

*MendelianIndexWeight* Definition: Mendelian-index weight used as modify selection criterion. The modified criterion for individual *i* is  $c_i = b \cdot (a_i - PA_i) + (1 - b) \cdot PA_i$ , where *b* is *MendelianIndexWeight*, *a<sub>i</sub>* is its breeding value, and *PA<sub>i</sub>* is its parental average (after Grundy et al. 1999, Wu & Schaeffer 2000).

Type: Real  
Options:  $0.0 \leq \textit{MendelianIndexWeight} \leq 1.0$   
Default: *MendelianIndexWeight* must be specified

*RunBlup* Definition: Estimate BLUP-breeding values  
Type: Integer  
Options:  
    0 Breeding values are not estimated  
    1 Breeding values are estimated  
Default: *RunBlup* must be specified

*numbers* Definition: Number of plants to be selected from each selection\_unit  
Type: Integer  
Options:  $\geq 1$   
Default: *numbers* must be specified

*related\_stage* Definition: Plants selected in the current stage of selection are automatically selected in selection stage *related\_stage* of the current time step. The total number of selected plants in selection stage *related\_stage* includes the number of plants selected in the current selection stage.  
Type: Integer  
Options: 0 No related stages  
         $2 \leq \textit{related\_stage} \leq \textit{selection\_groups}$   
Default: *related\_stage* must be specified

*tag* Definition: Plants with specified tag are selection candidates when *sex\_code* 5 or 6  
Type: Integer  
Options:  
    90 Selection among candidates tagged to be left alive  
    91 Selection among candidates tagged to reproduce

- (mate)
- 92 Selection among candidates tagged to have germ plasm stored
- 93 Selection among candidates tagged for genotyping
- 98 Selection among candidates tagged to have phenotypic observations realised at current selection stage
- 99 Selection among candidates tagged to be culled voluntarily
- 912 Selection among candidates tagged to reproduce and have germ plasm stored

Default: *tag* must be specified

*destiny\_sel*

Definition: Defines the destiny of selected plants

Type: Integer

Options:

- 0 Selected candidates are left alive
- 1 Selected candidates are reproduced (mated)
- 2 Selected candidates have germ plasm stored
- 3 Selected candidates are genotyped
- 8 Selected candidates have phenotypic observation(s) realised at current selection stage
- 9 Selected candidates are culled voluntarily (only for *selection\_method* 'select\_all')
- 12 Selected candidates are reproduced and have germ plasm stored
- 90 Selected candidates are tagged as candidates to be left alive
- 91 Selected candidates are tagged as candidates to reproduce (mate)
- 92 Selected candidates are tagged as candidates to have germ plasm stored
- 93 Selected candidates are tagged as candidates for genotyping

Default: *destiny\_sel* must be specified.

*destiny\_unsel*

Definition: Destiny of candidates that are not selected

Type: Integer

Options:

- 0 Plant is culled
- 1 Plant is left alive

Default: *destiny\_unsel* must be specified

*repro\_capacity*

Definition: Reproductive capacity (number of matings) of selected individuals (biologically constrained or otherwise)

Type: Integer

Options:  $\geq 1$

Default: *repro\_capacity* must be specified.

*litter\_size*

Definition: Number of offspring per mating

Type: Integer

Options:  $\geq 1$

Default: *litter\_size* must be specified

*sex\_ratio*

Definition: Probability of an offspring being a female

Type: Real  
Options:  $0.0 \leq \text{sex\_ratio} \leq 1.0$   
Default: *sex\_ratio* must be specified

*germ\_plasm* Definition: Number of units of germplasm stored per selected plant.  
Type: Integer  
Options: *germ\_plasm*  $\geq 0$   
Default: *germ\_plasm* must be specified

*SelectionRule* Definition: Selection rule number; only valid for truncation selection  
Type: Integer  
Options:  
    0 No selection rule  
     $\geq 1$  Selection rule. Rule number must correspond to a rule number specified in namelist rules, variable *SelectionRules*.  
Default: *SelectionRule* must be specified

**\*\*Relation to subsequent namelists\*\***

&PHENOTHRESHOLDS

Namelist &PHENOTHRESHOLDS is required when *selection\_criterion* 'phenothreshold' in any selection stage of namelist &SELECTION, variable *selection\_scheme*

&RULES

Namelist &RULES is required when *sex\_code* 0:6, *selection\_method* 'truncation', and *rule*  $> 0$ , in any selection stage of namelist &SELECTION, variable *selection\_scheme*

&EVA

Namelist &EVA is required when *sex\_code* 7 in any selection stage of namelist &SELECTION, variable *selection\_scheme*. The number of EVA-selection stages in namelist &EVA, variable *EvaSelection* must equal the number of selection stages in namelist &SELECTION, variable *selection\_scheme* with EVA-selection (i.e., *sex\_code* 7)

&PHENOWEIGHTS

Namelist &PHENOWEIGHTS is required when *selection\_criterion* 'phenoweight' in any selection stage of namelist &SELECTION, variable *selection\_scheme*

&DMUPARAMETERS

Namelist &DMUPARAMETERS is required when *selection\_criterion* 'polyblup', 'genomicblup', 'ibdblup', or 'gas' at any selection stage of namelist &SELECTION, variable *selection\_scheme*

&GAS\_PARAMETERS

Namelist &GAS\_PARAMETERS is required when *GeneticModel* 'qtl' in namelist &CONTROLPARAMETERS and *selection\_criterion* 'gas' in any selection stage of namelist &SELECTION, variable *selection\_scheme*

&GENOMICBLUPPARAMETERS

&IBDBLUPPARAMETERS

&BAYESPPARAMETERS

**\*\*Additional information\*\***

- 1) All variables in namelist &SELECTION, variable *selection\_scheme* are read and, therefore, must be specified. However, there are cases where some variables are not used. The most striking case is when *sex\_code* 7. This specifies that EVA selection is to be carried out. The information required to carry out EVA selection is not provided in *selection\_scheme*, but in namelist &EVA. Another case is when selected plants are not destined to be mated. In this case, variables, such as *repro\_capacity*, *litter\_size*, and *sex\_ratio*, are read, but not used. For variables that are not used, the input provided is irrelevant. However, for clarity, we recommend providing 0 for integer variables, 0.0 for *sex\_ratio* (the only real), and ' ' for character variables.
- 2) *sex\_code*
  - (a) *sex\_code* must be 0:7
  - (b) The number of selection stages with *sex\_code* 7 (selection stages with EVA-selection) must equal the number of EVA-selection stages provided in namelist &EVA
- 3)
  - (a) *live\_status* must be 0, 1, or 2 when *sex\_code* 0:6
  - (b) *live\_status* can only be 0 and 2 when
    - (i) *sex\_code* 1:4 and *destiny\_sel* 1
    - (ii) *sex\_code* 5 or 6, *tag* 91, and *destiny\_sel* 1
    - (iii) *sex\_code* 0:4 and *destiny\_sel* 91 or 95
    - (iv) *selection\_unit* not 'family'
  - (c) When *live\_status* 0 or 2, *destiny\_sel* 1, and a deceased plant with stored germ plasm is selected for reproduction, the plant's reproductive capacity is defined as follows. If the number of stored germ plasm is greater or equal to *repro\_capacity*, the plant's reproductive capacity is *repro\_capacity*. If, however, the number of stored germ plasm is less than *repro\_capacity*, the plant's reproductive capacity is the number of stored germ plasm. The consequence of this is that, insufficient stored germ plasm can lead to less matings being carried out than planned.
- 5) *population\_id* must be 1 when *sex\_code* 0:6
- 6)
  - (a) *selection\_unit* must be 'across\_pop', 'population', 'across\_herd', 'within\_herd', or 'family' when *sex\_code* 0:6
  - (b) *selection\_unit* cannot be 'family' with *sex\_code* 3:4, *live\_status* 0 or 2, or *selection\_method* 'select\_all'
  - (c) *selection\_unit* 'family' implies selection within all full-sib families in herds *herd\_id*(1) to *herd\_id*(2) with individuals from ages *age*(1) to *age*(2). The number of full-sib families is not specified explicitly. The number is determined at other selection stages where selection of plants for mating occurs.
- 7)
  - (a) *age*(1) and *age*(2) must be provided when *sex\_code* 0:6
  - (b)  $age(2) < \max(\text{OldAgeMales}, \text{OldAgeFemales})$  when *sex\_code* 0 and *live\_status* 1
  - (c)  $age(2) < \text{OldAgeMales}$  when *sex\_code* 1, 3, or 5 and *live\_status* 1
  - (d)  $age(2) < \text{OldAgeFemales}$  when *sex\_code* 2, 4, or 6 and *live\_status* 1
  - (e) There is no limit on *age*(1) and *age*(2) when *live\_status* 0 or 2
  - (f)  $age(2) \geq age(1) \geq 0$  implies that plants cannot be selected before they are born
- 8)
  - (a) *selection\_method* must be 'select\_all', 'threshold', or 'truncation' when *sex\_code* 0:6

- (b) When *selection\_method* 'select\_all', *selection\_criterion*, *MendelianIndexWeight*, *RunBlup*, *numbers*, *related\_stage*, *CheckHerdsSize*, *destiny\_unsel*, *repro\_capacity*, *litter\_size*, *sex\_ratio*, and *SelectionRule* are not used. They are set to 0; 0.5 for *MendelianIndexWeight*.
  - (c) When *selection\_method* 'threshold', *MendelianIndexWeight*, *RunBlup*, *numbers*, *related\_stage*, *CheckHerdsSize*, *repro\_capacity*, *litter\_size*, *sex\_ratio*, and *SelectionRule* are not used. They are set to 0; 0.5 for *MendelianIndexWeight*.
  - (d) When *selection\_method* 'select\_all' or 'threshold', the destiny of the selected candidates cannot include reproduction. That is, *destiny\_sel* cannot be 1, 12, 14, 16, 17, 126, 127, or 147.
  - (e) When *selection\_method* 'select\_all', *selection\_unit* cannot be 'family'
- 9) (a) *selection\_criterion* must be 'tbv', 'random', 'phenoweights', 'polyblup', 'genomicblup', 'ibdblup', or 'gas' when *sex\_code* 0:6 and *selection\_method* 'truncation'
- (b) *selection\_criterion* must be 'phenothreshold' when *sex\_code* 0:6 and *selection\_method* 'threshold'
  - (c) When *GeneticModel* 'polygenic', *selection\_criterion* cannot be 'genomicblup', 'ibdblup', or 'gas' at any selection stage
  - (d) When *GeneticModel* 'qtl', *selection\_criterion* cannot be 'genomicblup' or 'ibdblup' [should be ok with 'ibdblup?']
  - (e) When *GeneticModel* 'genomic', both 'genomicblup' and 'gas' cannot be used as selection criterion in a simulated breeding scheme. That is, both 'genomicblup' and 'gas' cannot be specified as *selection\_criterion* in *namelist &selection*, variable *selection\_scheme*, and/or as *MaleSelCrit* or *FemaleSelCrit* in any EVA-selection stage of *namelist &EVA*, variable *EvaSelection*.
  - (f) When *selection\_criterion* 'tbv', economic weight(s) provided in *economic\_weight* in *namelist &MATRICES* are used to weight the true breeding values for each trait  
When *selection\_criterion* 'polyblup', 'genomicblup', 'ibdblup', or 'gas', economic weight(s) provided in *economic\_weight* in *namelist &MATRICES* are used to weight the estimated breeding values for each trait  
When *selection\_criterion* 'phenoweights', phenotypic weight(s) provided in *namelist &PHENOWEIGHTS* are used to weight the phenotypes for each trait

When *bayesP*, *GeneticModel* must be 'genomic', *nebv*=1, and *genotyped\_at\_birth*)='yes'

- 10) (a) *MendelianIndexWeight* available when *selection\_method* 'truncation' and *selection\_criterion* 'random', 'polyblup', 'genomicblup', 'ibdblup', or 'gas'
- (b) Most-common values for *MendelianIndexWeight*:
- 0.0 Between-family selection
  - 0.5 Selection for breeding value
  - 1.0 Selection for Mendelian-sampling term

See Grundy et al. (1998) JABG 115:39-51 and Wu & Schaeffer (2000) JABG 117:361-374 for details

- 11) (a) *RunBlup* must be 0:1 when *sex\_code* 0:6, *selection\_method* 'truncation', and *selection\_criterion* 'polyblup', 'genomicblup', 'ibdblup', or 'gas'
- (b) *RunBlup* is not used when *sex\_code* 7, *selection\_method* 'select\_all' or 'threshold', or *selection\_criterion* 'tbv', 'random', 'phenothreshold', or 'phenoweights'. It is set to 0.
- (c) *RunBlup* must be 1 in the first selection stage(s) where *selection\_criterion* 'polyblup', 'genomicblup', or 'gas'. The first selection stage(s) can be a EVA-selection stage(s).
- (d) When *RunBlup* 1, *sex\_code* 0:6, *selection\_method* 'truncation', and *selection\_criterion* 'polyblup', 'ibdblup', or 'gas', and

selection stage not the first selection stage where *selection\_criterion* 'polyblup', 'genomicblup', or 'gas', BLUP-breeding values are only estimated if a phenotypic observation(s) has been realised. If BLUP-breeding values have been estimated previously, they are only re-estimated when phenotypic observations have been realised since the previous estimation.

- (e) When *RunBlup* 1, *sex\_code* 0:6, *selection\_method* 'truncation', and *selection\_criterion* 'genomicblup', BLUP-breeding values are only estimated if a phenotypic observation(s) has been realised and plants have been genotyped. If genomic-BLUP breeding values have been estimated previously, they are only re-estimated when phenotypic observations have been realised or additional plants have been genotyped since the previous estimation.
- 12) (a) *germ\_plasm*>0 when *sex\_code* 1:6 and *destiny\_sel* 2, 12, 26, 126, or 127
- (b) If an plant is reselected to have germ plasm stored within a time step or during a subsequent time step, the new number of germ plasm is added to the number currently stored for the plant. The exception is males and females in the base population.
- (c) When *live\_status* 0 or 2, *destiny\_sel* 1, and deceased plants with stored germ plasm are selected for reproduction, the number of stored germ plasm for each selected plant is reduced by the number of germ plasm used for reproduction. The number of germ plasm used for reproduction is *repro\_capacity* when the number of stored germ plasm is greater than or equal to *repro\_capacity*. Otherwise, it is the number of stored germ plasm.
- 13) *SelectionRule* can be used when *sex\_code* 0:6 and *selection\_method* 'truncation'
- 14) When the options of only using some selection groups in any particular time step, the user is extra responsible that all selection groups fits, as there are no internal checks to control irregularities across clusters of selection groups.

## &PHENOTHRESHOLDS

```
nPhenotypicThresholds=nPhenotypicThresholds
phenotypicThresholds=stage observation minThreshold maxThreshold /
```

NB! *nPhenotypicThresholds* must equal the number of selection stages with selection criterion 'phenothreshold' in namelist &SELECTION, variable *selection\_scheme*

The number of stages specified in *phenotypicThresholds* must equal *nPhenotypicThresholds*

**\*\*Task\*\***

Specify thresholds for phenotypic selection with associated thresholds

**\*\*Properties of names\*\***

*nPhenotypicThresholds* Definition: Number of selection stages where phenotypic selection with associated thresholds is applied

Type: Integer

Options: 1≤*nPhenotypicThresholds*≤*selection\_groups*

Default: 0

*stage*

Definition: Selection stage

Type: Integer

Options: 1≤*stage*≤*selection\_groups*

Default: *stage* must be specified

*observation* Definition: Observation number; observation to which phenotypic thresholds are applied  
Type: Integer  
Options:  $1 \leq \textit{observation} \leq \textit{nobs} + \textit{nCombinedObs}$   
Default: *observation* must be specified

*minThreshold* Definition: Minimum threshold; plants with an phenotypic value smaller than *minThreshold* are culled  
Type: Real  
Options:  $\geq -999.0$   
-9999.0 if minimum threshold not applied  
Default: *minThreshold* must be specified

*maxThreshold* Definition: Maximum threshold; plants with an phenotypic value greater than *maxThreshold* are culled  
Type: Real  
Options:  $\geq -999.0$   
-9999.0 if maximum threshold not applied  
Default: *maxThreshold* must be specified

**\*\*Additional information\*\***

- 1) *selection\_criterion* in namelist &SELECTION, variable *selection\_scheme* must be 'phenothreshold' at each *stage* specified in variable *phenotypicThresholds*
- 2) Each *stage* can only be represented once in *phenotypicThresholds*
- 3) Both *minThreshold* and *maxThreshold* cannot be -999.0 at the same *stage*

**&RULES**

SelectionRules=  
*rule SireTimeTotal DamTimeTotal FamilyTimeTotal SireMatingsTimeTotal*  
*DamMatingsTimeTotal SireTotal DamTotal FamilyTotal SireMatingsTotal*  
*DamMatingsTotal reselect*

*SireTimeTotals=SireTimeTotals*  
*DamTimeTotals=DamTimeTotals*  
*FamilyTimeTotals=FamilyTimeTotals*  
*SireMatingsTimeTotals=SireMatingsTimeTotals*  
*DamMatingsTimeTotals=DamMatingsTimeTotals*  
*SireTotals=SireTotals*  
*DamTotals=DamTotals*  
*FamilyTotals=FamilyTotals*  
*SireMatingsTotals=SireMatingsTotals*  
*DamMatingsTotals=DamMatingsTotals /*

NB! Number of selection rules provided in *SelectionRules* must equal the number of different rules specified by *SelectionRule* in namelist &SELECTION, variable *selection\_scheme*

**\*\*Task\*\***

Specify selection rule(s) for truncation selection.

**\*\*Properties of names\*\***

The following variables are single integers

*rule* Definition: Selection-rule number; must correspond to a selection rule in namelist &SELECTION, variable *SelectionRule*  
Type: Integer  
Options: ≥1  
Default: *rule* must be specified

*SireTimeTotal* Definition: Specifies which element of *SireTimeTotals* contains the maximum number of offspring that can be selected from each sire during each time step  
Type: Integer  
Options:  
≥1 Element of *SireTimeTotals* that contains the maximum number of offspring that can be selected from each sire during each time step  
-9 Maximum number of offspring not applicable  
Default: *SireTimeTotal* must be specified

*DamTimeTotal* Definition: Specifies which element of *DamTimeTotals* contains the maximum number of offspring that can be selected from each dam during each time step  
Type: Integer  
Options:  
≥1 Element of *DamTimeTotals* that contains the maximum number of offspring that can be selected from each dam during each time step  
-9 Maximum number of offspring not applicable  
Default: *DamTimeTotal* must be specified

*FamilyTimeTotal* Definition: Specifies which element of *FamilyTimeTotals* contains the maximum number of offspring that can be selected from each full-sib family during each time step  
Type: Integer  
Options:  
≥1 Element of *FamilyTimeTotals* that contains the maximum number of offspring that can be selected from each full-sib family during each time step  
-9 Maximum number of offspring not applicable  
Default: *FamilyTimeTotal* must be specified

*SireMatingsTimeTotal* Definition: Specifies which element of *SireMatingsTimeTotals* contains the maximum number of matings for each sire during each time step  
Type: Integer  
Options:  
≥1 Element of *SireMatingsTimeTotals* that contains the maximum number of matings for each sire during each time step  
-9 Maximum number of matings not applicable  
Default: *SireMatingsTimeTotals* must be specified

*DamMatingsTimeTotal* Definition: Specifies which element of *DamMatingsTimeTotals* contains the maximum number of matings for each dam during each time step  
Type: Integer  
Options:  
>1 Element of *DamMatingsTimeTotals* that contains the maximum number of matings for each dam during each time step  
-9 Maximum number of matings not applicable  
Default: *DamMatingsTimeTotals* must be specified

*SireTotal* Definition: Specifies which element of *SireTotals* contains the maximum number of offspring that can be selected from each sire across time steps  
Type: Integer  
Options:  
>1 Element of *SireTotals* that contains the maximum number of offspring that can be selected from each sire  
-9 Maximum number of offspring not applicable  
Default: *SireTotal* must be specified

*DamTotal* Definition: Specifies which element of *DamTotals* contains the maximum number of offspring that can be selected from each dam across time steps  
Type: Integer  
Options:  
>1 Element of *DamTotals* that contains the maximum number of offspring that can be selected from each dam  
-9 Maximum number of offspring not applicable  
Default: *DamTotal* must be specified

*FamilyTotal* Definition: Specifies which element of *FamilyTotals* contains the maximum number of offspring that can be selected from each full-sib family across time steps  
Type: Integer  
Options:  
>1 Element of *FamilyTotals* that contains the maximum number of offspring that can be selected from each full-sib family  
-9 Maximum number of offspring not applicable  
Default: *FamilyTotal* must be specified

*SireMatingsTotal* Definition: Specifies which element of *SireMatingsTotals* contains the maximum number of matings for each sire across time steps  
Type: Integer  
Options:  
>1 Element of *SireMatingsTotals* that contains the maximum number of matings for each sire  
-9 Maximum number of matings not applicable  
Default: *SireMatingsTotals* must be specified

*DamMatingsTotal* Definition: Specifies which element of *DamMatingsTotals* contains the maximum number of matings for each dam across time steps  
Type: Integer  
Options:  
    ≥1 Element of *DamMatingsTotals* that contains the maximum number of matings for each dam  
    -9 Maximum number of matings not applicable  
Default: *DamMatingsTotals* must be specified

*reselect* Definition: Specifies whether the highest-ranking candidates that do not fulfil the rule(s) are selected when there are insufficient selection candidates to fulfil the selection rule(s)  
Type: Integer  
Options:  
    0 Highest-ranking candidates are not selected  
    1 Highest-ranking candidates are selected  
Default: *reselect* must be specified

The following variables are arrays of integers

*SireTimeTotals* Definition: Array that contains the maximum number(s) of offspring that can be selected from each sire during each time step  
Type: Integer  
Dimension: 1 x maximum number specified for *SireTimeTotal* across rules  
Options:  
    ≥1 For each element specified in *SireTimeTotal*  
    0 For each element not specified in *SireTimeTotal*  
Default: *SireTimeTotals* must be specified when *SireTimeTotal* ≥ 1 for any rule

*DamTimeTotals* Definition: Array that contains the maximum number(s) of offspring that can be selected from each dam during each time step  
Type: Integer  
Dimension: 1 x maximum number specified for *DamTimeTotal* across rules  
Options:  
    ≥1 For each element specified in *DamTimeTotal*  
    0 For each element not specified in *DamTimeTotal*  
Default: *DamTimeTotals* must be specified when *DamTimeTotal* ≥ 1 for any rule

*FamilyTimeTotals* Definition: Array that contains the maximum number(s) of offspring that can be selected from each full-sib family during each time step  
Type: Integer  
Dimension: 1 x maximum number specified for *FamilyTimeTotal* across rules  
Options:  
    ≥1 For each element specified in *FamilyTimeTotal*  
    0 For each element not specified in *FamilyTimeTotal*

Default: *FamilyTimeTotals* must be specified when  
*FamilyTimeTotal* ≥ 1 for any rule

*SireMatingsTimeTotals* Definition: Array that contains the maximum number(s) of matings for each sire during each time step  
Type: Integer  
Dimension: 1 x maximum number specified for *SireMatingsTimeTotal* across rules  
Options:  
    ≥ 1 For each element specified in *SireMatingsTimeTotal*  
    0 For each element not specified in *SireMatingsTimeTotal*  
Default: *SireMatingsTimeTotals* must be specified when  
*SireMatingsTimeTotal* ≥ 1 for any rule

*DamMatingsTimeTotals* Definition: Array that contains the maximum number(s) of matings for each dam during each time step  
Type: Integer  
Dimension: 1 x maximum number specified for *DamMatingsTimeTotal* across rules  
Options:  
    ≥ 1 For each element specified in *DamMatingsTimeTotal*  
    0 For each element not specified in *DamMatingsTimeTotal*  
Default: *DamMatingsTimeTotals* must be specified when  
*DamMatingsTimeTotal* ≥ 1 for any rule

*SireTotals* Definition: Array that contains the maximum number(s) of offspring that can be selected from each sire across time steps  
Type: Integer  
Dimension: 1 x maximum number specified for *SireTotal* across rules  
Options:  
    ≥ 1 For each element specified in *SireTotal*  
    0 For each element not specified in *SireTotal*  
Default: *SireTotals* must be specified when *SireTotal* ≥ 1 for any rule

*DamTotals* Definition: Array that contains the maximum number(s) of offspring that can be selected from each dam across time steps  
Type: Integer  
Dimension: 1 x maximum number specified for *DamTotal* across rules  
Options:  
    ≥ 1 For each element specified in *DamTotal*  
    0 For each element not specified in *DamTotal*  
Default: *DamTotals* must be specified when  
*DamTotal* ≥ 1 for any rule

*FamilyTotals* Definition: Array that contains the maximum number(s) of offspring that can be selected from each full-sib family across time steps  
Type: Integer  
Dimension: 1 x maximum number specified for *FamilyTotal* across rules  
Options:

≥1 For each element specified in *FamilyTotal*  
 0 For each element not specified in *FamilyTotal*  
 Default: *FamilyTotals* must be specified when  
*FamilyTotal* ≥1 for any rule

*SireMatingsTotals* Definition: Array that contains the maximum number(s) of matings for each sire across time steps  
 Type: Integer  
 Dimension: 1 x maximum number specified for *SireMatingsTotal* across rules  
 Options:  
 ≥1 For each element specified in *SireMatingsTotal*  
 0 For each element not specified in *SireMatingsTotal*  
 Default: *SireMatingsTotals* must be specified when *SireMatingsTotal* ≥1 for any rule

*DamMatingsTotals* Definition: Array that contains the maximum number(s) of matings for each dam across time steps  
 Type: Integer  
 Dimension: 1 x maximum number specified for *DamMatingsTotal* across rules  
 Options:  
 ≥1 For each element specified in *DamMatingsTotal*  
 0 For each element not specified in *DamMatingsTotal*  
 Default: *DamMatingsTotals* must be specified when *DamMatingsTotal* ≥1 for any rule

**\*\*Additional information\*\***

- 1) Selection rules do not apply to plants in the base population
- 2) reselect
  - (a) When *reselect* 0 and an insufficient number of selection candidates fulfil the selection rule(s), the breeding program continues with fewer selected candidates from the corresponding selection stage
  - (b) When *reselect* 1 and an insufficient number of selection candidates fulfil the selection rule(s), the highest-ranking candidates that do not fulfil the rule(s) are selected until the required number of plants are selected. If there is still an insufficient number of selection candidates, the breeding program continues with fewer selected candidates for the corresponding selection stage.

## &EVA

EvaSelection=  
*stage MalesSelected FemalesSelected MaleSelCrit MaleRunBlup MaleDestinySel MaleTestHerd MaleDestinyUnsel MaleMaxMatings MaleGermplasm FemaleSelCrit FemaleRunBlup FemaleDestinySel FemaleTestHerd FemaleDestinyUnsel FemaleMaxMatings FemaleGermplasm relationshipMatrix startGenRelTime FutMaleBreeders FutFemaleBreeders nTracedGen birthGroups nMatings LitterSize SexRatio /*

**\*\*Task\*\***

Input for EVA-selection. Namelist is read when *sex\_code* 7 in any selection stage of namelist &SELECTION, variable *selection\_scheme*.

**\*\*Properties of names\*\***

*stage* Definition: Stage of selection; must correspond to a selection stage in namelist &SELECTION, variable selection\_scheme with sex\_code 7  
Type: Integer  
Options: 2≤*stage*≤*selection\_groups*  
Default: *stage* must be specified

*MalesSelected* Definition: Males EVA-selected  
Type: Character  
Options:  
    yes Males are selected  
    no Males are not selected  
Default: *MalesSelected* must be specified

*FemalesSelected* Definition: Females EVA-selected  
Type: Character  
Options:  
    yes Females are selected  
    no Females are not selected  
Default: *FemalesSelected* must be specified.

*MaleSelCrit* Definition: Criterion used to select males  
Type: Character  
Options:  
    tbv True breeding value  
    null No selection criterion  
    phenoweight Phenotypic selection with observations weighted  
    polyblup Polygenic-BLUP breeding value  
    genomicblup Genomic-BLUP breeding value  
    ibdblup IBD-BLUP breeding value  
    gas GAS-breeding value  
    bayesp BayesP-breeding values  
Default: *MaleSelCrit* must be specified

When bayesP, *GeneticModel* must be 'genomic', nebv==1, and genotyped\_at\_birth)/='yes'

*MaleRunBlup* Definition: Estimate BLUP breeding values  
Type: Integer  
Options:  
    0 Breeding values are not estimated  
    1 Breeding values are estimated  
Default: *MaleRunBlup* must be specified

*MaleDestinySel* Definition: Destiny of selected males  
Type: Integer  
Options:  
    0 Selected males are left alive  
    1 Selected males are reproduced (mated)  
    2 Selected males have germ plasm stored  
    3 Selected males are genotyped  
    4 Selected males are transferred to another (test) herd; the herd is specified by *MaleTestHerd*  
    6 Selected males have DYD sampled  
    8 Selected males have phenotypic observation(s)

- realised at current selection stage
- 12 Selected males are reproduced and have germ plasm stored
- 14 Selected males are reproduced after transfer to another (test) herd; the herd is specified by *MaleTestHerd*
- 16 Selected males are reproduced and have DYD sampled
- 26 Selected males have germ plasm stored and DYD sampled
- 126 Selected males are reproduced, have germ plasm stored, and DYD sampled
- 90 Selected males are tagged as candidates to be left alive
- 91 Selected males are tagged as candidates to reproduce (mate)
- 92 Selected males are tagged as candidates to have germ plasm stored
- 93 Selected males are tagged as candidates for genotyping
- 94 Selected males are tagged as candidates for transfer to another (test) herd
- 96 Selected males are tagged as candidates to have DYD sampled
- 98 Selected males are tagged as candidates to have a phenotypic observation(s) realised at a subsequent selection stage
- 99 Selected males are tagged as candidates to be culled voluntarily
- 912 Selected males are tagged as candidates to reproduce and have germ plasm stored
- 914 Selected males are tagged as candidates to reproduce after transfer to another (test) herd
- 916 Selected males are tagged as candidates to reproduce and have DYD sampled
- 926 Selected males are tagged as candidates to have germ plasm stored and DYD sampled
- 9126 Selected males are tagged as candidates to reproduce, have germ plasm stored, and DYD sampled

Default: *MaleDestinySel* must be specified

*MaleTestHerd*

Definition: Test herd to which selected males are transferred

Type: Integer

Options:  $1 \leq \text{MaleTestHerd} \leq n_{\text{herd}}$

Default: *MaleTestHerd* must be specified

*MaleDestinyUnsel*

Definition: Destiny of unselected males

Type: Integer

Options:

0 Males are culled

1 Males are left alive

Default: *MaleDestinyUnsel* must be specified

*MaleMaxMatings*

Definition: Maximum number of matings allocated to selected males; male reproductive capacity

Type: Integer  
Options:  $\geq 1$   
Default: *MaleMaxMatings* must be specified

*MaleGermplasm*

Definition: Number of units of germplasm stored for selected males

Type: Integer

Options:

$\geq 1$  Number of units stored for each selected male

-1 Number of units stored for each selected male is set to the number of matings allocated to each male

Default: *MaleGermplasm* must be specified

*FemaleSelCrit*

Definition: Criterion used to select females

Type: Character

Options:

tbv True breeding value

null No selection criterion

phenoweight Phenotypic selection with observations weighted

polyblup Polygenic-BLUP breeding value

genomicblup Genomic-BLUP breeding value

ibdblup IBD-BLUP breeding value

gas GAS-breeding value

bayesp BayesP-breeding values

Default: *FemaleSelCrit* must be specified

When bayesP, *GeneticModel* must be 'genomic', nebv==1, and genotyped\_at\_birth)/='yes'

*FemaleRunBlup*

Definition: Estimate BLUP breeding values

Type: Integer

Options:

0 Breeding values are not estimated

1 Breeding values are estimated

Default: *FemaleRunBlup* must be specified

*FemaleDestinySel*

Definition: Destiny of selected females

Type: Integer

Options:

0 Selected females are left alive

1 Selected females are reproduced (mated)

2 Selected females have germ plasm stored

3 Selected females are genotyped

4 Selected females are transferred to another (test) herd; the herd is specified by *FemaleTestHerd*

8 Selected females have phenotypic observation(s) realised at current selection stage

12 Selected females are reproduced and have germ plasm stored

14 Selected females are reproduced after transfer to another (test) herd; the herd is specified by *FemaleTestHerd*

17 Selected females are reproduced as bull-dams

127 Selected candidates are reproduced as bull-dams and have germ plasm stored

147 Selected females are reproduced as bull-dams

after transfer to another (test) herd; the herd is specified by *FemaleTestHerd*

90 Selected females are tagged as candidates to be left alive

91 Selected females are tagged as candidates to reproduce (mate)

92 Selected females are tagged as candidates to have germ plasm stored

93 Selected females are tagged as candidates for genotyping

94 Selected females are tagged as candidates for transfer to another (test) herd

98 Selected females are tagged as candidates to have a phenotypic observation(s) realised at a subsequent selection stage

99 Selected females are tagged as candidates to be culled voluntarily

912 Selected females are tagged as candidates to reproduce and have germ plasm stored

914 Selected females are tagged as candidates to reproduce after transfer to another (test) herd

917 Selected females are tagged as candidates to reproduce as bull-dams

9127 Selected females are tagged as candidates to reproduce as bull-dams and have germ plasm stored

9147 Selected females are tagged as candidates to reproduce as bull-dams after transfer to another (test) herd

Default: *FemaleDestinySel* must be specified

*FemaleTestHerd* Definition: Test herd to which selected females are transferred

Type: Integer

Options:  $1 \leq \text{FemaleTestHerd} \leq \text{nherd}$

Default: *FemaleTestHerd* must be specified

*FemaleDestinyUnsel* Definition: Destiny of unselected females

Type: Integer

Options:

- 0 Females are culled
- 1 Females are left alive

Default: *FemaleDestinyUnsel* must be specified

*FemaleMaxMatings* Definition: Maximum number of matings allocated to selected females; female reproductive capacity

Type: Integer

Options:  $\geq 1$

Default: *FemaleMaxMatings* must be specified

*FemaleGermplasm* Definition: Number of units of germplasm stored for selected females

Type: Integer

Options:

- $\geq 1$  Number of units stored for each selected female
- 1 Number of units stored for each selected female is set

to the number of matings allocated to each female  
Default: *FemaleGermplasm* must be specified

- relationshipMatrix* Definition: Method used to construct relationship matrix  
Type: Character  
Options:  
    pedigree Matrix constructed with pedigree  
    genomic Matrix constructed with markers and pedigree  
    ibs Matric constructed with IBS-markers  
    ibd Matrix constructed with IBD-markers  
  
Default: *RelationshipMatrix* must be specified
- FutMaleBreeders* Definition: Young males that are potential breeders at later  
time steps are included in the relationship  
matrix. All males younger than the maximum  
reproductive age of living males are included.  
Type: Character  
Options:  
    none Non-candidate males not included  
    herd Only non-candidate males from same herd(s)  
as candidates included  
    population All non-candidate males included  
Default: *FutMaleBreeders* must be specified
- FutFemaleBreeders* Definition: Young females that are potential breeders at  
later time steps are included in the  
relationship matrix. All females younger than  
the maximum reproductive age of living females  
are included.  
Type: Character  
Options:  
    none Non-candidate females not included  
    herd Only non-candidate females from same herd(s)  
as candidates included  
    population All non-candidate females included  
Default: *FutFemaleBreeders* must be specified
- birthGroups* Definition: Parameter used to allocate plants into birth  
groups when generating EVA-input data. Plants  
are allocated to birth groups as  
 $\text{abs}(\text{minval}(\text{pop}(\cdot)\% \text{birth})) +$   
 $\text{floor}(\text{real}(\text{pop}(\text{id})\% \text{birth}) /$   
 $(\text{birthGroups} + \text{gestation\_length}))$   
Type: Integer  
Options:  $1 \leq \text{birthGroups} \leq \text{rAge}_{\text{min}}$ , where  $\text{rAge}_{\text{min}}$  is the minimum  
reproductive age of EVA-selection candidates  
Default: *birthGroups* must be specified
- nMatings* Definition: Total number of matings  
Type: Integer  
Options:  $\geq 1$   
Default: *nMating* must be specified
- LitterSize* Definition: Number of offspring per mating  
Type: Integer  
Options:  $\geq 1$

Default: *LitterSize* must be specified

*SexRatio* Definition: Probability of an offspring being a female  
Type: Real  
Options:  $0.0 \leq \textit{SexRatio} \leq 1.0$   
Default: *SexRatio* must be specified

**\*\*Relation to subsequent namelists\*\***

&EVAPARAMETERS

Namelist &EVAPARAMETERS is required when EVA-selection. The number of stages in namelist &EVAPARAMETERS, variable parameters must equal the number of stages in namelist &EVA, variable *EvaSelection*.

&EVAPHENOWEIGHT

Namelist &EVAPHENOWEIGHTS is required when *MaleSelCrit* and/or *FemaleSelCrit* 'phenoweight' in any eva-selection stage of namelist &EVA, variable *EvaSelection*

&IBDBLUPPARAMETERS

&EVAGENOMICRELATIONSHIP

Namelist &EVAGENOMICRELATIONSHIPS is required when *relationshipMatrix* 'genomic' in any eva-selection stage of namelist &EVA, variable *EvaSelection*. The number of stages in namelist &EVAGENOMICRELATIONSHIPS, variable *genomicRelationships* must equal the number of stages in namelist &EVA, variable *relationshipMatrix* 'genomic'.

&EVAIBDRELATIONSHIPPARAMETERS

&DMUPARAMETERS

Namelist &DMUPARAMETERS is required when *selection\_criterion* 'polyblup', 'genomicblup', 'ibdblup', or 'gas' in any eva-selection stage of namelist &EVA, variable *EvaSelection*

&GAS\_PARAMETERS

Namelist &GAS\_PARAMETERS is required when *GeneticModel* 'qtl' in namelist &CONTROLPARAMETERS and *MaleSelCrit* and/or *FemaleSelCrit* 'gas' in any EVA-selection stage of namelist &EVA, variable *EvaSelection*

&BAYESPPARAMETERS

**\*\*Additional information\*\***

- 1) Only plants tagged for EVA-selection are selection candidates. That is, plants tagged in selection stages prior to the EVA-selection stage and, if there is more than one EVA-selection stage, after the previous EVA-selection stage. Plants are tagged for EVA selection in namelist *selection*, variable *selection\_scheme*.
- 2) EVA-selection tags are removed from all plants following a stage of EVA selection
- 3) All variables in namelist *eva*, variable *EvaSelection* are read and, therefore, must be specified. However, there are cases where some variables are not used. The most striking case is when *MalesSelected* or *FemalesSelected* set to 'no'. Other cases are when selected plants are not destined to be mated. In these cases, variables, such as *Littersize* and *SexRatio* are not used. For variables that are not used, the input provided is irrelevant. However, for clarity, we recommend providing 0 for integer

variables and 0.0 for *SexRatio* (the only real).

- 4) Variables that are always used are *stage*, *MalesSelected*, *FemalesSelected*, *FutMaleBreeders*, *FutFemaleBreeders*, *nTracedGen*, *nMatings*, and *EvaParameterFile*. The use of all other variables depends on the options specified for these and the other variables in namelist *eva*.
- 5) *stage* must correspond to a selection stage in namelist &SELECTION, variable *selection\_scheme* with *sex\_code* 7
- 6) (a) Either *MalesSelected* or *FemalesSelected*, or both, must be 'yes'. That is, EVA selection is not carried out when both *MalesSelected* and *FemalesSelected* are 'no'. In this case, the program stops.
  - (b) (i) When *MalesSelected* 'yes', *MaleSelCrit*, *MaleDestinySel*, *MaleDestinyUnsel*, and *MaleMaxMatings* are used and must be specified with valid options
  - (ii) When *FemalesSelected* 'yes', *FemaleSelCrit*, *FemaleDestinySel*, *FemaleDestinyUnsel*, and *FemaleMaxMatings* are used and must be specified with valid options
  - (c) (i) When *MalesSelected* 'no', *MaleSelCrit*, *MaleDestinySel*, *MaleDestinyUnsel*, *MaleMaxMatings*, *MaleRunBlup*, *MaleTestHerd*, and *MaleGermplasm* are not used. *MaleSelCrit* is set to ' ' and *MaleDestinySel*, *MaleDestinyUnsel*, *MaleMaxMatings*, *MaleRunBlup*, *MaleTestHerd*, and *MaleGermplasm*, are set to 0.
  - (ii) When *FemalesSelected* 'no', *FemaleSelCrit*, *FemaleDestinySel*, *FemaleDestinyUnsel*, *FemaleMaxMatings*, *FemaleRunBlup*, *FemaleTestHerd*, *FemaleGermplasm*, *Littersize*, and *SexRatio* are not used. *FemaleSelCrit* is set to ' ', *FemaleDestinySel*, *FemaleDestinyUnsel*, *FemaleMaxMatings*, *FemaleRunBlup*, *FemaleTestHerd*, *FemaleGermplasm*, and *Littersize* are set to 0, and *SexRatio* is set to 0.0.
- 7) (a) (i) When *MalesSelected* 'no', males are not EVA-selected. Females are EVA-selected while ignoring the genetic relationships of males.
  - (ii) When *FemalesSelected* 'no', females are not EVA-selected. Males are EVA-selected while ignoring the genetic relationships of females.(b) Setting *MalesSelected* or *FemalesSelected* to 'no' is different from setting *MalesSelected* and/or *FemalesSelected* to 'yes' and *MaleSelCrit* and/or *FemaleSelCrit* to 'null' (see information point 19)

Information points 8) to 16) assume that *MalesSelected* 'yes' and/or *FemalesSelected* 'yes'

phenoweights

- 8) (a) *MaleSelCrit* and *FemaleSelCrit* must be 'tbv', 'null', 'polyblup', 'genomicblup', 'ibdblup', or 'gas'
- (b) When *MaleSelCrit* and/or *FemaleSelCrit* 'tbv', economic weight(s) provided in namelist &MATRICES, variable *economic\_weight* in are used to weight the true breeding values for each trait  
When *MaleSelCrit* and/or *FemaleSelCrit* 'polyblup', 'genomicblup', 'ibdblup', or 'gas', economic weight(s) provided in namelist &MATRICES, variable *economic\_weight* are used to weight the estimated breeding values for each trait
- (c) When *GeneticModel* 'polygenic', *selection\_criterion* cannot be 'genomicblup', 'ibdblup', or 'gas' at any selection stage
- (d) When *GeneticModel* 'qtl', *selection\_criterion* cannot be 'genomicblup' or 'ibdblup' [should be ok with 'ibdblup?]
- (e) When *GeneticModel* 'genomic', both 'genomicblup' and 'gas' cannot be used as selection criterion in the same simulated breeding scheme. That is, both

'genomicblup' and 'gas' cannot be specified as *selection\_criterion* in *namelist &selection*, variable *selection\_scheme*, and/or as *MaleSelCrit* or *FemaleSelCrit* in any EVA-selection stage of *namelist &EVA*, variable *EvaSelection*.

When *bayesP*, *GeneticModel* must be 'genomic', *nebv*=1, and *genotyped\_at\_birth*)/'=yes'

- 9) (a) *MaleRunBlup* must be 0:1 when *MaleSelCrit* 'polyblup', 'genomicblup', 'ibdblup', or 'gas'; *FemaleRunBlup* must be 0:1 when *FemaleSelCrit* 'polyblup', 'genomicblup', 'ibdblup', or 'gas'
  - (b) *MaleRunBlup* is not used when *MaleSelCrit* 'tbv' or 'null'; *FemaleRunBlup* is not used when *FemaleSelCrit* 'tbv' or 'null'. They are set to 0.
  - (c) *MaleRunBlup* and/or *FemaleRunBlup* must be 1 if the EVA-selection stage is the first selection stage where *selection\_criterion* 'polyblup', 'genomicblup', or 'gas'. The first selection stage(s) can be a truncation-selection stage(s).
  - (d) When *MaleRunBlup* and/or *FemaleRunBlup* 1 and *selection\_criterion* 'polyblup', 'ibdblup', or 'gas', and selection stage not the first selection stage where *selection\_criterion* 'polyblup', 'genomicblup', or 'gas', BLUP-breeding values are only estimated if a phenotypic observation(s) has been realised. If BLUP-breeding values have been estimated previously, they are only re-estimated when phenotypic observations have been realised since the previous estimation.
  - (e) When *MaleRunBlup* and/or *FemaleRunBlup* 1 and *selection\_criterion* 'genomicblup', BLUP-breeding values are only estimated if a phenotypic observation(s) has been realised and plants have been genotyped. If genomic-BLUP breeding values have been estimated previously, they are only re-estimated if phenotypic observations have been realised or additional plants have been genotyped since the previous estimation.
- 10) (a) When males that are not alive can be amongst those males tagged for EVA selection (i.e., *live\_status* 0 or 2 in *namelist &SELECTION*, variable *selection\_scheme*),
    - (i) *MaleDestinySel* must be 1 or 91,
    - (ii) When *MaleDestinySel* 1, and a deceased plant with stored germ plasm is selected for reproduction, the plant's reproductive capacity is defined as follows. If the number of stored germ plasm is greater or equal to *MaleMaxMatings*, the plant's reproductive capacity is *MaleMaxMatings*. If, however, the number of stored germ plasm is less than *MaleMaxMatings*, the plant's reproductive capacity is the number of stored germ plasm. The consequence of this is that the total number of male matings available may be less than *nMatings*.
  - (b) 10)(a) applies to females
- 11) Females tagged for EVA selection can be either normal females or bull dams. That is, both normal females (*sex\_code* 2 or 6 in *namelist &SELECTION*, variable *selection\_scheme*) and bull dams (*sex\_code* 4) cannot be selected for EVA selection.
  - 12) (a) *MaleDestinySel* or *FemaleDestinySel* cannot be 3 (genotyping) at any EVA-selection stage when *MaleSelCrit* or *FemaleSelCrit* 'gas' at any EVA-selection stage or *selection\_criterion* 'gas' at any selection stage of *namelist &SELECTION*, variable *selection\_scheme*.
  - (b) *MaleDestinySel* can only be 4, 14, 94, and 914 [transfer to another (test) herd] when *nherd*>1; *FemaleDestinySel* can only be 4, 14, 147, 94, 914, and 9147

- (c) Plants can be tagged with a view to selection with in *sex\_code* 5 or 6 (namelist &SELECTION, variable *selection\_scheme*) at a subsequent selection stage during the same time step. That is, *MaleDestinySel* can be 90, 91, 92, 93, 94, 96, 98, 99, 912, 914, 916, 926, and 9126; *FemaleDestinySel* can be 91, 92, 93, 94, 98, 99, 912, 914, 917, 9127, and 9147.
  - (d) Plants cannot be tagged for EVA selection. That is, *MaleDestinySel* and *FemaleDestinySel* cannot be 95.
  - (e) Males cannot be bull-dams. That is, *destiny\_sel* cannot be 17, 127, 147, 917, 9127, or 9147 when *sex\_code* 0, 1, 3, or 5.
  - (f) Females cannot have DYD sampled. That is, *FemaleDestinySel* cannot be 6, 16, 26, 126, 96, 916, 926, or 9126.
  - (j) There is only a limited number of valid destinies for selected bull dams. They are *FemaleDestinySel* 0, 1, 2, 3, 8, and 12.
  - (k) Non-reproductive males cannot be among the candidates for selection when *MaleDestinySel* includes reproduction. That is, non-reproductive males are not candidates when *MaleDestinySel* 1, 12, 14, 16, 126, 91, 912, 914, 916, 9126. Non-reproductive females cannot be among the candidates for selection when *FemaleDestinySel* includes reproduction. They are not candidates when *FemaleDestinySel* 1, 12, 14, 17, 127, 147, 91, 912, 914, 917, 9127, or 9147.
  - (f) Non-reproductive plants are not candidates for selection when *destiny\_sel* includes reproduction. That is, non-reproductive males are not candidates when *destiny\_sel* 1, 12, 14, 16, 126, 91, 912, 914, 916, 9126. Non-reproductive females are not candidates when *destiny\_sel* 1, 12, 14, 17, 127, 147, 91, 912, 914, 917, 9127, or 9147.
  - (g) Non-reproductive plants are not candidates for EVA-selection when *destiny* for selection in the subsequent EVA-selection stage includes reproduction. That is, non-reproductive males are not candidates when *MaleDestinySel* in namelist &EVA, variable *EvaSelection* 1, 12, 14, 16, 126, 91, 912, 914, 916, 9126. Non-reproductive females are not candidates when *FemaleDestinySel* in namelist &EVA, variable *EvaSelection* 1, 12, 14, 17, 127, 147, 91, 912, 914, 917, 9127, or 9147.
- 13) (a) *MaleTestHerd* must be specified when *MaleDestinySel* includes transfer to another (test) herd. That is, *MaleDestinySel* 4 or 14.
- (b) *FemaleTestHerd* must be specified when *FemaleDestinySel* includes transfer to another (test) herd. That is, *FemaleDestinySel* 4, 14, or 147.
- 14) (a) *MaleMaxMatings*>0
- (b) *FemaleMaxMatings*>0
- 15) (a) *MaleGermplasm*>0 or -1 when *MaleDestinySel* 2, 12, 26, or 126
- (b) *FemaleGermplasm*>0 or -1 when *FemaleDestinySel* 2, 12, or 127
- (c) If an plant is reselected to have germ plasm stored within a time step or during a subsequent time step, the new number of germ plasm is added to the number currently stored for the plant. The exception is males and females in the base population.
- (d) When plants that are not alive can be amongst those tagged for EVA selection (i.e., *live\_status* 0 or 2 in namelist &SELECTION, variable *selection\_scheme*), *destiny\_sel* 1, and deceased plants with stored germ plasm are selected for reproduction, the number of stored germ plasm for each selected plant is reduced by the number of germ plasm used for reproduction. The number of of germ plasm used for reproduction is the number of matings allocated to each male or female.
- 16) *LitterSize*>0 and  $0.0 \leq \text{SexRatio} \leq 1.0$  when the destiny for selected females includes reproduction. That is, *FemaleDestinySel* 1, 2, 14, 17, 127, or 147.

- 17) *relationshipMatrix* can be 'pedigree', 'genomic', 'ibs', or 'ibd' when *GeneticModel* 'genomic' in *namelist &CONTROLPARAMETERS*. It can only be 'pedigree' when *GeneticModel* 'polygenic' or 'qtl'. [Should it be possible to use 'ibd' with *GeneticModel* 'qtl']. Genotyping is considered with *relationshipMatrix* 'genomic'; it is ignored with 'ibs' and 'ibd'. It is ignored with 'ibd' because this is a theoretical situation; it is ignored with 'ibs' because we have not implemented a way to build relationship matrices for a mixture of genotyped and non-genotyped plants.

If *relationshipMatrix* 'genomic' and no plants have been genotyped, *relationshipMatrix* 'pedigree' is used. Any other problems will be detected when constructing genomic-relationship matrices.

- 18) *FutMaleBreeders* and *FutFemaleBreeders* must be 'none', 'herd', or 'population'
- 19) *nTracedGen* is applied to increase the speed of EVA-calculations. It reduces the size of the relationship matrix, the main restricter of speed.
- 20) (a) *birthGroups* can determine the speed of EVA-calculations. The speed is quickest when *birthGroups* is equal to the minimum reproductive age of the candidates for EVA-selection.
- (b) If *birthGroups* is greater than the minimum reproductive age, no input error or warning is given, but the program will crash during EVA-calculations. The reason being that some offspring will be allocated to the same birth group as their parents.
- (c) *birthGroups* can be smaller than the minimum reproductive age of the candidates for EVA-selection. The only drawback is that this may slow the speed of the EVA-calculations.
- 20) Setting *MalesSelected* or *FemalesSelected* to 'no' is different from setting *MalesSelected* and/or *FemalesSelected* to 'yes' and *MaleSelCrit* and/or *FemaleSelCrit* to 'null'
- (a) (i) When *MalesSelected* 'no', males are not selected. Females are EVA-selected without considering the genetic relationships of males.
- (ii) When *FemalesSelected* 'no', females are not selected. Males are EVA-selected without considering the genetic relationships of females.
- (b) (i) When *MalesSelected* 'yes' and *MaleSelCrit* 'null', males are EVA-selected. The selection criterion of the males is set to 0.0 and the genetic relationships of the males is considered in the selection of the males and, possibly, the females.
- (ii) When *FemalesSelected* 'yes' and *FemaleSelCrit* 'null', females are EVA-selected. The selection criterion of the females is set to 0.0 and the genetic relationships of the females is considered in the selection of the females and, possibly, the males.

A description of the program EVA is provided in Appendix I

## &EVAPARAMETERS

```
parameters=
stage optimise wMerit wRelationship dFconstraint limitMaleMatings nGenerations
popSize nOffspring restartInterval exchangeAlgorithm mutateProb crossoverProb
directedMutateProb /
```

**\*\*Task\*\***

Input to run EVA, including parameters for the evolutionary algorithm

**\*\*Properties of names\*\***

*stage* Definition: Stage of selection. Must correspond to a selection stage in *select\_scheme* with *sex\_code* 7  
Type: Integer  
Options:  $2 \leq \textit{stage} \leq \textit{selection\_groups}$   
Default: *stage* must be specified

*optimise* Definition:  
Type: Character  
Options:  
    *penalty* Penalty applied to average relationship  
    *constraint* Rate of inbreeding constrained to specified rate  
    *merit* Selection on merit  
Default: *optimise* must be specified

'*penalty*' uses *wMerit* and *wRelationship*. '*constraint*' uses *dFconstraint*. '*merit*' uses neither *wMerit*, *wRelationship*, or *dFconstraint*; it sets *wMerit* 1 and *wRelationship* 0.

*wMerit* Definition: Weight on genetic merit; estimated breeding value or index  
Type: Real  
Option: Any real; negative values impose a penalty on genetic merit  
Default: *wMerit* must be specified

Applied when *optimise* '*penalty*'

*wRelationship* Definition: Weight applied to the average additive-genetic relationship of the current generation, which includes the new cohort  
Type: Real  
Options: Any real; negative values impose a penalty on additive-genetic relationship  
Default: *wRelationship* must be specified

Applied when *optimise* '*penalty*'

*dFconstraint* Definition: Pre-defined rate of inbreeding  
Type: Real  
Options:  $0.0 \leq \textit{dFconstraint} \leq 1.0$   
Default: *dFconstraint* must be specified

Applied when *optimise* '*constraint*'

*limitMaleMatings* Definition: Multiple by which matings are allocated to male selection candidates. For example, when *limitMaleMatings* 5, matings are allocated in multiples of 5 and males can only be allocated 0, 5, 10, 15, ... *MaleMaxMatings<sub>i</sub>* matings, where *MaleMaxMatings<sub>i</sub>* is the maximum number of matings that can be allocated to the *i*th male.  
Type: Integer  
Options:  $\textit{limitMaleMatings} \geq 1$   
Default: *limitMaleMatings* must be specified

The following variables control the evolutionary algorithm

*nGenerations* Definition: Maximim number of generations run by the

evolutionary algorithm

Type: Integer  
Options: *nGenerations* ≥ 1  
Default: *nGenerations* must be specified

*popSize*                    Definition: Size of population of solutions maintained by  
the evolutionary algorithm  
Type: Integer  
Options: *popSize* ≥ 1  
Default: *popSize* must be specified

*nOffspring*                Definition: Number of new solutions generated in each  
generation of the evolutionary algorithm  
Type: Integer  
Options: *nOffspring* ≥ 1  
Default: *nOffspring* must be specified

*restartInterval*            Definition: Number of generations after which more variation  
is generated by the evolutionary algorithm. More  
variation is generated by increasing the  
mutation variance in a single generation.  
Increasing the variance is only applied when a  
better solution is not been found for  
*restartInterval* generations. Better solutions  
are those that increase the optimisation  
criterion, which is a function of genetic merit,  
average additive-genetic relationship, *wMerit*,  
and *wRelationship*.  
Type: Integer  
Options: *restartInterval* ≥ 1  
Default: *restartInterval* must be specified

*exchangeAlgorithm*        Definition: Number of generations after which an exchange  
algorithm is used to iteratively optimise  
solutions generated by the evolutionary  
algorithm  
Type: Integer  
Options: *exchangeAlgorithm* ≥ 1  
Default: *exchangeAlgorithm* must be specified

*mutateProb*                 Definition: Probability of mutating an (each) individual in a  
solution generated by the evolutionary  
algorithm by randomly exchanging the  
individual for another individual (in the  
solution or resampling?). Suggested value  
1/(4·*Nmatings*).  
Type: Real  
Options: 0.0 ≤ *mutateProb* ≤ 1.0  
Default: *mutateProb* must be specified

*crossoverProb*             Definition: Probability of crossovers when the evolutionary  
algorithm generates new solutions from two  
parental solutions. Suggested value between  
1/*nMatings* : 1/(2·*nMatings*).  
Type: Real  
Options: 0.0 ≤ *crossoverProb* ≤ 1.0  
Default: *crossoverProb* must be specified

*directedMutateProb* Definition: Probability of mutating an individual in a solution generated by the evolutionary algorithm by exchanging the individual for an individual that increases the evaluation of the solution. Suggested value  $1/(2*nMatings)$ .

Type: Real  
Options:  $0.0 \leq \textit{directedMutateProb} \leq 1.0$   
Default: *directedMutateProb* must be specified

*nGenNoImprovement* Definition: Number of generations of the evolutionary algorithm that are run without generating an improved solution before EVA stops

Type: Integer  
Options:  $nGenNoImprovement \geq 1$   
Default: *nGenNoImprovement* must be specified

**\*\*Additional information\*\***

A description of the program EVA is provided in the Appendix

## &PHENOWEIGHTS

*nPhenotypicWeights*=*nPhenotypicWeights*  
*phenotypicWeights*=*stage sex observation weight /*

NB! The number of lines specified in *phenotypicWeights* must equal *nPhenotypicWeights*

**\*\*Task\*\***

Specify weights applied to each observation when aggregate phenotype used as selection criterion

**\*\*Properties of names\*\***

*nPhenotypicWeights* Definition: Number of stage-observation combinations specified in *phenotypicWeights*

Type: Integer  
Options:  $1 \leq nPhenotypicWeights \leq (n_p + n_m + n_f) * (nobs + nCombinedObs)$ ,  
where  $n_p$  is the number of selection stages with *sex\_code* 0:6, *selection\_method* 'truncation', and *selection\_criterion* 'phenoweight';  $n_m$  is the number of EVA-selection stages with *MaleSelCrit* 'phenoweight'; and  $n_f$  is the number of EVA-selection stages with *FemaleSelCrit* 'phenoweight'.

Default: 0

*stage* Definition: Stage of selection at which phenotypic selection is applied. Must correspond to a selection stage in *select\_scheme*.

Type: Integer  
Options:  $1 \leq \textit{stage} \leq \textit{selection\_groups}$   
Default: *stage* must be specified

*sex* Definition: Sex of selection candidates to which phenotypic selection is applied

Type: Integer  
Options:  
0 Sex ignored, weights applied to both sexes

1 Males  
2 Females  
Default: *sex* must be specified

*observation* Definition: Observation number  
Type: Integer  
Options:  $1 \leq \textit{observation} \leq \textit{obs}$   
Default: *observation* must be specified

*weight* Definition: Weight applied to observation  
Type: Real  
Options: Any real value  
Default: *weight* must be specified

**\*\*Additional information\*\***

- 1) Namelist &PHENOWEIGHTS must be provided when (i) *selection\_criterion* 'phenoweight' at any selection stage of namelist &SELECTION, variable *selection\_scheme* with *sex\_code* 0:6, or (ii) *MaleSelCrit* 'phenoweight' or *FemaleSelCrit* 'phenoweight' at any EVA-selection stage of namelist &EVA, variable *EvaSelection*
- 2) At least one *weight* must be provided for each selection stage with phenotypic selection
- 3) Each combination of *stage*, *sex*, and *observation* can only be provided once in *phenotypicWeights*
- 4) *sex* must be 0 for all *stages* corresponding to selection stages of namelist &SELECTION, variable *selection\_scheme* with *sex\_code* 0:6 and *selection\_criterion* 'phenoweight'
- 5) *weight* is set to 0.0 for all observations not specified in *phenotypicWeights*
- 6) Observations with *weight* 0.0 do not contribute to the aggregate phenotype used as the selection criterion
- 7) Plants must have realised all observations allocated a *weight* to be candidates for phenotypic selection at selection stage *stage*. That is, if a plant has not had an observation realised, and the observation has *weight* ≠ 0.0 at selection stage *stage*, the plant is not considered a candidate for phenotypic selection.

**&GENOMICBLUPPARAMETERS**

*parameters=stage genomicBase firstChrom lastChrom loci maf mafInclude  
locusWeight scaleMethod adjustGScale propAToG addDiagG diagGOne /*

NB! Number of lines in *parameters* must equal the number of selection stages using genomic-breeding value as selection criterion

**\*\*Task\*\***

Input to construct genomic-**G** matrices using Guosheng's program, *invhmatrix*. Genomic-**G** matrices are used by DMU to predict genomic-breeding values.

**\*\*Properties of names\*\***

*stage* Definition: Stage of selection. Must correspond with a selection stage that uses (i) *selection\_criterion* 'genomicblup', and *RunBlup* 1 in namelist

&SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* and/or *FemaleSelCrit* 'genomicblup' and *MaleRunBlup* and/or *FemaleRunBlup* 1 in namelist &EVA, variable *EvaSelection*.

Type: Integer  
Options:  $1 \leq \text{stage} \leq \text{selection\_groups}$   
Default: *stage* must be specified

*genomicBase*

Definition: Define plants in genomic-base population that are used to calculate marker-allele frequencies, *p* and *1-p*. Allele frequencies are used to 'centre' and 'scale' genotypes at loci used as genetic markers in prediction.

Type: Character  
Options:  
    *all*                   All genotyped plants in the population, <included in *dmudat*>  
    *base*                 All plants in the base population ignoring genotyping  
    *genotypedbase*       All genotyped plants in the base population  
    *tracedbase*          All plants in the base population <included in *dmudat*> ignoring genotyping  
    *tracedgenotypedbase* All genotyped plants in the base population <included in *dmudat*>  
Default: *genomicBase* must be specified

*firstChrom*

Definition: First chromosome used to construct genomic-relationship matrices

Type: Integer  
Options:  $1 \leq \text{firstChrom} \leq \text{nchrom}$   
Default: *firstChrom* must be specified

*lastChrom*

Definition: Last chromosome with loci used to construct genomic-relationship matrices

Type: Integer  
Options:  $\text{firstChrom} \leq \text{lastChrom} \leq \text{nchrom}$   
Default: *lastChrom* must be specified

Loci on chromosomes *firstChrom*:*lastChrom* are used to construct matrices

*loci*

Definition: Loci used as genetic markers

Type: Character  
Options:  
    *all* QTL and markers  
    *qtl* QTL  
    *markers* Markers  
Default: *loci* must be specified

*maf*

Definition: Threshold for minimum-allele frequency

Type: Real  
Options:  $0.0 \leq \text{maf} \leq 0.50$   
Default: *maf* must be specified

*mafInclude*

Definition: Minimum-allele frequency of loci included. Fixed loci, loci with minimum-allele frequency 0.0, are excluded.

Type: Character  
Options:  
    above Include loci with minimum-allele frequency greater than or equal to *maf*  
    below Include loci with minimum-allele frequency less than or equal to *maf*  
Default: *mafInclude* must be specified

*locusWeight* Definition: Weight applied to each locus  
Type: Character  
Options:  
    one Weight 1.0 applied to each locus; each locus has equal weight  
    goddard Weight applied to each locus as a function of allele frequency,  $1.0/(p_i(1-p_i))$ , where  $p_i$  is the minimum-allele frequency at locus  $i$  (after Goddard 2009)  
    jannink Weight applied to each locus as a function of allele frequency,  $(\arcsin(1)-\arcsin(\sqrt{p_i}))/p_i(1-p_i)$  (after Jannink 2010)  
Default: *locusWeight* must be specified

*scaleMethod* Definition: Method to scale **G**-matrix  
Type: Integer  
Options:  
    1 Divide by sum of  $2p(1-p)$   
    2 Divide each locus genotype by  $\sqrt{2p_i(1-p_i)}$ , where  $p_i$  is frequency of an allele at locus  $i$   
Default: *scaleMethod* must be specified

*adjustGScale* Definition: Adjust **G** to same scale as **A**  
Type: Integer  
Options:  
    0 **G**-matrix not adjusted  
    1 **G**-matrix is adjusted, where  $\alpha$  and  $\beta$  are estimated from all genotyped plants  
    2 **G**-matrix is adjusted, where  $\alpha$  and  $\beta$  are estimated from all genotyped plants in the genomic-base population  
Default: *adjustGScale* must be specified

Note: For 'prediction', 'eva', and 'evaRelationships', genomic-base population used by *adjustGScale* 2 is plants defined by *genomicBase* that are both genotyped and traced back from selection candidates. For 'inbreeding', it is all plants defined by *genomicBase*.

*propAToG* Definition: Proportion of **A**-matrix to modify **G**-matrix  
Type: Real  
Options:  $0.0 \leq \text{propAToG} \leq 1.0$   
Default: *percentAToG* must be specified

*addDiagG* Definition: Value added to diagonal elements of **G**-matrix <to make the matrix positive-definite>  
Type: Real  
Options: *addDiagG*  $\geq 0.0$  [Set to 0.0 if **A**-matrix used]  
Default: *addDiagG* must be specified

*diagGOne* Definition: Scale mean of diagonal elements of **G**-matrix so the mean of the diagonal equals *diagGOne*

Type: Real

Options: *diagGOne* ≥ 0.0, where 0.0 does not bring about scaling

Default: *diagGOne* must be specified

**\*\*Additional information\*\***

- 1) An overview of the program *invhmatrix* is provided in section 13. The manual is provided in the Appendix.
- 2) Namelist *&GENOMICBLUPPARAMETERS* is only read when there is a selection stage(s) using genomic-breeding value as the selection criterion.
- 3) The character variables, *genomicBase*, *loci*, *mafInclude*, and *locusWeight*, must be provided in inverted commas ('').
- 4) Fixed loci, loci with minimum-allele frequency 0.0, are not used to construct genomic matrices.
- 5)

When constructing base file for AGSCALE 2:

```
do iid=1,maxid
  if (.not. genomicBasePopulation(iid)) cycle
  select case (genomicBase)
    case ('base', 'genotypedbase', 'tracedbase')
      select case (gMatrixTask)
        case ('prediction')
          if (.not. lpedGenoBlup(iid) .or. .not. pop(iid)%genotyped) cycle
        case ('eva')
          if (.not. lpedEva(iid) .or. .not. pop(iid)%genotyped) cycle
      end select
  end select
```

The 'base' specified for *adjustGScale*==2 is the same group of plants defined by *genomicBase* to calculate allele frequencies for centering and scaling.

- 6) Selection stages using genomic-breeding value as selection criterion are stages of namelist *&SELECTION*, variable *selection\_groups* with (i) *sex\_code* 0:6, *selection\_criterion* 'genomicblup', and *RunBlup* 1, and (ii) *sex\_code* 7, *MaleSelCrit* or *FemaleSelCrit* 'genomicblup', and *MaleRunBlup* and/or *FemaleRunBlup* 1 in corresponding EVA-selection stage of namelist *&EVA*, variable *EvaSelection*.
- x) Stages can be provided in any order; all stages must be provided
- x) Selection stages using genomic-breeding value as selection criterion must be represented once in variable *economicValueEbv*.

***&IBDBLUPPARAMETERS***

```
parameters=stage firstChrom lastChrom loci /
```

NB! Number of lines in parameters must equal the number of selection stages using IBD-breeding value as selection criterion

**\*\*Task\*\***

Input to generate IBD-relationship matrices for IDB-BLUP.

**\*\*Properties of names\*\***

*stage* Definition: Stage of selection. Must correspond with a selection stage that uses (i) *selection\_criterion*

'ibdblup', and *RunBlup* 1 in namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* and/or *FemaleSelCrit* 'ibdblup' and *MaleRunBlup* and/or *FemaleRunBlup* 1 in namelist &EVA, variable *EvaSelection*.

Type: Integer  
Options:  $1 \leq \text{stage} \leq \text{selection\_groups}$   
Default: *stage* must be specified

*firstChrom* Definition: First chromosome used to construct IBD-relationship matrices

Type: Integer  
Options:  $1 \leq \text{firstChrom} \leq \text{nchrom}$   
Default: *firstChrom* must be specified

*lastChrom* Definition: Last chromosome with loci used to construct IBD-relationship matrices

Type: Integer  
Options:  $\text{firstChrom} \leq \text{lastChrom} \leq \text{nchrom}$   
Default: *lastChrom* must be specified

Loci on chromosomes *firstChrom:lastChrom* are used to construct matrices

*loci* Definition: Loci used as genetic markers

Type: Character  
Options:  
    *markers* Markers  
    *qtl* QTL  
    *all* QTL and markers  
Default: *loci* must be specified

**\*\*Additional information\*\***

1) Namelist &IBDBLUPPARAMETERS is only read when there is a selection stage(s) using *ibd-breeding* value as the selection criterion.

*GeneticModel* must be 'genomic'. Should we allow 'ibdblup' with *GeneticModel* 'qtl'?

'ibdblup' does not rely on genotypings. Plants do not need to be genotyped to be part of *ibd-relationship* matrix.

2) The character variable, *loci*, must be provided in inverted commas ('').

3) Selection stages using *ibd-breeding* value as selection criterion are stages of namelist &SELECTION, variable *selection\_groups* with (i) *sex\_code* 0:6, *selection\_criterion* 'ibdblup', and *RunBlup* 1, and (ii) *sex\_code* 7, *MaleSelCrit* or *FemaleSelCrit* 'ibdblup', and *MaleRunBlup* and/or *FemaleRunBlup* 1 in corresponding EVA-selection stage of namelist &EVA, variable *EvaSelection*.

x) Stages can be provided in any order; all stages must be provided

x) Selection stages using *ibd-breeding* value as selection criterion must be represented once in variable *economicValueEbv*.

#### &IBSBLUPPARAMETERS

*parameters=stage firstChrom lastChrom loci /*

NB! Number of lines in parameters must equal the number of selection stages using IBS-breeding value as selection criterion

**\*\*Task\*\***

Input to generate IBS-relationship matrices for IDB-BLUP.

**\*\*Properties of names\*\***

*stage* Definition: Stage of selection. Must correspond with a selection stage that uses (i) *selection\_criterion* 'ibsblup', and *RunBlup* 1 in namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* and/or *FemaleSelCrit* 'ibsblup' and *MaleRunBlup* and/or *FemaleRunBlup* 1 in namelist &EVA, variable *EvaSelection*.  
Type: Integer  
Options:  $1 \leq \textit{stage} \leq \textit{selection\_groups}$   
Default: *stage* must be specified

*firstChrom* Definition: First chromosome used to construct IBS-relationship matrices  
Type: Integer  
Options:  $1 \leq \textit{firstChrom} \leq \textit{nchrom}$   
Default: *firstChrom* must be specified

*lastChrom* Definition: Last chromosome with loci used to construct IBS-relationship matrices  
Type: Integer  
Options:  $\textit{firstChrom} \leq \textit{lastChrom} \leq \textit{nchrom}$   
Default: *lastChrom* must be specified

Loci on chromosomes *firstChrom*:*lastChrom* are used to construct matrices

*loci* Definition: Loci used as genetic markers  
Type: Character  
Options:  
    *markers* Markers  
    *qtl* QTL  
    *all* QTL and markers  
Default: *loci* must be specified

**\*\*Additional information\*\***

1) Namelist &IBSBLUPPARAMETERS is only read when there is a selection stage(s) using ibs-breeding value as the selection criterion.

*GeneticModel* must be 'genomic'. Should we allow 'ibsblup' with *GeneticModel* 'qtl'?

'ibsblup' does not rely on genotypings. Plants do not need to be genotyped to be part of ibs-relationship matrix.

2) The character variable, *loci*, must be provided in inverted commas ('').

3) Selection stages using ibs-breeding value as selection criterion are stages of namelist &SELECTION, variable *selection\_groups* with (i) *sex\_code* 0:6, *selection\_criterion* 'ibsblup', and *RunBlup* 1, and (ii) *sex\_code* 7, *MaleSelCrit* or *FemaleSelCrit* 'ibsblup', and *MaleRunBlup* and/or *FemaleRunBlup* 1 in corresponding EVA-selection stage of namelist &EVA, variable *EvaSelection*.

- x) Stages can be provided in any order; all stages must be provided
- x) Selection stages using *ibs-breeding* value as selection criterion must be represented once in variable *economicValueEbv*.

#### &EVAGENOMICRELATIONSHIPPARAMETERS

```
parameters= stage genomicBase firstChrom lastChrom loci maf mafInclude
             locusWeight scaleMethod adjustGScale propAToG addDiagG diagGOne /
```

NB! Number of lines in parameters must equal the number of selection stages using genomic-relationship matrix to constrain average relationship in EVA-selection.

##### \*\*Task\*\*

Input to construct genomic-**H** matrices using the program, *invhmatrix*. Genomic-**H** matrices are used by EVA to constrain average relationship. The namelist is read when *relationshipMatrix* 'genomic' in any EVA-selection stage of namelist &EVA, variable *EvaSelection*.

##### \*\*Properties of names\*\*

Description of variables in parameters is as described for namelist &GENOMICBLUPPARAMETERS with the exception that:

- (i) *genomicBase* 'all' includes all genotyped plants that are candidates for EVA-selection (tagged for EVA-selection) or too young to be selection candidates and all genotyped individuals traced back from these plants, 'tracedbase' are base plants traced back from candidates for EVA-selection (tagged for EVA-selection) or too young to be selection candidates, and 'tracedgenotypedbase' are genotyped base plants traced back from candidates for EVA-selection (tagged for EVA-selection) or too young to be selection candidates.

#### &EVAIBDRELATIONSHIPPARAMETERS

```
parameters=stage firstChrom lastChrom loci /
```

NB! Number of lines in parameters must equal the number of selection stages using ibd-relationship matrix to constrain average relationship in EVA-selection.

##### \*\*Task\*\*

Loci used to generate IBD-relationship matrices that constrain average relationship in EVA-selection.

##### \*\*Properties of names\*\*

*stage* Definition: Stage of selection. Must correspond with a selection stage that uses (i) *selection\_criterion* 'ibdblup', and *RunBlup* 1 in namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* and/or *FemaleSelCrit* 'ibdblup' and *MaleRunBlup* and/or *FemaleRunBlup* 1 in namelist &EVA, variable *EvaSelection*.

Type: Integer

Options:  $1 \leq \textit{stage} \leq \textit{selection\_groups}$

Default: *stage* must be specified

*firstChrom* Definition: First chromosome used to construct IBD-relationship matrices

Type: Integer  
Options:  $1 \leq \text{firstChrom} \leq \text{nchrom}$   
Default: *firstChrom* must be specified

*lastChrom* Definition: Last chromosome with loci used to construct IBD-relationship matrices  
Type: Integer  
Options:  $\text{firstChrom} \leq \text{lastChrom} \leq \text{nchrom}$   
Default: *lastChrom* must be specified

Loci on chromosomes *firstChrom:lastChrom* are used to construct matrices

*loci* Definition: Loci used as genetic markers  
Type: Character  
Options:  
    markers Markers  
    qtl QTL  
    all QTL and markers  
Default: *loci* must be specified

**\*\*Additional information\*\***

- 1) Namelist &IBDBLUPPARAMETERS is only read when there is a selection stage(s) using ibd-breeding value as the selection criterion.

*GeneticModel* must be 'genomic'. Should we allow 'ibd' with *GeneticModel* 'qtl'?

'ibdblup' does not rely on genotypings. Plants do not need to be genotyped to be part of ibd-relationship matrix.

- 2) The character variable, *loci*, must be provided in inverted commas ('').
  - 3) Selection stages using ibd-breeding value as selection criterion are stages of namelist &SELECTION, variable *selection\_groups* with (i) *sex\_code* 0:6, *selection\_criterion* 'ibdblup', and *RunBlup* 1, and (ii) *sex\_code* 7, *MaleSelCrit* or *FemaleSelCrit* 'ibdblup', and *MaleRunBlup* and/or *FemaleRunBlup* 1 in corresponding EVA-selection stage of namelist &EVA, variable *EvaSelection*.
- x) Stages can be provided in any order; all stages must be provided
- x) Selection stages using ibd-breeding value as selection criterion must be represented once in variable *economicValueEbv*.

**&EVAIBSRELATIONSHIPPARAMETERS**

parameters=stage *firstChrom lastChrom loci /*

NB! Number of lines in parameters must equal the number of selection stages using ibs-relationship matrix to constrain average relationship in EVA-selection.

**\*\*Task\*\***

Loci used to generate IBS-relationship matrices that constrain average relationship in EVA-selection.

**\*\*Properties of names\*\***

*stage* Definition: Stage of selection. Must correspond with a selection stage that uses (i) *selection\_criterion*

'ibsblup', and *RunBlup* 1 in namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* and/or *FemaleSelCrit* 'ibsblup' and *MaleRunBlup* and/or *FemaleRunBlup* 1 in namelist &EVA, variable *EvaSelection*.

Type: Integer  
Options:  $1 \leq \text{stage} \leq \text{selection\_groups}$   
Default: *stage* must be specified

*firstChrom* Definition: First chromosome used to construct IBS-relationship matrices

Type: Integer  
Options:  $1 \leq \text{firstChrom} \leq \text{nchrom}$   
Default: *firstChrom* must be specified

*lastChrom* Definition: Last chromosome with loci used to construct IBS-relationship matrices

Type: Integer  
Options:  $\text{firstChrom} \leq \text{lastChrom} \leq \text{nchrom}$   
Default: *lastChrom* must be specified

Loci on chromosomes *firstChrom:lastChrom* are used to construct matrices

*loci* Definition: Loci used as genetic markers

Type: Character  
Options:  
    *markers* Markers  
    *qtl* QTL  
    *all* QTL and markers  
Default: *loci* must be specified

**\*\*Additional information\*\***

1) Namelist &IBSBLUPPARAMETERS is only read when there is a selection stage(s) using *ibs-breeding* value as the selection criterion.

*GeneticModel* must be 'genomic'. Should we allow 'ibs' with *GeneticModel* 'qtl'?

'ibsblup' does not rely on genotypings. Plants do not need to be genotyped to be part of *ibs-relationship* matrix.

2) The character variable, *loci*, must be provided in inverted commas ('').

3) Selection stages using *ibs-breeding* value as selection criterion are stages of namelist &SELECTION, variable *selection\_groups* with (i) *sex\_code* 0:6, *selection\_criterion* 'ibsblup', and *RunBlup* 1, and (ii) *sex\_code* 7, *MaleSelCrit* or *FemaleSelCrit* 'ibsblup', and *MaleRunBlup* and/or *FemaleRunBlup* 1 in corresponding EVA-selection stage of namelist &EVA, variable *EvaSelection*.

x) Stages can be provided in any order; all stages must be provided

x) Selection stages using *ibs-breeding* value as selection criterion must be represented once in variable *economicValueEbv*.

## &DMUPARAMETERS

*dmuPolyBlup*=*dmuPolyBlup*  
*dmuGenomicBlup*=*dmuGenomicBlup*

```
dmuIbdBlup=dmuIbdBlup
dmuGasBlup=dmuGasBlup
ebv_observation=ebv_observation
printDmuLstFiles=printDmuLstFiles /
```

**\*\*Task\*\***

Input for estimation of breeding values using DMU

**\*\*Properties of names\*\***

```
dmuPolyBlup          Definition: DMU version used to estimate polygenic breeding
                        values
                        Type: Character
                        Options:
                          dmuai DMUAI used
                          dmu4 DMU4 used
                          dmu5 DMU5 used
                        Default: dmu5

dmuGenomicBlup      Definition: DMU version used to estimate genomic breeding
                        values
                        Type: Character
                        Options:
                          dmuai DMUAI used
                          dmu4 DMU4 used
                          dmu5 DMU5 used
                        Default: dmu5

dmuIbdBlup          Definition: DMU version used to estimate ibd breeding values
                        Type: Character
                        Options:
                          dmuai DMUAI used
                          dmu4 DMU4 used
                          dmu5 DMU5 used
                        Default: dmu5

dmuGasBlup          Definition: DMU version used to estimate GAS breeding values
                        Type: Character
                        Options:
                          dmu4 DMU4 used
                          dmu5 DMU5 used
                        Default: dmu5

ebv_observation     Definition: Matrix relating observations to BLUP-breeding
                        values. Used to create DMU-input data and read
                        breeding values predicted by DMU.
                        Dimension: (nobs+nCombinedObs)*nebv
                        Options: Matrix elements 0 or 1
                        Type: Integer
                        Default: ebv_observation must be specified

printDmuLstFiles    Definition: Write DMU-lst files to subdirectory,
                        dmuLstFiles. Subdirectory DmuLstFiles
                        is created in the output directory specified
                        in namelist &OUTPUTDIRECTORY, variable
                        OutDirectory.
                        Type: Character
                        Options:
```

no DMU-1st files are not written to subdirectory  
yes DMU-1st files are written  
Default: no

**\*\*Additional information\*\***

- 1) *dmuPolyBlup* is used when polygenic breeding values are used as selection criterion at any selection stage, *dmuGenomicBlup* is used when genomic breeding values are used, and *dmuGasBlup* when GAS breeding values are used.
- 2) (a) *dmuPolyBlup* is also used when genomic breeding values are specified as the selection criterion but polygenic breeding values are estimated instead of genomic breeding values. This occurs when there is a lack of genotypic and/or phenotypic observations (see section *Genetic model and selection*; ADAM's motor), or when *startGenomicSelectionTime*>1 (namelist &CONTROL\_GENOME).  
(b) *dmuPolyBlup* is also used when gas breeding values are specified as the selection criterion but polygenic breeding values are estimated instead of gas breeding values. This occurs when there is a lack of phenotypic observations (see section *Genetic model and selection*), or when *startGasTime*>1 (namelist &CONTROL\_GENOME).
- 3) When *printDmuLstFiles* 'yes':
  - (a) DMU-1st files are written to directory *dmuLstFiles* at selection stages with (i) truncation or EVA selection, and (ii) selection criterion polygenic, genomic, or GAS breeding values
  - (b) Directory *dmuLstFiles* is a subdirectory of the output directory *OutDirectory* (namelist &OUTPUTDIRECTORY, variable *OutDirectory*)
  - (c) DMU-1st files are written as *dmuAdamRep*<rep>*Time*<time>*Stage*<stage>.lst, where <rep> is replicate number, <time> is time step, and <stage> is selection stage
  - (d) If the subdirectory *dmuLstFiles* does not exist, it is created
  - (e) If the subdirectory *dmuLstFiles* exists and it contains old DMU-1st files (files from an earlier simulation), the old DMU-1st files are renamed *dmuAdamRep*<rep>*Time*<time>*Stage*<stage>.prev

## **&BAYESPPARAMETERS**

There is now a version of ADAM that can use BayesP instead of GBLUP for genomic prediction. It is restricted to fewer cases than GBLUP, e.g. only a single trait and all plants genotyped.

BayesP can be used when specifying 'bayesp' in &SELECTION rather than 'polyblup' or 'genomicblup' as SelectionCriterion.

The attached input.prm works with the new version of ADAM. Here are some comments to the additional parameters involved.

There is a new namelist with up to seven parameters:

```
&BAYESPPARAMETERS
nIterations=1000
priorProbability=0.05
priorResidualVariance=1.0
priorGeneticVariance=1.0
bayesPLoci='markers'
bayespMafInclude='above'
mafBayesP=0.0
```

/

The values given for the parameters in the example above are the default values. That means that if these values suit you, you don't need to put them in the namelist.

nIterations Is the number of rounds run in the BayesP program. This is a parameter that Theo knows a lot more about than me.

priorProbability Is the mixing proportion in the program, i.e. the proportion of loci with big effect.

priorResidualVariance Is the residual variance. This should almost always fit the parameter given in r\_matrix.

priorGeneticVariance is the genetic variance. This should almost always fit the parameter given in genomicMatrix.

bayesPLoci controls which loci to use whether 'all', 'markers', or 'qtl'.

bayesPmafInclude specifies whether to use loci with MAF 'above' or 'below' the MAF-threshold.

mafBayesP is the MAF-threshold.

### &MATINGPARAMETERS

```
Mating_groups=mating_groups
Selection_scheme=
FirstTime LastTime NtimeSteps generation repro_method mating_design mating_unit
max_numberMating
/
```

#### \*\*Task\*\*

Method to mate selected plants

#### \*\*Properties of names\*\*

<i>FirstTime</i>	Definition: First time step where the selection group is used Type: Integer Options: 1-gestation_length≤FirstTime≤LastTime Default: <i>FirstTime</i> must be specified
<i>LastTime</i>	Definition: Last time step where the selection group is used Type: Integer Options: <i>FirstTime</i> ≤ <i>LastTime</i> ≤ <i>ntime</i> Default: <i>LastTime</i> must be specified
<i>Treproductive</i>	Definition: time steps fro mating to birth Type: Integer Options: ≥0 Default: 0
<i>Generation</i>	Definition: generation in a breeding cycle Type: Integer Options: ≥0 Default: must be specified
repro_method	Definition: method of reproduction Type: Character Options: clone, selfing, crossing, DHs.
<i>mating_design</i>	Definition: Method to mate selected plants.

Type: Character  
Options:  
random\_mating Parents mated randomly  
assortative\_mating Best male parents mated to the best females, where best is the criterion used to select males and females  
desortative\_mating Best male parents mated to the worse females, where best is the criterion used to select males and females  
mc\_mating Minimum-coancestry mating  
mcac\_mating Mating by minimising covariance of ancestral genetic contributions as described by Henryon et al. (2010)  
Default: random\_mating

*McacGenerations* Definition: Number of generations ancestors of selected plants are traced back when using minimum-coancestry-covariance mating (MCAC mating).  
Type: Integer  
Options:  $\geq 0$   
Default: 5

max\_numberMating Definition: maximum number of crosses.  
Type: Integer  
Options:  $\geq 1$   
Default: 1

## &MATRICES

polygenicMatrix=*polygenicMatrix*  
genomicMatrix=*genomicMatrix*  
residualMatrix=*residualMatrix*  
geneticMeanVector=*geneticMeanVector*  
femaleDeviationVector=*femaleDeviationVector* /

### \*\*Task\*\*

Provide genetic and residual (co)variance matrices and vectors of genetic means and female deviations (fixed-sex effects)

### \*\*Properties of names\*\*

*polygenicMatrix* Definition: Polygenic (co)variance matrix. Elements are read in the following order: (row 1,column 1), (1,2), ..., (1,column n), (2,1), (2,2) ...  
Dimension: *ntbv\*ntbv*  
Type: Real  
Default: Matrix of 0.0

*genomicMatrix* Definition: Genomic (co)variance matrix. Elements are read in the following order: (row 1,column 1), (1,2), ..., (1,column n), (2,1), (2,2) ...  
Dimension: *ntbv\*ntbv*  
Type: Real

Default: Matrix of 0.0

*residualMatrix* Definition: Residual (co)variance matrix. Elements are read in the following order: (row 1, column 1), (1,2), ..., (1,column n), (2,1), (2,2) ...  
 Dimension: *nres\*nres*  
 Type: Real  
 Default: Matrix of 0.0

*geneticMeanVector* Definition: Vector of genetic means  
 Dimension: *ntbv*  
 Type: Real  
 Default: Vector of 0.0

*femaleDeviationVector* Definition: Vector of female deviations  
 Dimension: *ntbv*  
 Type: Real  
 Default: Vector of 0.0

**\*\*Additional information\*\***

- 1) Matrix of total-genetic (co)variances is the sum of *polygenicMatrix* and *genomicMatrix*
- 2) *genomicMatrix* is only used when *GeneticModel* 'genomic' in namelist &CONTROLPARAMETERS

**&DESIGN\_MATRICES**

ZDirectGenetic=ZDirectGenetic  
 WDirectError=WDirectError  
 ZPaternalGenetic=ZPaternalGenetic  
 WPaternalError=WPaternalError  
 ZMaternalGenetic=ZMaternalGenetic  
 WMaternalError=WMaternalError  
 ZMateGenetic=ZMateGenetic  
 WMateError=WMateError  
 XFemales=XFemales /

**\*\*Task\*\***

Provide design matrices

**\*\*Properties of names\*\***

*ZDirectGenetic* Definition: Design matrix associating true direct-genetic effects to observations  
 Dimension: *nobs\*ntbv*  
 Type: Integer  
 Default: Matrix of 0

*WDirectError* Definition: Design matrix associating direct-residual effects to observations  
 Dimension: *nobs\*nres*  
 Type: Integer  
 Default: Matrix of 0

*ZPaternalGenetic* Definition: Design matrix associating paternal-genetic effects to observations  
 Dimension: *nobs\*ntbv*

Type: Integer  
Default: Matrix of 0

*WPaternalError* Definition: Design matrix associating paternal-residual effects to observations  
Dimension: *nobs\*nres*  
Type: Integer  
Default: Matrix of 0

*ZMaternalGenetic* Definition: Design matrix associating maternal-genetic effects to observations  
Dimension: *nobs\*ntbv*  
Type: Integer  
Default: Matrix of 0

*WMaternalError* Definition: Design matrix associating maternal-residual effects to observations  
Dimension: *nobs\*nres*  
Type: Integer  
Default: Matrix of 0

*ZMateGenetic* Definition: Design matrix associating mate-genetic effects to observations  
Dimension: *nobs\*ntbv*  
Type: Integer  
Default: Matrix of 0

*WMateError* Definition: Design matrix associating mate-residual effects to observations  
Dimension: *nobs\*nres*  
Type: Integer  
Default: Matrix of 0

*XFemales* Definition: Design matrix associating female deviations to observations  
Dimension: *nobs\*ntbv*  
Type: Integer  
Default: Matrix of 0

**\*\*Additional information\*\***

1) *ZMateGenetic* and *WMateError* apply to maternal traits; id of sire mated to dam prior to phenotyping of maternal traits.

**&COMBINEDOBSERVATIONS**

combinations=*obs a b c d e /*

NB! Number of lines in combinations must equal *nCombinedObs*

**\*\*Task\*\***

Input to generate combined traits. The *i*th combined trait (*i=nobs+1 ... nobs+nCombinedObs*) for the *j*th plant,  $y_{ij}$ , is generated as  $y_{ij}=(a_j+b_j-c_j)*d_j/e_j$ , where  $a_j$ ,  $b_j$ ,  $c_j$ ,  $d_j$ , and  $e_j$  are phenotypic observations generated for plant *j* and the observation numbers allocated to *a*, *b*, *c*, *d*, and *e* can be 1 ... *nobs*.

**\*\*Properties of names\*\***

*obs* Definition: Observation number

Type: Integer  
Options:  $nobs+1 \leq obs \leq nobs+nCombinedobs$   
Default: *obs* must be specified

*a* Definition: Observation allocated to *a*  
Type: Integer  
Options:  
    -9 No observation is allocated to *a*  
    1:*nobs* Observation allocated to *a*  
Default: *a* must be specified

*b* Definition: Observation allocated to *b*  
Type: Integer  
Options:  
    -9 No observation is allocated to *b*  
    1:*nobs* Observation allocated to *b*  
Default: *b* must be specified

*c* Definition: Observation allocated to *c*  
Type: Integer  
Options:  
    -9 No observation is allocated to *c*  
    1:*nobs* Observation allocated to *c*  
Default: *c* must be specified

*d* Definition: Observation allocated to *d*  
Type: Integer  
Options:  
    -9 No observation is allocated to *d*  
    1:*nobs* Observation allocated to *d*  
Default: *d* must be specified

*e* Definition: Observation allocated to *e*  
Type: Integer  
Options:  
    -9 No observation is allocated to *e*  
    1:*nobs* Observation allocated to *e*  
Default: *e* must be specified

**\*\*Additional information\*\***

- 1) Namelist &COMBINEDTRAITS is only read and used when *GeneticModel* 'polygenic' or 'genomic' in namelist &CONTROLPARAMETERS and *nCombinedTraits*>0 in namelist &POPULATIONPARAMETERS
- 2) An observation number can only be represented once in variable combinations, *obs*. This implies that all observation numbers in the sequence *nobs*+1 ... *nobs*+*nCombinedObs* must be represented in combinations, *obs*.
- 3) At least one of *a*, *b*, *c*, *d*, and *e* must be allocated an observation number (1:*nobs*) for each combined observation. That is, all of *a*, *b*, *c*, *d*, and *e* cannot be -9.
- 4) (i) If *a* -9, *b* -9, and *c* -9, *a* for each plant is set to 1.0, *b* to 0.0, and *c* to 0.0.  
    (ii) If *d* -9, *d* for each plant is set to 1.0.  
    (iii) If *e* -9, *e* for each plant is set to 1.0.

5) All component observations (1 ... *nobs*) that make up a combined observation must be realised by an plant for the combined observation to be realised by the plant.  
CHECK!!!!!!!!!!!!

6) DYD???

## &OBSERVATIONCONSTRAINTS

constraints=a b c d e sign y /

NB! Number of lines in constraints must equal *nObsConstraints*

### \*\*Task\*\*

Input for imposing constraints on sampled observations, where a constraint is a restriction by which observations must comply. Each constraint is imposed on the *j*th plant as  $(a_j+b_j-c_j)*d_j/e_j \text{ sign } y$ , where  $a_j$ ,  $b_j$ ,  $c_j$ ,  $d_j$ , and  $e_j$  are phenotypic observations generated for plant *j*, the observation numbers allocated to *a*, *b*, *c*, *d*, and *e* can be 1 ... *nobs+nCombinedObs*, and *sign* is > or <. When an observation(s) for plant *j* does not fulfil all constraints, all observations for that plant are resampled.

### \*\*Properties of names\*\*

*a* Definition: Observation allocated to *a*  
Type: Integer  
Options:  
-9 No observation is allocated to *a*  
1:*nobs+nCombinedObs* Observation allocated to *a*  
Default: *a* must be specified

*b* Definition: Observation allocated to *b*  
Type: Integer  
Options:  
-9 No observation is allocated to *b*  
1:*nobs+nCombinedObs* Observation allocated to *b*  
Default: *b* must be specified

*c* Definition: Observation allocated to *c*  
Type: Integer  
Options:  
-9 No observation is allocated to *c*  
1:*nobs+nCombinedObs* Observation allocated to *c*  
Default: *c* must be specified

*d* Definition: Observation allocated to *d*  
Type: Integer  
Options:  
-9 No observation is allocated to *d*  
1:*nobs+nCombinedObs* Observation allocated to *d*  
Default: *d* must be specified

*e* Definition: Observation allocated to *e*  
Type: Integer  
Options:  
-9 No observation is allocated to *e*  
1:*nobs+nCombinedObs* Observation allocated to *e*  
Default: *e* must be specified

*sign* Definition: Equation sign  
Type: Character  
Options:  
    < Less than  
    > Greater than  
Default: *sign* must be specified

*y* Definition: Equation sign  
Type: Real  
Options: Any real number  
Default: *y* must be specified

**\*\*Additional information\*\***

- 1) Namelist &OBSERVATIONCONSTRAINTS is only read and used when *nObsConstraints*>0 in namelist &POPULATIONPARAMETERS
- 2) At least one of *a*, *b*, *c*, *d*, and *e* must be allocated an observation number (1:*nobs*) for each combined observation. That is, all of *a*, *b*, *c*, *d*, and *e* cannot be -9.
- 3) (i) If *a* -9, *b* -9, and *c* -9, *a* for each plant is set to 1.0, *b* to 0.0, and *c* to 0.0.  
(ii) If *d* -9, *d* for each plant is set to 1.0.  
(iii) If *e* -9, *e* for each plant is set to 1.0.
- 4) When an observation(s) for an plant does not fulfil all constraints, all observations for the plant are resampled by resampling the residual effects for all observations.
- 5) If the observation(s) does not fulfil all constraints after 100 rounds of resampling, the program stops. This implies that the constraints are too strict.

**&ECONOMICVALUES**

*economicValueTbv=economicValueTbv*  
*nEconomicValuePbv=nEconomicValuePbv*  
*economicValuePbv=stage sex values*  
*nEconomicValueEbv=nEconomicValueEbv*  
*economicValueEbv=stage sex values /*

NB! Number of lines in *economicValuePbv* and *economicValueEbv* must equal *nEconomicValuePbv* and *nEconomicValueEbv*

**\*\*Task\*\***

Provide economic values

**\*\*Properties of names\*\***

*economicValueTbv* Definition: Vector of *ntbv* economic values used to calculate true aggregate-breeding value. The aggregate-breeding value is calculated by weighting *ntbv* true-breeding values by *economicValueTbv*.  
Dimension: *ntbv*  
Type: Real  
Options: Any reals  
Default: *economicValueTbv* must be specified

*nEconomicValuePbv*

economicValuePbv=  
stage

Definition: Stage of selection. Must correspond with a selection stage using pseudo-true aggregate-breeding value ('tbv') as selection criterion

Type: Integer

Options:

1 Values applied to all selection stages

1≤stage≤selection\_groups

Default: stage must be specified when economicValuePbv

provided

sex

Definition: Sex of selection candidates

Type: Integer

Options:

0 Sex ignored, economic values applied to both sexes

1 Males

2 Females

Default: sex must be specified

values

Definition: Vector of *ntbv* economic values used to calculate pseudo-true aggregate-breeding value. The pseudo-true aggregate-breeding value is calculated by weighting *ntbv* true-breeding values by *values*.

Dimension: *ntbv*

Type: Real

Options: Any reals

Default: values must be specified

*nEconomicValueEbv*

economicValueEbv=  
stage

Definition: Stage of selection. Must correspond with a selection stage using estimated aggregate-breeding value as selection criterion

Type: Integer

Options:

1 Values applied to all selection stages and sexes

1≤stage≤selection\_groups

Default: stage must be specified

sex

Definition: Sex of selection candidates

Type: Integer

Options:

0 Sex ignored, economic values applied to both sexes

1 Males

2 Females

Default: sex must be specified

values

Definition: Vector of *nebv* economic values used to calculate estimated aggregate-breeding value. The estimated aggregate-breeding value is calculated by weighting *nebv* selection criteria by *values*.

Dimension: *nebv*

Type: Real

Options: Any reals  
Default: values must be specified

**\*\*Additional information\*\***

- 1) Namelist &ECONOMICVALUES is always read and variable *economicValueTbv* is always used. Variables *economicValuePbv* and *economicValueEbv* are only used when there are selection stage(s) using pseudo-true and estimated aggregate-breeding values as selection criterion.
- 2) Economic values can be allocated to *economicValuePbv* and *economicValueEbv* in three ways:
  - (i) No input provided for *economicValuePbv* and *economicValueEbv*. The economic values provided in *economicValueTbv* are allocated to all selection stages of *economicValuePbv* and *economicValueEbv* where pseudo-true and estimated aggregate-breeding values are used as selection criterion. To be able to provide input this way for *economicValueEbv*, *ntbv* must equal *nebv*. If this is used, *nEconomicValuePbv* and *nEconomicValueEbv* must be -9, the default value. Don't override by adding a value not equal to -9.
  - (ii) Provide one row of input that is allocated to all selection stages of *economicValuePbv* and *economicValueEbv* where pseudo-true and estimated aggregate-breeding values are used as selection criterion. *nEconomicValuePbv* and *nEconomicValueEbv* must be 1, and this row must have *stage* -9 and *sex* 0.
  - (iii) Provide economic values for all stages and sexes of *economicValuePbv* and *economicValueEbv* where pseudo-true and estimated aggregate-breeding values are used as selection criterion. The number of rows provided must equal *nEconomicValuePbv* and *nEconomicValueEbv*.

When economic values for all stages and sexes of *economicValuePbv* and *economicValueEbv* are provided, *sex* can be:

*sex\_code* 0: *sex* can only be 0, 1, or 2. When *sex* 0, no other rows of *economicValuePbv* or *economicValueEbv* can have this *stage*. When *sex* 1, there must be another row with same *stage* and *sex* 2. When *sex* 2, there must be another row with same *stage* and *sex* 1.

*sex\_code* 1, 3, or 5: *sex* must be 1. No other rows of *economicValuePbv* or *economicValueEbv* can have this *stage*.

*sex\_code* 2, 4, or 6: *sex* must be 2. No other rows of *economicValuePbv* or *economicValueEbv* can have this *stage*.

*sex\_code* 7, *sex* can be 0, 1, or 2. When *sex* 0, no other rows of *economicValuePbv* or *economicValueEbv* can have this *stage*. When *sex* 1, there must be another row with same *stage* and *sex* 2. When *sex* 2, there must be another row with same *stage* and *sex* 1.

where *sex\_code* is provided in namelist &SELECTION, variable *selection\_groups*.

*sex* must be 0 when namelist &SELECTION, variable *selection\_groups* with (i) *sex\_code* 0:6 and *selection\_criterion*, 'polyblup', 'genomicblup', 'ibdblup', 'gas', or 'bayesp'.

Can be 0, 1, or 2 when *sex\_code* 7 and *MaleSelCrit* or *FemaleSelCrit*, 'polyblup', 'genomicblup', 'ibdblup', 'gas', or 'bayesp' in corresponding EVA-selection stage of namelist &EVA, variable *EvaSelection*.

- 2) Selection stages using pseudo-true aggregate-breeding value as selection criterion must be specified in variable *economicValuePbv*.

- 3) Selection stages using pseudo-true aggregate-breeding value as selection criterion are stages of namelist &SELECTION, variable *selection\_groups* with (i) *sex\_code* 0:6 and *selection\_criterion* 'tbv', and (ii) *sex\_code* 7 and *MaleSelCrit* or *FemaleSelCrit* 'tbv' in corresponding EVA-selection stage of namelist &EVA, variable *EvaSelection*.
- 4) Selection stages using estimated aggregate-breeding value as selection criterion must be specified in variable *economicValueEbv*.
- 5) Selection stages using estimated aggregate-breeding value as selection criterion are stages of namelist &SELECTION, variable *selection\_groups* with (i) *sex\_code* 0:6 and *selection\_criterion*, 'polyblup', 'genomicblup', 'ibdblup', 'gas', or 'bayesp', and (ii) *sex\_code* 7 and *MaleSelCrit* or *FemaleSelCrit*, 'polyblup', 'genomicblup', 'ibdblup', 'gas', or 'bayesp' in corresponding EVA-selection stage of namelist &EVA, variable *EvaSelection*.

## &OBSERVATIONS

```
nMaleObs=nMaleObs
nFemaleObs=nFemaleObs
nDydObs=nDydObs
nCategoricalObs=nCategoricalObs
```

```
MaleObservations=
obs RealisedSelectionStage FirstHerd LastHerd age alive selection
CullingUnselected CullingOldAge CullingInvoluntary
```

```
FemaleObservations=
obs RealisedSelectionStage FirstHerd LastHerd age alive selection
CullingUnselected CullingOldAge CullingInvoluntary parity parityTime
```

```
DydObservations=
Obs RealisedSelectionStage nOffspring TimeLag AgeMates
```

```
CategoricalObservations=CategoricalObservations /
```

NB! Number of observations for MaleObservations, FemaleObservations, DydObservations, and CategoricalObservations must equal *nMaleObs*, *nFemaleObs*, *nDydObs*, and *nCategoricalObs*

When *nMaleObs*, *nFemaleObs*, *nDydObs*, and/or *nCategoricalObs* are 0, MaleObservations, FemaleObservations, DydObservations, and/or CategoricalObservations are not required

**\*\*Task\*\***

Input for realising observations

**\*\*Properties of names\*\***

```
nMaleObs          Definition: Number of observations recorded for males
                  Type: Integer
                  Options: nMaleObs≥0
                  Default: 0
```

```
nFemaleObs        Definition: Number of observations recorded for females
```





culled involuntary to have observation  
 obs realised  
 Type: Integer  
 Options:  
 Males  
 1≤CullingInvoluntary<OldAgeMales when gestation\_length 0  
 0≤CullingInvoluntary<OldAgeMales when gestation\_length>0  
 Females  
 1≤CullingInvoluntary<OldAgeFemales when gestation\_length 0  
 0≤CullingInvoluntary<OldAgeFemales when gestation\_length>0  
 -1 Observation obs realised at culling regardless of age  
 -9 Culling not considered  
 Default: *CullingInvoluntary* must be specified

*parity* Definition: Parity during which an observation is realised  
 for females that have been selected to produce  
 offspring  
 Type: Integer  
 Options:  
 1≤*parity*≤1+MaxAge-MinAge when *gestation\_length* 0, where  
 MaxAge and MinAge are the maximum and minimum  
 reproductive ages for living females, derived from input  
 provided in namelist selection, variable  
*selection\_scheme*  
 1≤*parity*≤1+floor((MaxAge-MinAge)/(*gestation\_length*+*daysOpen*))  
 when *gestation\_length*>0  
 -9 Parity not considered  
 Default: *parity* must be specified

*parityTime* Definition: Parity timestep at which an observation is  
 realised for females that have been selected to  
 produce offspring  
 Type: Integer  
 Options:  
 0 when *gestation\_length*+*daysOpen*=0  
 0≤*parityTime*<*gestation\_length*+*daysOpen* when  
*gestation\_length*+*daysOpen*>0  
 -9 *ParityTime* not considered  
 Default: *parityTime* must be specified

*nOffspring* Definition: Number of offspring in progeny group.  
 Type: Integer  
 Options: ≥1  
 Default: *noffspring* must be specified

*TimeLag* Definition: Time lag (in time steps) from selection  
 until the DYD is realised  
 Type: Integer  
 Options: 0≤*TimeLag*≤*ntime*  
 Default: *TimeLag* must be specified

*AgeMates* Definition: Age of mates when offspring are born.  
 Type: Integer  
 Options: 1≤*AgeMates*≤*ntime*, where 1 means that mates  
 are one time step older than offspring.  
 Default: *AgeMates* must be specified

*ObservationTypes* Definition: Age of mates when offspring are born.  
 Type: Character  
 Options:  
     normal Normally-distributed trait  
     categorical Categorical trait  
 Default: normal

*CategoricalObservations* Definition: List of categorical observations  
 Type: Integer  
 Options: 1≤*CategoricalObservations*≤*nobs*  
 Default: *CategoricalObservations* must be specified

**\*\*Relation to subsequent namelists\*\***

&CATEGORICALS

Namelist &CATEGORICALS is required when *nCategoricalObs*>0 in namelist  
 &OBSERVATIONS

**\*\*Additional information\*\***

- 1) At least one observation must be realised. That is, at least one observation in *nMaleObs*, *nFemaleObs*, and/or *nDydObs* must be greater than zero. Not all observations need to be realised.
- 2) Male observations in *MaleObservations* can be realised in two ways. First, at the start of each time step (*RealisedSelectionStage* -9 in namelist &OBSERVATIONS, variable *MaleObservations*). Second, via selection (*destiny\_sel* 8 in namelist SELECTION, variable *selection\_scheme* or *MaleDestinySel* 8 in namelist EVA, variable *EvaSelection*).
- 3) Female observations in *FemaleObservations* can be realised in three ways. First, at the start of each time step (*RealisedSelectionStage* -9 in namelist &OBSERVATIONS, variable *FemaleObservations*). Second, via selection (*destiny\_sel* 8 in namelist SELECTION, variable *selection\_scheme* or *FemaleDestinySel* 8 in namelist EVA, variable *EvaSelection*). Third, maternal traits for females in gestation or days open. Maternal traits are realised after offspring are sampled/born. Females in gestation or days open that fulfil the criteria specified in *FemaleObservations*, including *parity* and *parityTime*, have traits realised.

Note: Maternal traits can only be realised as maternal traits; they cannot be realised at the start of each time step and via selection. Maternal traits are defined as having as those having *parity* and *parityTime* specified (i.e., not equal to -9).

- 4) When *RealisedSelectionStage*≥1, *FirstHerd*, *LastHerd*, *age*, *alive*, *selection*, *CullingUnselected*, *CullingOldAge*, *CullingInvoluntary*, *parity*, and *parityTime* Must be -9.
- 5) When *FirstHerd* -9, *LastHerd* must be -9. When *LastHerd* -9, *FirstHerd* must be -9.
- 6) When *alive* 1 in *MaleObservations*, *age* must be less than *OldAgeMales*. When *live* 1 in *FemaleObservations*, *age* must be less than *OldAgeFemales*.
- 7) When *selection*≥0, *age* must be greater than *selection*. *alive* can be 1 or -9.
- 8) (a) When *CullingUnselected*≠-9, *age* must be -9. When *age*≠-9, *CullingUnselected* must be -9.  
 (b) When *CullingUnselected*≠-9, *alive* must be -9. When *alive*≠-9, *CullingUnselected* must be -9.

- 9) (a) When *CullingOldAge*≠-9, *age* must be -9. When *age*≠-9, *CullingOldAge* must be -9.  
 (b) When *CullingOldAge*≠-9, *alive* must be -9. When *alive*≠-9, *CullingOldAge* must be -9.
- 10) (a) When *CullingInvoluntary*≠-9, *age* must be -9. When *age*≠-9, *CullingInvoluntary* must be -9.  
 (b) When *CullingInvoluntary*≠-9, *alive* must be -9. When *alive*≠-9, *CullingInvoluntary* must be -9.
- 11) (a) The largest parity derived from the input provided in namelist selection, variable *selection\_scheme* is the largest possible parity a female can obtain. It does not necessarily mean that females obtain this parity. All females may, for example, be culled before they obtain this or earlier parities. In these cases, some observations will not be realised.  
 (b) When *parity*≠-9, *alive* must be 1. When *alive* = -9, *parity* must be -9.  
 (c) When *parity*≠-9, *age*≠-9, *FirstHerd*≠-9, and *LastHerd*≠-9 are valid options
- 12) (a) When *parity*≠-9, *parityTime* must not be -9. When *parity* = -9, *parityTime* must be -9.  
 (b) When *gestation\_length+daysOpen*=0, maternal traits can only be realised in the same time step in which females were mated  
 (c) When *gestation\_length+daysOpen*>0, maternal traits can be realised in the same time step in which females were mated and in the next *gestation\_length+daysOpen*-1 time steps. This implies that when *gestation\_length+daysOpen*=1, maternal traits can only be realised in the same time step in which the females were mated. Maternal traits are realised after mating and have no influence in the current time step, and are first used in the next time step.
- 13) (a) Only one of the following options can be set to a value other than -9 for each observation in MaleObservations: *selection*, *CullingUnselected*, *CullingOldAge*, and *CullingInvoluntary*.  
 (b) Only one of the following options can be set to a value other than -9 for each observation in FemaleObservations: *selection*, *CullingUnselected*, *CullingOldAge*, *CullingInvoluntary*, and *parity*.
- 14) DYDs cannot be sampled for traits influenced by maternal effects, whether genetic or environmental  
 ) Obs cannot for combined traits in DydObservations
- 15) Observations not specified in MaleObservations, FemaleObservations, or DydObservations are not realised
- 16) The same combination of *obs* and *RealisedSelectionStage* can only be represented once in MaleObservations and FemaleObservations
- 17) Females in gestation or days open can have any traits realised
- 18) (a) (i) When *sex\_code* 0 and *destiny\_sel* 8 [observation(s) realised] at selection stage *stage* in namelist &SELECTION, variable *selection\_scheme*, *RealisedSelectionStage* must be *stage* for at least one observation in MaleObservations and/or FemaleObservations  
 (ii) When *sex\_code* 0 and *destiny\_sel* not 8 at selection stage *stage*, *RealisedSelectionStage* must not be *stage* for any observation in MaleObservations and FemaleObservations

- (b) (i) When *sex\_code* 1, 3, or 5 and *destiny\_sel* 8 at selection stage *stage*, *RealisedSelectionStage* must be *stage* for at least one observation in *MaleObservations*
- (ii) When *sex\_code* 1, 3, or 5 and *destiny\_sel* not 8 at selection stage *stage*, *RealisedSelectionStage* must not be *stage* for any observation in *MaleObservations*
- (c) (i) When *sex\_code* 2, 4, or 5 and *destiny\_sel* 8 at selection stage *stage*, *RealisedSelectionStage* must be *stage* for at least one observation in *FemaleObservations*
- (ii) When *sex\_code* 2, 4, or 5 and *destiny\_sel* not 8 at selection stage *stage*, *RealisedSelectionStage* must not be *stage* for any observation in *FemaleObservations*
- (d) (i) When *sex\_code* 7 at selection stage *stage* and *MaleDestinySel* 8 in corresponding EVA-selection stage, *RealisedSelectionStage* must be *stage* for at least one observation in *MaleObservations*
- (ii) When *sex\_code* 7 at selection stage *stage* and *FemaleDestinySel* 8 in corresponding EVA-selection stage, *RealisedSelectionStage* must be *stage* for at least one observation in *FemaleObservations*
- (iii) When *sex\_code* 7 at selection stage *stage* and *MaleDestinySel* not 8 in corresponding EVA-selection stage, *RealisedSelectionStage* must not be *stage* for any observation in *MaleObservations*
- (iv) When *sex\_code* 7 at selection stage *stage* and *FemaleDestinySel* not 8 in corresponding EVA-selection stage, *RealisedSelectionStage* must not be *stage* for any observation in *FemaleObservations*

19) Observation only recorded once. The first observation. If already recorded, cannot be overwritten when plant falls into phenotyping category again.

Ja, R-matricen er uændret og gælder for en enkelt observation, både i input.prm og i .parm. Vægten bliver beregnet i ADAM og skrevet til dmutat og .dir fortæller DMU, at der skal bruges vægte for forskellige observationer. Hvis alle dyr med den pågældende fænotype havde DYD'er, så kunne man også gøre det i R-matricen, men hvis der både er DYD'er og enkelte fænotyper, så er man nødt til at bruge vægten i DMU.

DYD can only be realised via *destiny\_sel* 6 in *&selection* and *&eva*.

## &CATEGORICALS

```
NCategories=NCategories
Proportions=Proportions /
```

**\*\*Task\*\***

Information specific to categorical traits

**\*\*Properties of names\*\***

```
NCategories      Definition: Number of categories for each categorical trait
                  Type: Integer
                  Dimension: nCategoricalObs
                  Options: ≥2
                  Default: -1
```

```
Proportions      Definition: Proportion of observations that fall within
                  Category intervals
                  Type: Real
                  Dimension: nCategoricalObs*Max(NCategories)
                  Options:
```

0.0<*Proportions*<1.0 Proportion for each category  
 -9.0 Otherwise  
 Default: -1.0

**\*\*Additional information\*\***

- 1) Proportions provided in *Proportions* must sum to 1 for each categorical trait
- 2) Unused elements in *Proportions* must be -9.0

**&MARKER\_NUMBERS**

markers=markers /

**\*\*Task\*\***

Number of markers on each chromosome

**\*\*Properties of names\*\***

*markers* Definition: Number of markers on each chromosome  
 Type: Integer  
 Dimension: *nchrom*  
 Number required for each chromosome; the number of chromosomes is *nchrom*  
 Options: ≥0  
 Default: -1

**\*\*Example\*\***

The following illustrates how the input for this namelist is provided. In the example, seven markers are located on two chromosomes (*nchrom*=2); four markers are located on the first chromosome, three markers are on the second.

**&MARKER\_NUMBERS**

markers=  
 4  
 3 /

**&MARKER\_PARAMETERS**

m\_positions=m\_positions  
 m\_alleles=m\_alleles /

**\*\*Task\*\***

Positions and numbers of alleles at each marker locus

**\*\*Properties of names\*\***

*m\_positions* Definition: Position (cM) of the markers on each chromosome  
 Type: Real  
 Dimension: Sum of array *markers*  
 Real required for each marker; the number of markers on each chromosome is provided in *markers*  
 Options: ≥0.0  
 Default: -1.0

*m\_alleles* Definition: Number of alleles at each marker locus  
 Type: Integer  
 Dimension: Sum of array *markers*  
 Integer required for each marker; the number of markers on each chromosome is provided in *markers*

Options:  $\geq 0$   
Default: -1

**\*\*Example\*\***

The following illustrates how the input for this namelist is provided. In the example, seven markers are located on two chromosomes (*nchrom=2*); four markers are located on the first chromosome, three markers are on the second (*markers=4 3*).

&MARKER\_PARAMETERS

m\_positions=

13.2  
17.6  
45.1  
47.3 [Positions (cM) of the four marker loci on the first chromosome]

67.1  
71.7  
77.4 [Positions of the three markers loci on the second chromosome]

m\_alleles=

4  
3  
2 [Four, three, two, and two alleles are at the four marker loci  
2 located on the first chromosome]  
  
2  
3 [Two, three and two alleles are at the three marker loci located on  
2 / the second chromosome]

&MARKER\_ALLELE\_FREQUENCIES

m\_al\_freq=m\_al\_freq /

**\*\*Task\*\***

Frequencies of each marker allele

**\*\*Properties of names\*\***

*m\_al\_freq* Definition: Frequencies of marker alleles  
Type: Real  
Dimension: Sum of array *m\_alleles*  
Real required for each marker allele; the number of alleles on each chromosome is provided in *m\_alleles*  
Options:  $\geq 0.0$   
Default: -1.0

**\*\*Example\*\***

The following illustrates how the input for this namelist is provided. In the example, seven marker loci are located on two chromosomes (*nchrom=2*); four markers are located on the first chromosome, three markers are on the second (*markers=4 3*). The numbers of alleles at the four marker loci on the first chromosome are four, three, two, and two; the numbers at the three loci located on the second chromosome are two, three, and two (*m\_alleles*).

&MARKER\_ALLELE\_FREQUENCIES

```

m_al_freq=
  0.86 0.07 0.05 0.02 [Frequencies of the four alleles at the first marker
locus located on the first chromosome]
  0.65 0.30 0.05      [Frequencies of the three alleles at the second marker
locus located on the first chromosome]
  0.50 0.50
  0.70 0.30

  0.55 0.45          [Frequencies of the two alleles at the first marker locus
located on the second chromosome]
  0.40 0.30 0.30
  0.90 0.10 /

```

### &SAMPLE\_MARKER\_PARAMETERS

```

marker_type=marker_type
marker_coverage=marker_coverage
msat_density=msat_density
snp_density=snp_density
marker_spacing=marker_spacing /

```

#### \*\*Task\*\*

Parameters to sample marker loci; type, number, density, and distribution of the loci

#### \*\*Properties of names\*\*

```

marker_type          Definition: Type of markers sampled
                    Type: Character
                    Options:
                      msat  Microsatellites
                      snps  SNPs
                      both  Both SNPs and microsatellites
                    Default: snps

marker_coverage      Definition: Number of markers sampled
                    Type: Integer
                    Options:
                      1 Number is provided in namelist &MARKER_PARAMETERS
                      2 Number is a function of marker density, where
                        marker density is provided as msat_density or
                        snp_density
                    Default: 1

msat_density         Definition: Number of microsatellite markers per cM
                    Type: Real
                    Options: ≥0.0
                    Default: 0.1

snp_density          Definition: Number of SNPs markers per cM
                    Type: Real
                    Options: ≥0.0
                    Default: 1.0

marker_spacing       Definition: Spacing of markers along the genome
                    Type: Integer
                    Options:

```

1 Markers evenly spaced across the genome  
2 Markers randomly spaced across the genome  
Default: 2

#### &QTL\_PARAMETERS

*qtls*=*qtls*  
*q\_positions*=*q\_positions*  
*q\_alleles*=*q\_alleles*  
*qtl\_wt*=*qtl\_wt* /

#### \*\*Task\*\*

Number and position of QTLs, the number of alleles at each QTL, and the weight of each QTL

#### \*\*Properties of names\*\*

*qtls*                    Definition: Number of QTLs on each chromosome  
                          Type: Integer  
                          Dimension: *nchrom*  
  Integer required for each chromosome; the  
  number of chromosomes is *nchrom*  
Options: ≥0  
Default: -1

*q\_positions*            Definition: Position (cM) of each QTL on each chromosome  
                          Type: Real  
                          Dimension: Sum of array *qtls*  
  Real required for each QTL; the number of QTLs  
  on each chromosome is provided in *qtls*  
Options: ≥0.0  
Default: -1.0

*q\_alleles*              Definition: Number of alleles at each QTL  
                          Type: Integer  
                          Dimension: Sum of array *qtls*  
  Integer required for each QTL; the number of QTLs  
  on each chromosome is provided in *qtls*  
Options: ≥0  
Default: -1

*qtl\_wt*                 Definition: Weight placed on each QTL during selection;  
  the weight is relative to polygenic effects  
                          Type: Real  
                          Dimension: Sum of array *qtls*  
  Real required for each QTL; the number of QTLs  
  on each chromosome is provided in *qtls*  
Options: ≥0.0  
Default: -1.0

#### \*\*Example\*\*

The following illustrates how the input for this namelist is provided. In the example, five QTLs are located on two chromosomes (*nchrom*=2); three QTLs are located on the first chromosome, two QTLs on the second.

#### &QTL\_PARAMETERS

*qtls*=

```

3
    [Two chromosomes; three QTLs are located on the first chromosome,
2    two are located on the second]

q_positions=
3.2
7.6
15.1    [Positions (cM) of the three QTLs on the first chromosome]

17.1
54.7    [Positions of the two QTLs on the second chromosome]

q_alleles=
3
2    [Three, two, and two alleles are at the three QTL loci located on
2    the first chromosome]

3    [Three and two alleles are at the two QTL loci located on the
2    second chromosome]

qtl_wt=
1.0    [Equal weight given to the first QTL on the first chromosome and
polygenic effects]
0.9    [Less weight given to the second QTL]
1.7    [More weight given to the second QTL]

2.2    [More weight given to the first QTL on the second chromosome]
0.5    /

```

#### **&QTL\_EFFECTS\_FREQUENCIES**

```

q_effects=q_effects
q_al_freq=q_al_freq /

```

##### **\*\*Task\*\***

Effects and frequencies of each QTL allele

##### **\*\*Properties of names\*\***

```

q_effects    Definition: Effect of each QTL allele
              Type: Real
              Dimension: Sum of array q_alleles
                       Real required for each QTL allele; the number of
                       QTLs on each chromosome is provided in qtls
                       The block of input is repeated for each true
                       breeding value simulated

              Options: ≥0.0
              Default: -1.0

```

```

q_al_freq    Definition: Frequencies of QTL alleles
              Type: Real
              Dimension: Sum of array q_alleles
                       Real required for each QTL allele; the number of
                       QTLs on each chromosome is provided in qtls
                       The block of input is repeated for each true
                       breeding value simulated

              Options: ≥0.0

```

Default: -1.0

**\*\*Example\*\***

The following illustrates how the input for this namelist is provided. In the example, QTLs are located on two chromosomes (*nchrom=2*); three QTLs are located on the first chromosome, two QTLs on the second. The numbers of alleles at the three QTLs on the first chromosome are three, two, and two; the numbers at the two loci on the second chromosome are two and three (*q\_alleles*).

```
&QTL_EFFECTS_FREQUENCIES
q_effects=
  10.7 -3.0 -7.7          [Effects of the three alleles at the first QTL located
on the first chromosome]
  2.2 -2.2              [Effects of the two alleles at the second QTL located on
the first chromosome]
  5.1 -5.1

  1.9 -1.9              [Effects of the two alleles at the first QTL located on
the second chromosome]
  5.2 2.0 -7.2

q_al_freq=
  0.07 0.23 0.70        [Frequencies of the three alleles at the first QTL
located on the first chromosome]
  0.05 0.95             [Frequencies of the two alleles at the second QTL located
on the first chromosome]
  0.50 0.50

  0.75 0.25             [Frequencies of the two alleles at the first QTL located
on the second chromosome]
  0.20 0.30 0.50 /
```

**&SAMPLE\_QTL\_PARAMETERS**

```
qtl_effect_input=qtl_effect_input
gene_distribution=gene_distribution
gamma_scale=gamma_scale
gamma_shape=gamma_shape /
```

**\*\*Task\*\***

Parameters to sample QTLs; sample QTLs by number or QTL variance, distribution of QTL across the genome, and distribution of QTL effects

**\*\*Properties of names\*\***

```
qtl_effect_input      Definition: Specifies whether a (1) given number of QTL,
                      (2) given amount of variance explained by
                      QTL, or (3) given number of QTL explaining a
                      given amount of variance is sampled
                      Type: Integer
                      Options: 1 Number of QTL sampled
                               2 Amount of variance explained by QTL is sampled
                               3 Number of QTL explaining given amount of variance
                               is sampled
                      Default: 1

gene_distribution      Definition: QTL are uniformly or multinomially
```

distributed across the genome  
 Type: Integer  
 Options: 1 Uniform distribution  
 2 Multinomial distribution  
 Default: 1

*gamma\_scale* Definition: Scale parameter of gamma distribution; QTL effects assumed to follow a gamma distribution  
 Type: Real  
 Options:  $\geq 0.0$   
 Default: 5.4

*gamma\_shape* Definition: Shape parameter of gamma distribution; QTL effects assumed to follow a gamma distribution  
 Type: Real  
 Options:  $\geq 0.0$   
 Default: 0.42

### &SAMPLE\_QTL\_NUMBERS

*n\_qtl\_trait*=*n\_qtl\_trait*  
*var\_qtl\_trait*=*var\_qtl\_trait* /

#### \*\*Task\*\*

Parameters to sample QTLs; number of QTLs affecting each trait and the variance of the traits explained by the QTLs

#### \*\*Properties of names\*\*

*n\_qtl\_trait* Definition: Number of QTL affecting each trait  
 Type: Integer  
 Dimension: Integer required for each trait; where the number of traits, *ntbv*, is provided in namelist &POPVARIABLES.  
 Options:  $\geq 0$   
 Default: -1

*var\_qtl\_trait* Definition: Variance of each trait explained by QTL  
 Type: Real  
 Dimension: Real required for each trait; where the number of traits, *ntbv*, is provided in namelist &POPVARIABLES.  
 Options:  $\geq 0.0$   
 Default: -1.0

#### \*\*Example\*\*

The following illustrates how the input for this namelist is provided. In the example, two traits (*ntbv*=2) are affected by 2 and 4 QTLs

#### &SAMPLE\_QTL\_NUMBERS

*n\_qtl\_trait*=  
 2  
 4 [Two traits affected by two and four QTLs]

*var\_qtl\_trait*=  
 0.2  
 100.0 / [QTL variance 0.2 for the first trait, 100.0 for the second trait]

## &GAS\_PARAMETERS

gas\_weight=gas\_weight /

### \*\*Task\*\*

Parameters used in gene-assisted selection

### \*\*Properties of names\*\*

*gas\_weight* Definition: Weight placed on known gene effect; the weight is relative to polygenic effects  
Type: Real  
Options:  $\geq 0.0$   
Default: 1.0; gene and polygenic effects weighted equally

## &TEMPLATE\_PARAMETERS

template\_density=template\_density  
founder\_representation=founder\_representation  
print\_genotypes=print\_genotypes /

### \*\*Task\*\*

Parameters used to specify the use of a marker template. The marker template is a dense marker map that provides unique genotypes for all base individuals. It is sampled for all offspring according to Mendelian sampling terms allowing for recombination. The markers are not available for selection purposes but only serve to monitor inbreeding.

### \*\*Properties of names\*\*

*template\_density* Definition: Number of markers per cM  
Type: Real  
Options:  $\geq 0.0$   
Default: 2.0

*print\_genotypes* Definition: Controls whether the template genotype for each plants in each timestep is written to the output file 'template\_info<timestep>.res'  
Type: Integer  
Options:  
1 Output written to file  
2 Output not written to file  
Default: 1

*founder\_representation* Definition: Specify if founder representation should be calculated. For each time step, the representation of each base plant in specific loci are given. These loci includes all QTL and a number of template loci specified in &FOUNDER\_PARAMETERS.  
Type: Integer  
Options:  
1 Founder representation is not calculated  
2 Founder representation is calculated  
Default: 1

### \*\*Relation to subsequent namelists\*\*

&FOUNDER\_PARAMETERS

Namelist &FOUNDER\_PARAMETERS is required if *founder\_representation* 2

**\*\*Additional information\*\***

1) do ichrom=1,nchrom ! Number of template markers on each chromosome

chrom(ichrom)%nmarkers\_template=nint(template\_density\*chrom(ichrom)%length)  
end do

The number of template markers is rounded to the nearest integer. So, if *template\_density\*chrom(ichrom)%length* is not a whole number, the number of markers differs slightly from the specified number.

## &REPORT

firstReportHerd=*firstReportHerd*

lastReportHerd=*lastReportHerd*

nGenomicF=*nGenomicF*

genomicFParameters=*stage genomicBase firstChrom lastChrom loci maf mafInclude*  
*locusWeight scaleMethod adjustGScale propAToG addDiagG*  
*diagGOne*

printBiasAccuracy=*printBiasAccuracy*

printBreedingValues=*printBreedingValues*

printEvaRelationships=*printEvaRelationships*

genomicRelationshipParameters=*stage genomicBase firstChrom lastChrom loci maf*  
*mafInclude locusWeight scaleMethod adjustGScale*  
*propAToG addDiagG diagGOne*

ibdRelationshipParameters=*stage firstChrom lastChrom loci*

ibsRelationshipParameters=*stage firstChrom lastChrom loci*

printGenomicHomozygosity=*printGenomicHomozygosity*

firstReportTime=*firstReportTime*

lastReportTime=*lastReportTime*

reportSelectionStages=*reportSelectionStages*

printIbd=*printIbd*

ibdParameters=*founderRepresentation printIbdGenotypes*

time\_steps\_year=*time\_steps\_year*

print\_replicate=*print\_replicate*

printLdHayesFiles=*printLdHayesFiles*

printLdMutations=*printLdMutations*

debugOutput=*debugOutput /*

**\*\*Task\*\***

Controls generation of output files. Output files are written to the output directory specified in namelist &OUTPUTDIRECTORY, variable *OutDirectory*. Contents of the output file are provided in section 'Output files'.

**\*\*Properties of names\*\***

*firstReportHerd* Definition: First herd-of-birth of plants used to calculate genetic trends written to output files, 'geneticTrendsRep<rep>.res', 'geneticTrendsMeans.res', and 'geneticTrendsPlots.pdf', where <rep> is replicate number ... and phenotypic-trends and genomic-inbreeding file.

Type: Integer

Options: *lastReportHerd*≥1

Default: 1

*lastReportHerd* Definition: Last herd-of-birth of plants used to calculate genetic trends written to output files, 'geneticTrendsRep<rep>.res', 'geneticTrendsMeans.res', and 'geneticTrendsPlots.pdf', where <rep> is replicate number ... and phenotypic-trends and genomic-inbreeding file

Type: Integer  
Options: *firstReportHerd* ≤ *lastReportHerd* ≤ *nherd*  
Default: *nherd*

*nGenomicF* Definition: Number of genomic-inbreeding coefficients to calculate

Type: Integer  
Options: *nGenomicF* ≥ 0  
Default: 0

Ignored when *GeneticModel* not 'genomic'

*genomicFParameters*

As for &GENOMICBLUPPARAMETERS parameters with the exception that:

(i) *genomicBase* can only be 'all' and 'base', where 'all' includes all plants in the population and 'base' includes all plants in the base population. Genotyping is ignored.

*stage* dummy variable; *stage* is not used, but a integer must be provided.  
Parameters to generate genomic-relationship matrices used to calculate genomic-inbreeding coefficients  
Number of lines in parameters must equal *nGenomicF*

Input to construct genomic-**H** matrices using the program, *invmatrix*. Genomic-**H** matrices are used by EVA to constraint average relationship. The namelist is read when *relationshipMatrix* 'genomic' in any EVA-selection stage of namelist &EVA, variable *EvaSelection*.

Description of variables in parameters is as described for namelist &GENOMICBLUPPARAMETERS

If present in namelist, *genomicFParameters* read in. However, it is only used when when *GeneticModel* 'genomic' and *genomicF* 'yes'. When when *GeneticModel* 'genomic' and *genomicF* 'yes', all variables in *genomicFParameters* must be present.

'parental' genomic/blended inbreeding set to zero for base plants. That means, genomic-F 0.0 at time 0.

*printBiasAccuracy* Definition: Write bias and accuracy at each specified time step and selection stage to output files, 'biasAccuracyRep<rep>.res', 'biasAccuracyMeans.res', and 'biasAccuracyPlots.pdf', where <rep> is replicate number

Type: Character  
Options:  
no Biases and accuracies are not written to output files  
yes Biases and accuracies are written to output files

*printBreedingValues*      Default: no  
 Definition: Write true and estimated breeding values of each selection candidate at each specified time step and selection stage to output files, 'breedingValuesRep<rep>.res', where <rep> is replicate number. Files are compressed by the linux command, 'bzip2 -f breedingValuesRep<rep>.res'.  
 Type: Character  
 Options:  
     no Breeding values are not written to output files  
     yes Breeding values are written to output files  
 Default: no

*printEvaRelationships* Definition: Write genetic contributions, average relationships of selected plants, and summaries of relationship matrices for candidates and selected plants to output files 'averageRelationshipsReps.res' and 'averageRelationshipsMeans.res'; EVA-selection stages only,  
 Type: Character  
 Options:  
     no Contributions, relationships, and summaries are not written to output files  
     yes Contributions, relationships, and summaries are written to output files  
 Default: no

printEvaRelationships can only be yes when EVA-selection is carried out; this is, there are selection stages with EVA-selection.

#### *genomicRelationshipParameters*

As for &GENOMICBLUPPARAMETERS parameters with the exception that:

stage dummy variable; stage is not used, but a integer must be provided; parameters apply to all EVA-selection stages

This is optional input. It is used to construct genomic-relationship matrix after stages of EVA selection when *printEvaRelationships* 'yes', *GeneticModel* 'genomic', and *relationshipMatrix* in namelist &EVA, variable *EvaSelection* is not 'genomic'. When *relationshipMatrix* is 'genomic', the genomic-relationship matrix used to constrain rates of inbreeding with EVA-selection is used. These relationship matrices are used to calculate average relationships of selected plants and summaries of relationship matrices for candidates and selected plants. At times *firstReportTime:lastReportTime*. When all constraints are 'genomic' at times *firstReportTime:lastReportTime*, *genomicRelationshipParameters* is not required.

Plants need to be genotyped to have their genotypes included in genomic-relationship matrix. So, genotyping strategy is critical to *printEvaRelationships* when not using genomic information to constrain rates of inbreeding in EVA.

Genotyping is ignored when constructing 'ibs' and 'ibd' relationship matrices; as for matrices to constrain rates of inbreeding with EVA-selection.

Note: If *relationshipMatrix* is 'genomic' in EVA-selection, but 'pedigree' used because no plants are genotyped at times *firstReportTime:lastReportTime*, then output associated with genomic-relationship matrices in *genomicRelationshipParameters* is not generated.

It is assumed that if genomic-relationship matrix cannot be created during EVA-selection, it cannot be created during report.

Input to construct genomic-**H** matrices using the program, invgmatrix.

All *genomicBase* options available; genotyping is considered.

When *relationshipMatrix* is not 'genomic' in EVA-selection, the genomic-relationship matrix generated with *printEvaRelationships* 'yes' is based on plants traced back from the candidates for EVA-selection:

```
do i=1,nCandidates
  call tracePedigreeGRM(contributions(i)%id)
end do
```

Note: This option considers all stages of EVA-selection; selected plants may or may not be destined for reproduction. Number of matings allocated to selected plants is used to calculate genetic contributions; litter size is ignored. This is not a problem at this stage as litter size is constant within selection stages.

#### *ibdRelationshipParameters*

Parameters used to construct IBD-relationship matrix after stages of EVA-selection when *printEvaRelationships* 'yes', *GeneticModel* 'genomic', and *relationshipMatrix* in namelist &EVA, variable *EvaSelection* is not 'ibd';

!

EVA-selection stages only

#### *ibsRelationshipParameters*

Parameters used to construct IBS-relationship matrix after stages of EVA-selection when *printEvaRelationships* 'yes', *GeneticModel* 'genomic', and *relationshipMatrix* in namelist &EVA, variable *EvaSelection* is not 'ibs';

!

EVA-selection stages only; required when *printEvaRelationships* 'yes', *GeneticModel* 'genomic', EVA-selection in breeding scheme, and not all EVA-selection stages are 'ibd'/'ibs'. If all EVA-selection stages, for example, are 'ibd', then do not need to specify *ibdRelationshipParameters*, but will require *ibsRelationshipParameters* and *genomicRelationshipParameters*.

*ibdRelationshipParameters* and *ibsRelationshipParameters* have same structure as &IBDBLUPPARAMETERS, variable parameters ... [and the three other ibd and ibs namelists]

*printGenomicHomozygosity* Definition: Write genomic homozygosity at QTL, marker, template-QTL, and template-marker loci to output files,

'averageRelationshipsReps.res' and  
'averageRelationshipsMeans.res'

Type: Character

Options:

no Genomic homozygosity is not written to output files  
yes Genomic homozygosity is written to output files

Default: no

```
ibdRelationshipParameters=stage firstChrom lastChrom loci
```

```
ibsRelationshipParameters=stage firstChrom lastChrom loci
```

Both as for earlier ibd and ibs namelists

*firstReportTime* Definition: First time step for which output is written to output files when *printBreedingValues* and/or *printBiasAccuracy* 'yes'  
Type: Integer  
Options: *firstReportTime*≥1  
Default: 1

*lastReportTime* Definition: Last time step for which output is written to output files when *printBreedingValues* and/or *printBiasAccuracy* 'yes'  
Type: Integer  
Options: *firstReportTime*≤*lastReportTime*≤*ntime*  
Default: *ntime*

*reportSelectionStages* Definition: List of selection stages for which output is written to output files when *printBreedingValues* and/or *printBiasAccuracy* 'yes'  
Type: Integer  
Dimension:  $1 \leq nStages \leq selection\_groups$ , where *nStages* is the number of selection stages for which output variables are to be written  
Options:  $1 \leq reportSelectionStages_i \leq selection\_groups$  ( $i=1, \dots, nStages$ ), where *reportSelectionStages<sub>i</sub>* is the *i*th integer of *reportSelectionStages* and *reportSelectionStages<sub>i</sub>*≠*reportSelectionStages<sub>j</sub>* ( $i \neq j$ )  
Default: 1 ... *selection\_groups*

*printIbd* Definition: Write IBD output to output files  
Type: Character  
Options:  
no Output is not written to output files  
yes Output is written to output files  
Default: no

*founderRepresentation* Definition: Specify if founder representation should be calculated. For each time step, the representation of each base plant in specific loci are given. These loci includes all QTL and a number of template loci specified in &FOUNDERPARAMETERS.  
Type: Integer  
Options:  
1 Founder representation is not calculated  
2 Founder representation is calculated  
Default: 1

*printIbdGenotypes* Definition: Controls whether the template genotype for each plants in each timestep is written to the output file 'template\_info<timestep>.res'  
Type: Integer  
Options:  
1 Output is not written to file  
2 Output is written to file  
Default: 1

*time\_steps\_year* Definition: Number of time steps per year; used to write

(delete) results to output files  
Type: Integer  
Options:  $\geq 1$   
Default: 1

*print\_replicate* Definition: Controls whether information on each individual is outputted in files  
Type: Integer  
Options:  
0 Simulated datasets are not stored.  
1 Simulated datasets are stored in several files.  
Default: 0

*printLdHayesFiles* Definition: Write output from analysis of linkage disequilibrium to output files, heterozygosity.dat, QTLdistribution.dat, markerDistribution.dat, LD\_bin.dat, ldPlots.pdf, ldSummaryOutputOverTime.dat, and ldVersusDistanceOverTime.dat  
Type: Character  
Options:  
no Output is not written to output files  
yes Output is written to output files  
Default: no

*printLdMutations* Definition: Write sampled positions of mutations from analysis of linkage disequilibrium to output file, mutations.dat  
Type: Character  
Options:  
no Output is not written to output file  
yes Output is written to output file  
Default: no

*debugOutput* Definition: Working-data and script files are copied to the output directory. These files are listed in 'Output files'. They are copied after they have been created; newly-created files overwrite older files. They will be the last files created, should the program crash.  
Type: Character  
Options:  
no Files are not copied to output directory  
yes Files are copied to output directory  
Default: no

**\*\*Relation to subsequent namelists\*\***

&FOUNDERPARAMETERS

Namelist &FOUNDERPARAMETERS is required if *founderRepresentation* 2

**\*\*Additional information\*\***

1) Namelist &REPORT must be provided, even if it does not contain input

2) Files with genetic trends, 'geneticTrendsRep<rep>.res', geneticTrendsMeans.res', and 'geneticTrendsPlots.pdf' are always written to the output directory

Base population and calculating genetic merit at time 0?

- 3) (a) When *firstReportHerd* and *firstReportHerd* are not provided, all plants born at the current time step are used to calculate genetic trends
- (b) *firstReportHerd* and *firstReportHerd* only apply to output files 'geneticTrendsRep<rep>.res', 'geneticTrendsMeans.res', and 'geneticTrendsPlots.pdf'

4) No genomic-inbreeding coefficients calculated when *nGenomicF* 0

If present in namelist, *genomicF* is read in. However, it is only used when *GeneticModel* 'genomic'.

If present in namelist, *genomicFParameters* read in. However, it is only used when when *GeneticModel* 'genomic' and *genomicF* 'yes'. When when *GeneticModel* 'genomic' and *genomicF* 'yes', all variables in *genomicFParameters* must be present.

- 5) Files *breedingValuesRep<rep>.res* are compressed with the linux command, 'bzip2 -f *breedingValuesRep<rep>.res*'. bzip2 compresses files using the Burrows-Wheeler block-sorting text-compression algorithm and Huffman coding. They can be decompressed with the command, 'bunzip2 *breedingValuesRep<rep>.res.bz2*'.

5) *printGenomicHomozygosity* can only be 'yes' when *GenomicModel* 'qtl' or 'genomic'

*firstReportHerd*, *lastReportHerd*, *firstReportTime*, and *lastReportTime* apply with *printGenomicHomozygosity*=='yes'

[Outline when *firstReportHerd*, *lastReportHerd*, *firstReportTime*, *lastReportTime*, and *reportSelectionStages* do and don't apply]

Required when `lowercase(printBiasAccuracy)=='yes'` .or.  
`lowercase(printBreedingValues)=='yes'` .or. &  
`lowercase(printEvaRelationships)=='yes'` .or.  
`lowercase(printGenomicHomozygosity)=='yes'`

- 6) (a) *firstReportTime* and *lastReportTime* only apply when *printBreedingValues* and/or *printBiasAccuracy* 'yes'
- (b) `current_time>0`

7) (a) *reportSelectionStages* only applies when *printBreedingValues*, *printBiasAccuracy*, *printEvaRelationships*, and/or *printGenomicHomozygosity* 'yes'

(b) Selection stages specified in *reportSelectionStages* will generate output result when *SelectionMethod*='truncation' or 'eva'. When *SelectionMethod* 'truncation', *SelectionCriterion* can be 'tbv', 'phenoweight', 'polyblup', 'genomicblup', 'ibdblup', 'gas', or 'bayesp'. When *SelectionMethod* 'eva', *MaleSelCrit* can be 'tbv', 'polyblup', 'genomicblup', 'ibdblup', 'gas', or 'bayesp'. *FemaleSelCrit* can be 'tbv', 'polyblup', 'genomicblup', 'ibdblup', 'gas', or 'bayesp'. In all other cases, output is not written to the files.

- (c) Selection stages specified in *reportSelectionStages* need not be ordered by Selection stage
- (d) Selection stages specified in *reportSelectionStages* cannot be repeated

*printIbd* can only be 'yes' when variable *templateDensity* in namelist& *control\_genome* is greater than 0.0.

*ibdParameters* is only used when *printIbd* 'yes'

8) When GeneticModel 'ldonly', *printLdHayesFiles* and *printLdMutations* are the only report parameters used; *debugOutput* is used when *printLdHayesFiles* 'yes'.

#### &FOUNDERPARAMETERS

```
pos_founderloci=pos_founderloci
n_founderloci=n_founderloci /
```

##### \*\*Task\*\*

Specifies for which loci founder representation should be determined

##### \*\*Properties of names\*\*

```
n_founderloci      Definition: Number of template loci on each chromosome for
                    which founder representation should be determined
                    Type: Integer
                    Dimension: nchrom*1; a number required for each chromosome
                    Options: ≥0
                    Default: -1
```

```
pos_founderloci  Definition: Positions of template loci in which founder
                    representation should be determined
                    Type: Real
                    Dimension:  $\Sigma$  or  $\text{sum}(n\_founderloci)*1$ ; a number required for
                    each locus position
                    Options: ≥0.0
                    Default: -1.0
```

##### \*\*Relation to subsequent namelists\*\*

Namelist &FOUNDERPARAMETERS is required if *printIbd* 'yes' and *founderRepresentation* 2 in namelist &REPORT, variable *ibdParameters*

## 15. Output files

Output files that are generated and written to output directory specified in namelist &OUTPUTDIRECTORY, variable *OutDirectory*:

geneticTrendsMeans.res

geneticTrendsRep<rep>.res (*rep*=*start\_rep* ... *start\_rep*+*nrep*-1)

geneticTrendsPlots.pdf

input.log

seeds.in

error.txt

memory.log

adam\_log.txt

adamlog.log

biasAccuracyMeans.res

biasAccuracyRep<rep>.res

breedingValuesRep<rep>.res.bz2

dmuAdamRep<rep>Time<time>Stage<stage>.lst

plant#.res (optional)

marker#.res (optional)

mean\_timesteps.res

mean\_timesteps\_replicate.res

number\_genotyped.res (optional)

obs#.res (optional)

qtl#.res (optional)

template#.res

template\_info#.res (optional)

mean\_template#.res (optional)

mean\_founder#.res (optional)

## geneticTrendsMeans.res

Description: Means of genetic trends as a function of time across replicates

Column variables:

timeStep generation nReps BV sdBV polyBV sdPolyBV qtlBV sdQtlBV varBV sdVarBV  
varPolyBV sdVarPolyBV varQtlBV sdVarQtlBV varMend sdVarMend F sdF GI sdGI

When  $ntbv > 1$ , variables specific to each trait are also presented:

timeStep generation nReps [necessary?] BV1 sdBV1 polyBV1 sdPolyBV1 qtlBV1 sdQtlBV1  
varBV1 sdVarBV1 varPolyBV1 sdVarPolyBV1 varQtlBV1 sdVarQtlBV1 varMend1 sdVarMend1 ...  
BVntbv sdBVntbv polyBVntbv sdPolyBVntbv qtlBVntbv sdQtlBVntbv varBVntbv sdVarBVntbv  
varPolyBVntbv sdVarPolyBVntbv varQtlBVntbv sdVarQtlBVntbv varMendntbv sdVarMendntbv

timeStep	Birth time (0 ... $ntime$ )
generation	Mean generation number across $nrep$ replicates of plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$ . Generation number of plant $i$ is calculated as $\frac{1}{2}(gNSire_i + gNDam_i) + 1.0$ , where $gNSire_i$ and $gNDam_i$ are the generation numbers of the sire and dam of plant $i$ . Generation numbers of base plants is 0.0.
nReps	Number of replicates ( $nrep$ )
BV	Mean aggregate-breeding value of plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$ . BV is the mean of $nrep$ replicate means.
sdBV	Standard deviation of BV (variation for replicate means)
polyBV	Mean aggregate polygenic-breeding value across $nrep$ replicates of plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
sdPolyBV	Standard deviation of polyBV
qtlBV	Mean aggregate QTL-breeding value across $nrep$ replicates of plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
sdQtlBV	Standard deviation of qtlBV
varBV	Mean variance of aggregate-breeding values across $nrep$ replicates for plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
sdVarBV	Standard deviation of varBV
varPolyBV	Mean variance of aggregate polygenic-breeding values across $nrep$ replicates for plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
sdVarPolyBV	Standard deviation of varPolyBV
varQtlBV	Mean variance of aggregate QTL-breeding values across $nrep$ replicates for plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
sdVarQtlBV	Standard deviation of varQtlBV
varMend	Mean variance of aggregate-Mendelian deviations across $nrep$ replicates for plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
sdVarMend	Standard deviation of varMend
F	Mean inbreeding coefficient based on pedigree across $nrep$ replicates for plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
sdF	Standard deviation of F
GI	Mean generation interval across $nrep$ replicates for plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$ . GI for the $ith$

plant is calculated as  $\frac{1}{2}(2*b_i - s_i - d_i)$ , where  $b_i$  is the birth time of the  $i$ th plant born at time  $timeStep$ , and  $s_i$  and  $d_i$  are the birth times of the sire and dam of plant  $i$ .

sdGI Standard deviation of GI  
 BVj Mean breeding value for trait  $j$  ( $j = 1 \dots ntbv$ ) across  $nrep$  replicates of plants born at time  $timeStep$  in herds  
*FirstReportHerd*≤*herd*≤*LastReportHerd*  
 sdBVj Standard deviation of BVj (variation for replicate means)  
 polyBVj Mean polygenic-breeding value for trait  $j$  across  $nrep$  replicates of plants born at time  $timeStep$  in herds  
*FirstReportHerd*≤*herd*≤*LastReportHerd*  
 sdPolyBVj Standard deviation of polyBVj  
 qtlBVj Mean QTL-breeding value for trait  $j$  across  $nrep$  replicates of plants born at time  $timeStep$  in herds *FirstReportHerd*≤*herd*≤*LastReportHerd*  
 sdQtlBVj Standard deviation of qtlBVj  
 varBVj Mean variance of breeding values for trait  $j$  across  $nrep$  replicates for plants born at time  $timeStep$  in herds  
*FirstReportHerd*≤*herd*≤*LastReportHerd*  
 sdVarBVj Standard deviation of varBVj  
 varPolyBVj Mean variance of polygenic-breeding values for trait  $j$  across  $nrep$  replicates for plants born at time  $timeStep$  in herds  
*FirstReportHerd*≤*herd*≤*LastReportHerd*  
 sdVarPolyBVj Standard deviation of varPolyBVj  
 varQtlBVj Mean variance of QTL-breeding values for trait  $j$  across  $nrep$  replicates for plants born at time  $timeStep$  in herds  
*FirstReportHerd*≤*herd*≤*LastReportHerd*  
 sdVarQtlBVj Standard deviation of varQtlBVj  
 varMendj Mean variance of aggregate-Mendelian deviations for trait  $j$  across  $nrep$  replicates for plants born at time  $timeStep$  in herds  
*FirstReportHerd*≤*herd*≤*LastReportHerd*  
 sdVarMendj Standard deviation of varMendj

Criteria for output: File always generated and written to *OutDirectory*

Additional information: Means are generated using the replicates run during the current simulation

geneticTrendsRep<rep>.res

(**rep=start\_rep ... start\_rep+nrep-1**)

Description: Means of genetic trends as a function of time within replicates

Column variables:

timeStep generation nPlants BV polyBV qtlBV varBV varPolyBV varQtlBV varMend F GI

When  $ntbv > 1$ , variables specific to each trait are also presented:

timeStep generation BV1 polyBV1 qtlBV1 varBV1 varPolyBV1 varQtlBV1 varMend1 ...  
 polyBV $ntbv$  qtlBV $ntbv$  varBV $ntbv$  varPolyBV $ntbv$  varQtlBV $ntbv$  varMend $ntbv$

timeStep Birth time (0 ...  $ntime$ )  
 generation Mean generation number of plants born at time  $timeStep$  in herds  
*FirstReportHerd*≤*herd*≤*LastReportHerd*. Generation number of plant  $i$  is calculated as  $\frac{1}{2}(gNSire_i + gNDam_i) + 1.0$ , where  $gNSire_i$  and  $gNDam_i$  are the

generation numbers of the sire and dam of plant  $i$ . Generation numbers of base plants is 0.0.

nPlants	Number of plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
BV	Mean aggregate-breeding value of plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
polyBV	Mean aggregate polygenic-breeding value of plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
qtlBV	Mean aggregate QTL-breeding value of plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
varBV	Mean variance of aggregate-breeding values of plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
varPolyBV	Mean variance of aggregate polygenic-breeding values of plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
varQtlBV	Mean variance of aggregate QTL-breeding values of plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
varMend	Mean variance of aggregate-Mendelian deviations for plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
F	Mean inbreeding coefficient based on pedigree for plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
GI	Generation interval for plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$ . GI is calculated as $\frac{1}{2}(2*birth_i - sireBirth_i - damBirth_i)$ , where $birth_i$ is the birth time of the $i$ th plant born at time $timeStep$ , and $sireBirth_i$ and $damBirth_i$ are the birth times of the sire and dam of plant $i$ .
BVj	Mean breeding value for trait $j$ ( $j = 1 \dots ntbv$ ) of plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
polyBVj	Mean polygenic-breeding value for trait $j$ of plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
qtlBVj	Mean QTL-breeding value for trait $j$ of plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
varBVj	Mean variance of breeding values for trait $j$ for plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
varPolyBVj	Mean variance of polygenic-breeding values for trait $j$ for plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
varQtlBVj	Mean variance of QTL-breeding values for trait $j$ for plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$
varMendj	Mean variance of Mendelian deviations for trait $j$ for plants born at time $timeStep$ in herds $FirstReportHerd \leq herd \leq LastReportHerd$

Criteria for output: Files are always generated and written to *OutDirectory*

Additional information: Means are generated using the replicates run during the current simulation

#### geneticTrendsPlots.pdf

Description: Plots of genetic gain, inbreeding, variances, and generation interval as functions of time

Plots:

Total genetic gain	Mean aggregate-breeding value ( $\pm$ 95% confidence interval) as a function of time for plants born in
--------------------	---

herds  $FirstReportHerd \leq herd \leq LastReportHerd$ . BV is the mean of  $nrep$  replicate means.

Total polygenic gain Mean aggregate polygenic-breeding value ( $\pm 95\%$  confidence interval) as a function of time across  $nrep$  replicates of plants born at time  $timeStep$  in herds  $FirstReportHerd \leq herd \leq LastReportHerd$

Total QTL gain Mean aggregate QTL-breeding value ( $\pm 95\%$  confidence interval) as a function of time across  $nrep$  replicates of plants born at time  $timeStep$  in herds  $FirstReportHerd \leq herd \leq LastReportHerd$

Total genetic variance Mean variance of aggregate-breeding values ( $\pm 95\%$  confidence interval) as a function of time across  $nrep$  replicates for plants born at time  $timeStep$  in herds  $FirstReportHerd \leq herd \leq LastReportHerd$

Polygenic variance Mean variance of aggregate polygenic-breeding values ( $\pm 95\%$  confidence interval) as a function of time across  $nrep$  replicates for plants born at time  $timeStep$  in herds  $FirstReportHerd \leq herd \leq LastReportHerd$

QTL variance Mean variance of aggregate QTL-breeding values ( $\pm 95\%$  confidence interval) as a function of time across  $nrep$  replicates for plants born at time  $timeStep$  in herds  $FirstReportHerd \leq herd \leq LastReportHerd$

Mendelian variance Mean variance of aggregate-Mendelian deviations ( $\pm 95\%$  confidence interval) as a function of time across  $nrep$  replicates for plants born at time  $timeStep$  in herds  $FirstReportHerd \leq herd \leq LastReportHerd$

Inbreeding coefficient Mean inbreeding coefficient based on pedigree ( $\pm 95\%$  confidence interval) as a function of time across  $nrep$  replicates for plants born at time  $timeStep$  in herds  $FirstReportHerd \leq herd \leq LastReportHerd$

Generation interval Mean generation interval ( $\pm 95\%$  confidence interval) as a function of time across  $nrep$  replicates for plants born at time  $timeStep$  in herds  $FirstReportHerd \leq herd \leq LastReportHerd$ . GI for the  $i$ th plant is calculated as  $\frac{1}{2}(2*b_i - s_i - d_i)$ , where  $b_i$  is the birth time of the  $i$ th plant born at time  $timeStep$ , and  $s_i$  and  $d_i$  are the birth times of the sire and dam of plant  $i$ .

When  $ntbv > 1$ , the following plots are also generated:

Genetic gain for trait  $j$  Mean breeding value for trait  $j$  ( $j = 1 \dots ntbv$ ) ( $\pm 95\%$  confidence interval) as a function of time across  $nrep$  replicates of plants born at time  $timeStep$  in herds  $FirstReportHerd \leq herd \leq LastReportHerd$

Polygenic gain for trait  $j$  Mean polygenic-breeding value for trait  $j$  ( $\pm 95\%$  confidence interval) as a function of time across  $nrep$  replicates of plants born at time  $timeStep$  in herds  $FirstReportHerd \leq herd \leq LastReportHerd$

QTL gain for trait  $j$  Mean QTL-breeding value for trait  $j$  ( $\pm 95\%$  confidence interval) as a function of time across  $nrep$  replicates of plants born at time  $timeStep$  in herds  $FirstReportHerd \leq herd \leq LastReportHerd$

Genetic variance for trait <i>j</i>	Mean variance of breeding values for trait <i>j</i> ( $\pm$ 95% confidence interval) as a function of time across <i>nrep</i> replicates for plants born at time <i>timeStep</i> in herds <i>FirstReportHerd</i> $\leq$ herd $\leq$ <i>LastReportHerd</i>
Polygenic variance for trait <i>j</i>	Mean variance of polygenic-breeding values for trait <i>j</i> ( $\pm$ 95% confidence interval) as a function of time across <i>nrep</i> replicates for plants born at time <i>timeStep</i> in herds <i>FirstReportHerd</i> $\leq$ herd $\leq$ <i>LastReportHerd</i>
QTL variance for trait <i>j</i>	Mean variance of QTL-breeding values for trait <i>j</i> ( $\pm$ 95% confidence interval) as a function of time across <i>nrep</i> replicates for plants born at time <i>timeStep</i> in herds <i>FirstReportHerd</i> $\leq$ herd $\leq$ <i>LastReportHerd</i>
Mendelian varaiance for trait <i>j</i>	Mean variance of Mendelian deviations for trait <i>j</i> ( $\pm$ 95% confidence interval) as a function of time across <i>nrep</i> replicates for plants born at time <i>timeStep</i> in herds <i>FirstReportHerd</i> $\leq$ herd $\leq$ <i>LastReportHerd</i>

#### input.log

Description: Reconstruction of input file, input.prm

Criterion for output: Always generated

#### seeds.in

Description:

#### error.txt

Description: Error message

Criterion for output: Program stops because of an error in input file(s) or program code

#### memory.log

Description: Memory usage

Criterion for output: Always generated

#### adam\_log.txt

Description: Log file with a description of simulation at each time step of each replicate

Criterion for output: Always generated

#### adamlog.log

Description:

## biasAccuracyMeans.res

Description: Mean bias and accuracy for each sex of selection candidates at each time and selection stage

Column variables:

time	stage	trait	sex	nReps	mnNPlants	mnBias	mnAccuracy	sdNPlants	sdBias	sdAccuracy
time	Time stage (time= <i>firstReportTime</i> ... <i>lastReportTime</i> )									
stage	Selection stage (stage= <i>reportSelectionStages</i> )									
trait	Trait number (trait=0 ... <i>ntbv</i> , where 0 is aggregate-breeding value and 1 ... <i>ntbv</i> is trait number)									
sex	Sex (sex=1 male, 2 female)									
nReps	Number of replicates									
mnNPlants	Mean number of selection candidates across <i>nrep</i> replicates									
mnBias	Mean bias for selection candidates across <i>nrep</i> replicates, where bias is the regression of true-breeding value on estimated breeding value									
mnAccuracy	Mean accuracy for selection candidates across <i>nrep</i> replicates, where accuracy is the correlation of true-breeding value and estimated breeding value									
sdNPlants	Standard deviation of mnNPlants									
sdBias	Standard deviation of mnBias									
sdAccuracy	Standard deviation of mnAccuracy									

Criteria for output: *printBiasAccuracy* 'yes' in namelist &REPORT

Additional information: No output written for times, stages, traits, and sex with no plants. No output is written at selection stages with no selection candidates or  $n < 2$ . No output written when ... (selection criterion) [CHECK]

(c) Selection scheme includes GAS breeding values

TotalAccuracy: AllCand GenoCand NonGenoCand, correlation between estimated and true breeding values for all, genotyped, and non-genotyped selection candidates

PolygenicAccuracy: AllCand GenoCand NonGenoCand, correlation between estimated and true polygenic breeding values for all, genotyped, and non-genotyped selection candidates

Derived from rep-files. So, excludes missing rep means and rep means with  $n < 2$ .

Truncation: 'tbv', 'phenoweight', 'polyblup', 'genomicblup', 'gas', 'bayesp'

EVA: 'tbv', 'polyblup', 'genomicblup', 'gas', 'bayesp'

All combinations of time, stage, trait, sex presented?

biasAccuracyRep<rep>.res (rep=start\_rep ... start\_rep+nrep-1)

Description: Mean bias and accuracy for each sex of selection candidates at each time and selection stage

Column variables:

time	stage	trait	sex	nReps	mnNPlants	mnBias	mnAccuracy	sdNPlants	sdBias	sdAccuracy
------	-------	-------	-----	-------	-----------	--------	------------	-----------	--------	------------

time            Time stage (time=*firstReportTime* ... *lastReportTime*)  
 stage           Selection stage (stage=*reportSelectionStages*)  
 trait           Trait number (trait=0 ... *ntbv*, where 0 is aggregate-breeding value and 1 ... *ntbv* is trait number)  
 sex             Sex (sex=1 male, 2 female)  
 nPlants        Mean number of selection candidates across *nrep* replicates  
 bias            Mean bias for selection candidates across *nrep* replicates, where bias is the regression of true-breeding value on estimated breeding value  
 accuracy       Mean accuracy for selection candidates across *nrep* replicates, where accuracy is the correlation of true-breeding value and estimated breeding value

Criteria for output: *printBiasAccuracy* 'yes' in namelist &REPORT

nPlants>1 for output line is written

Truncation: 'tbv', 'phenoweight', 'polyblup', 'genomicblup', 'gas', 'bayesp'  
 EVA: 'tbv', 'polyblup', 'genomicblup', 'gas', 'bayesp'

breedingValuesRep<rep>.res.bz2 (rep=start\_rep ... start\_rep+nrep-1)

Description: Estimated and true breeding values of selection candidates at each time, selection stage, sex

Column variables:

time stage id sire dam sex age herd trait genotyped phenotyped selected tbv ebv  
  
 time            Time step (time=*firstReportTime* ... *lastReportTime*)  
 stage           Selection stage (stage=*reportSelectionStages*)  
 id              Plant id  
 sire            Sire of plant  
 dam             Dam of plant  
 sex             Sex of plant (sex=1 male, 2 female)  
 age             Age of plant  
 herd            Herd of plant  
 trait           Trait number (trait=0 ... *ntbv*, where 0 is aggregate-breeding value and 1 ... *ntbv* is trait number)  
 genotyped      Plant genotyped (genotyped=0 not genotyped, 1 genotyped)  
 phenotyped     Plant phenotyped for specific trait (phenotyped=0 not phenotyped, 1 phenotyped, -1 trait is 0 and number of traits>1). When  
 selected        Plant selected in time and stage (selected=0 not selected, 1 selected)  
 tbv             True-breeding value  
 ebv             Estimated breeding value

Criteria for output: *printBreedingValues* 'yes' in namelist &REPORT

Additional information: Files are compressed by the linux command, 'bzip2 -f breedingValuesRep<rep>.res'. They can be decompressed with the command, 'bunzip2 breedingValuesRep<rep>.res.bz2'.

Breeding values are written to an output file at each selection stage with (i) truncation or EVA selection, and (ii) selection criterion weighted phenotypes, polygenic, genomic, or GAS breeding values

No output is written at selection stages with no selection candidates

### **breedingValuesRep<rep>.res (optional)**

Estimated and true breeding values of selection candidates at each selection stage

Breeding values are written to an output file at each selection stage with (i) truncation or EVA selection, and (ii) selection criterion weighted phenotypes, polygenic, genomic, or GAS breeding values

No output is written at selection stages with no selection candidates

Only non-missing rows and values included. If specified and not included, it is because not valid step or  $n < 2$ , where  $n$  is the number of candidates in the calculation of  $b$  and  $r$ .

**dmuAdamRep<rep>Time<time>Stage<stage>.lst**

**(rep=start\_rep ... start\_rep+nrep-1, time=1 ... ntime, stage=1 ... selection\_groups where breeding values predicted using DMU)**

Description: DMU-lst file generated by DMU when predicting breeding values

Criteria for output: *printDmuLstFiles* 'yes' in namelist &DMUPARAMETERS

Additional information: A unique file is created at each selection stage involving DMU calculations:

<rep>, replicate number  
<time>, time step  
<stage>, selection stage

Files are written to directory *dmuLstFiles*, a subdirectory of the output directory *OutDirectory* (namelist &OUTPUTDIRECTORY, variable *OutDirectory*)

DMU-lst file is written to an output file at each selection stage with DMU Calculations. These selection stages have (i) truncation or EVA selection, and (ii) selection criterion polygenic, genomic, or GAS breeding values.

### **heterozygosity.dat**

Description: LD-summary parameters as a function time; exponential distribution; summary of each replicate

Column variables:

```
igen ld_irep npar (count_seg-nqtl) nqtl count_mut count_cul nneg  
heterozygosity(igen,ld_irep,:) MeanFitness total_var genic_var ld_quant
```

```
igen          generation number of founder population  
ld_irep  
npar  
nmarkers     number of segregating markers in generation igen  
nqtl         number of segregating QTL in generation igen  
count_mut    number of new mutations in generation igen  
count_cul    number of culled offspring (not selected) in generation igen  
nneg  
heterozygosity(igen,ld_irep,:)  
MeanFitness
```

```
total_var
genic_var
ld_quant
```

Criteria for output: *printLdHayesFiles* 'yes' in namelist &REPORT

Additional information: *ld\_irep* is always 1 when *GeneticModel* 'genomic' in namelist &CONTROLPARAMETERS, *LD\_method* 'genomicld' in namelist &LD. It ranges from 1:*nrep* when *GeneticModel* 'ld\_Only'.

#### ldSummaryOutputOverTime.dat

Description: LD-summary parameters as a function time; exponential distribution; means of heterozygosity.dat across replicates

Column variables:

```
gen nReps nPar nMarkers nQTL nMutations nCulled nNegatives hetAll hetQtl meanFitness
varA varG ld
```

```
gen
nReps
nPar
nMarkers
nQTL
nMutations
nCulled
nNegatives
hetAll
hetQtl
meanFitness
varA
varG
ld
```

Criteria for output: *printLdHayesFiles* 'yes' in namelist &REPORT

#### LD\_bin.dat

Description: LD versus genomic distance markers as a function time; summary of each replicate

Column variables:

```
igen ld_irep bin1 bin2 ... bin40

igen          Final generation number of LD-analysis
ld_irep       Replicate number
bin1          r2 at specified distance between markers
bin2
bin40
```

Criteria for output: *printLdHayesFiles* 'yes' in namelist &REPORT

Additional information: `ld_irep` is always 1 when *GeneticModel* 'genomic' in namelist &CONTROLPARAMETERS, *LD\_method* 'genomicld' in namelist &LD. It ranges from 1:nrep when *GeneticModel* 'ld\_Only'.

#### ldVersusDistanceOverTime.dat

Description: LD versus genomic distance as a function time; exponential distribution; mean of LD\_bin.dat

Column variables:

```
gen nReps bin1 bin2 ... bin40

gen      Generation number of LD-analysis
nReps    Number of replicates
bin1
bin2
bin40
```

Criteria for output: *printLdHayesFiles* 'yes' in namelist &REPORT

#### QTLdistribution.dat

Description: Allele frequency and effect for each QTL locus at the end of the LD-analysis; summary of each replicate

Column variables:

```
igen ld_irep frequency effect

igen      Final generation number of LD-analysis
ld_irep   Replicate number
frequency Allele frequency at a QTL locus
effect    QTL effect at a QTL locus
```

Criteria for output: *printLdHayesFiles* 'yes' in namelist &REPORT

Additional information: `ld_irep` is always 1 when *GeneticModel* 'genomic' in namelist &CONTROLPARAMETERS, *LD\_method* 'genomicld' in namelist &LD. It ranges from 1:nrep when *GeneticModel* 'ld\_Only'.

#### markerDistribution.dat

Description: Allele frequency for each marker locus at the end of the LD-analysis; summary of each replicate

Column variables:

```
igen ld_irep frequency

igen      Final generation number of LD-analysis
ld_irep   Replicate number
frequency Allele frequency at a marker locus
```

Criteria for output: *printLdHayesFiles* 'yes' in namelist &REPORT

Additional information: *ld\_irep* is always 1 when *GeneticModel* 'genomic' in namelist &CONTROLPARAMETERS, *LD\_method* 'genomicld' in namelist &LD. It ranges from 1:*nrep* when *GeneticModel* 'ld\_Only'.

#### ldPlots.pdf

Description: Plots genetic gain, inbreeding, variances, and generation interval as functions of time; plots of *ldSummaryOutputOverTime.dat*, *ldVersusDistanceOverTime.dat*, *QTLdistribution.dat*, and *markerDistribution.dat*

#### Plots:

Number of segregating markers	Number of segregating-marker loci as a function of founder generation
Number of segregating QTL	Number of segregating-qt1 loci as a function of founder generation
Number of mutations	Number of new mutations as a function of founder generation
Number of culled plants	Number of culled plants as a function of founder generation
Average heterozygosity of markers and QTL	Average heterozygosity of markers and QTL as a function of founder generation
Average heterozygosity of QTL	Average heterozygosity of QTL as a function of founder generation

LD between segregating markers vs distance at generation *LD\_ngen*

LD between segregating markers <0.125> cM apart

Distribution of segregating-marker frequencies at generation *LD\_ngen*  
Only frequencies from replicate 1 presented. If *GeneticModel* 'ld\_Only' and *nrep*>1 in namelist &CONTROLPARAMETERS in namelist &LD, replicates 2:*nrep* not plotted.

Distribution of segregating-QTL frequencies at generation *LD\_ngen*

Distribution of segregating-QTL effects at generation *LD\_ngen*

Distribution of segregating-QTL variances at generation *LD\_ngen*

Effect versus frequency of segregating-QTL at generation *LD\_ngen*

#### baseHaplotypes.dat

Description: Sampled haplotypes generated by LD

Criteria for output: *GeneticModel* 'genomic' in namelist &CONTROLPARAMETERS, *LD\_method* 'genomicld' in namelist &LD, and *StoreHaplotypes* 'yes' in namelist &LD

#### geneticArchitecture.dat

Description: Sampled genetic architecture generated by LD

Criteria for output: *GeneticModel* 'genomic' in namelist &CONTROLPARAMETERS, *LD\_method* 'genomicld' in namelist &LD, and *StoreHaplotypes* 'yes' in namelist &LD

*plant#.res*

(Optional: Only printed if *print\_replicate* in namelist &CONTROLPARAMETERS has value yes)

File includes information on each individual plant including sire, dam, sex, birth, death, herd, true and estimated breeding values etc.

**founder\_representation#.res**

(Optional: Only printed if *founder\_representation=2* in namelist TEMPLATE\_PARAMETERS)

For all QTL and a specified number of template loci the representation of each founder (base plant) is given for each time step in replicate #. The representation is given as the number of each founder allele and the number of homozygotes for these alleles that the founder has contributed to the population in the given time step.

**marker#.res**

(Optional: Only printed if *print\_replicate* in namelist &CONTROLPARAMETERS has value yes)

File includes marker genotypes for all individuals.

*mean\_obs#.res*

*mean\_QTL#.res*

*mean\_template#.res*

*mean\_obs#.res*

*mean\_QTL#.res*

*mean\_template#.res*

-all of the above output files are to be replaced by the following two files:  
*mean\_timesteps.res*

*mean\_timesteps\_replicate.res*

*obs#.res*

(Optional: Only printed if *print\_replicate* in namelist &REPORT has value yes)

File includes realised phenotype, weight (ratio of residual variance to variance of phenotype given breeding value), time of recording and herd-year-season class associated with the recording for each observation for each plant.

#### **qt#.#.res**

(Optional: Only printed if *print\_replicate* in namelist &REPORT has value yes)

File includes QTL genotypes for all individuals.

#### **template#.#.res**

(Optional: Only printed if *use\_marker\_template=2* in Namelist &CONTROL\_GENOME)

File includes average number of plants that are IBD in each of the marker template loci for each time step in replicate #.

#### **template\_info#.#.res**

(Optional: Only printed if *use\_marker\_template=2* in Namelist &CONTROL\_GENOME)

File includes IBD information based on marker template for all individuals in each time step for replicate #. If *print\_genotypes=1* in Namelist &TEMPLATE\_PARAMETERS marker template genotypes for all individuals are printed as well.

When *debugOutput* 'yes' in namelist &REPORT, the following output files are generated and written to output directory specified in namelist &OUTPUTDIRECTORY, variable *OutDirectory*. Many of these files are regenerated during simulations. New files replace older files.

[Initialise]

#### **dmu4.polyblup.script**

Description: Script used to execute DMU4 when predicting polygenic-breeding values

Criteria for output: (i) *selection\_criterion* 'polyblup' in any selection stage of namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* or *FemaleSelCrit* 'polyblup' in any EVA-selection stage of namelist &EVA, variable *EvaSelection*, and (iii) variable *dmuPolyBlup* 'dmu4' in namelist &DMUPARAMETERS

#### **dmu5.polyblup.script**

Description: Script used to execute DMU5 when predicting polygenic-breeding values

Criteria for output: (i) *selection\_criterion* 'polyblup' in any selection stage of namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* or *FemaleSelCrit* 'polyblup' in any EVA-selection stage of namelist &EVA, variable *EvaSelection*, and (iii) variable *dmuPolyBlup* 'dmu5' in namelist &DMUPARAMETERS

#### **dmu4.genomicblup.script**

Description: Script used to execute DMU4 when predicting genomic-breeding values

Criteria for output: (i) *selection\_criterion* 'genomicblup' in any selection stage of namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* or *FemaleSelCrit* 'genomicblup' in any EVA-selection stage of namelist &EVA, variable *EvaSelection*, and (iii) variable *dmuGenomicBlup* 'dmu4' in namelist &DMUPARAMETERS

### ***dmu5.genomicblup.script***

Description: Script used to execute DMU5 when predicting genomic-breeding values

Criteria for output: (i) *selection\_criterion* 'genomicblup' in any selection stage of namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* or *FemaleSelCrit* 'genomicblup' in any EVA-selection stage of namelist &EVA, variable *EvaSelection*, and (iii)variable *dmuGenomicBlup* 'dmu5' in namelist &DMUPARAMETERS

### ***dmu4.gas.script***

Description: Script used to execute DMU4 when predicting GAS-breeding values

Criteria for output: (i) *selection\_criterion* 'gas' in any selection stage of namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* or *FemaleSelCrit* 'gas' in any EVA-selection stage of namelist &EVA, variable *EvaSelection*, and (iii)variable *dmuGasBlup* 'dmu4' in namelist &DMUPARAMETERS

### ***dmu5.gas.script***

Description: Script used to execute DMU4 when predicting GAS-breeding values

Criteria for output: (i) *selection\_criterion* 'gas' in any selection stage of namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* or *FemaleSelCrit* 'gas' in any EVA-selection stage of namelist &EVA, variable *EvaSelection*, and (iii)variable *dmuGasBlup* 'dmu5' in namelist &DMUPARAMETERSS

[Selection]

### ***eva.dat***

Description: Input-data file used by EVA to carry out EVA-selection

Criteria for output: *sex\_code* 7 in namelist &SELECTION, variable *selection\_scheme*. New data files replace older files written to output directory.

### ***eva.prm***

Description: Parameter file used by EVA to carry out EVA-selection

Criteria for output: *sex\_code* 7 in namelist &SELECTION, variable *selection\_scheme*. New data files replace older files written to output directory.

### ***map.hmatrix***

Description: Input-data file with marker loci. The file is used as input for Guosheng's program, *invgenmatrix*, to construct genomic-relationship matrix with markers and pedigree

Criteria for output: *sex\_code* 7 in namelist &SELECTION, variable *selection\_scheme* and *relationshipMatrix* 'genomic', *current\_time*≥*startGenRelTime*, and *startGenRelTime*≠-9 in namelist &EVA, variable *EvaSelection*. New data files replace older files written to output directory.

### ***marker.hmatrix***

Description: Input-data file with genotypes for each genotyped plant. The file is used as input to Guosheng's program, *invmatrix*, to construct genomic-relationship matrix with markers and pedigree

Criteria for output: *sex\_code* 7 in namelist &SELECTION, variable *selection\_scheme* and *relationshipMatrix* 'genomic', *current\_time*≥*startGenRelTime*, and *startGenRelTime*≠-9 in namelist &EVA, variable *EvaSelection*. New data files replace older files written to output directory.

#### ***ped.hmatrix***

Description: Input-data file with pedigree of selection candidates. The file is used as input to Guosheng's program, *invmatrix*, to construct genomic-relationship matrix with markers and pedigree

Criteria for output: *sex\_code* 7 in namelist &SELECTION, variable *selection\_scheme* and *relationshipMatrix* 'genomic', *current\_time*≥*startGenRelTime*, and *startGenRelTime*≠-9 in namelist &EVA, variable *EvaSelection*. New data files replace older files written to output directory.

#### ***par.hmatrix***

Description: Parameter file used by Guosheng's program, *invmatrix*, to construct genomic-relationship matrix with markers and pedigree

Criteria for output: *sex\_code* 7 in namelist &SELECTION, variable *selection\_scheme* and *relationshipMatrix* 'genomic', *current\_time*≥*startGenRelTime*, and *startGenRelTime*≠-9 in namelist &EVA, variable *EvaSelection*. New data files replace older files written to output directory.

#### ***hMatrix.dat***

Description: H-matrix; genomic-relationship matrix constructed with markers and pedigree. The matrix is output from Guosheng's program, *invmatrix*. It is used as input by DMU to generate genomic breeding values.

Criteria for output: Criteria for output: *sex\_code* 7 in namelist &SELECTION, variable *selection\_scheme* and *relationshipMatrix* 'genomic', *current\_time*≥*startGenRelTime*, and *startGenRelTime*≠-9 in namelist &EVA, variable *EvaSelection*. New data files replace older files written to output directory.

#### ***hMatrix.lst***

Description: Log-file from Guosheng's program, *invmatrix*, when constructing genomic-relationship matrix with markers and pedigree.

Criteria for output: Criteria for output: *sex\_code* 7 in namelist &SELECTION, variable *selection\_scheme* and *relationshipMatrix* 'genomic', *current\_time*≥*startGenRelTime*, and *startGenRelTime*≠-9 in namelist &EVA, variable *EvaSelection*. New data files replace older files written to output directory.

#### ***eva.log***

Description: Log-file generated by EVA when carrying out EVA-selection

Criteria for output: *sex\_code* 7 in namelist &SELECTION, variable *selection\_scheme*. New data files replace older files written to output directory.

### ***eva\_MatingList.txt***

Description: Solution file with list of matings allocated by EVA when carrying out EVA-selection

Criteria for output: *sex\_code* 7 in namelist &SELECTION, variable *selection\_scheme*. New data files replace older files written to output directory.

[EBV]

### ***dmudat***

Description: Input-data file used by DMU to predict breeding values

Criteria for output: (i) *selection\_criterion* 'polyblup', 'genomicblup', or 'gas' and *RunBlup* 1 in namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* and/or *FemaleSelCrit* 'polyblup', 'genomicblup', or 'gas' and *MaleRunBlup* and/or *FemaleRunBlup* 1 in namelist &EVA, variable *EvaSelection*, and (iii) and phenotypes and/or genotypes realised since breeding values last predicted

### ***dmuped***

Description: Pedigree-file used by DMU to predict breeding values

Criteria for output: (i) *selection\_criterion* 'polyblup', 'genomicblup', or 'gas' and *RunBlup* 1 in namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* and/or *FemaleSelCrit* 'polyblup', 'genomicblup', or 'gas' and *MaleRunBlup* and/or *FemaleRunBlup* 1 in namelist &EVA, variable *EvaSelection*, and (iii) and phenotypes and/or genotypes realised since breeding values last predicted

### ***map.gmatrix***

Description: Input-data file with marker loci. The file is used as input for Guosheng's program, *gmatrix*, to generate genomic-relationship matrix.

Criteria for output: (i) *selection\_criterion* 'genomicblup' and *RunBlup* 1 in namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* or *FemaleSelCrit* 'genomicblup' and *MaleRunBlup* and/or *FemaleRunBlup* 1 in namelist &EVA, variable *EvaSelection*, and (iii) and phenotypes and/or genotypes realised since breeding values last predicted

### ***marker.gmatrix***

Description: Input-data file with genotypes for each genotyped plant. The file is used as input to Guosheng's program, *gmatrix*, to generate genomic-relationship matrix.

Criteria for output: (i) *selection\_criterion* 'genomicblup' and *RunBlup* 1 in namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* or *FemaleSelCrit* 'genomicblup' and *MaleRunBlup* and/or *FemaleRunBlup* 1 in namelist &EVA, variable *EvaSelection*, and (iii) and phenotypes and/or genotypes realised since breeding values last predicted

### ***par.gmatrix***

Description: Parameter file used by Guosheng's program, *gmatrix*, to generate genomic-relationship matrix.

Criteria for output: (i) *selection\_criterion* 'genomicblup' and *RunBlup* 1 in namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* or *FemaleSelCrit* 'genomicblup' and *MaleRunBlup* and/or *FemaleRunBlup* 1 in namelist &EVA, variable *EvaSelection*, and (iii) and phenotypes and/or genotypes realised since breeding values last predicted

#### ***gMatrix.dat***

Description: Genomic-relationship matrix constructed by Guosheng's program, *gmatrix*. It is used as input by DMU to predict genomic-breeding values.

Criteria for output: (i) *selection\_criterion* 'genomicblup' and *RunBlup* 1 in namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* or *FemaleSelCrit* 'genomicblup' and *MaleRunBlup* and/or *FemaleRunBlup* 1 in namelist &EVA, variable *EvaSelection*, and (iii) and phenotypes and/or genotypes realised since breeding values last predicted

#### ***gMatrix.lst***

Description: Log-file from Guosheng's program, *gmatrix*, when constructing genomic-relationship matrix

Criteria for output: (i) *selection\_criterion* 'genomicblup' and *RunBlup* 1 in namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* or *FemaleSelCrit* 'genomicblup' and *MaleRunBlup* and/or *FemaleRunBlup* 1 in namelist &EVA, variable *EvaSelection*, and (iii) and phenotypes and/or genotypes realised since breeding values last predicted

#### ***genotyped.dat***

Description: Data file with list of genotyped plants. It is used as input by DMU to predict genomic-breeding values.

Criteria for output: (i) *selection\_criterion* 'genomicblup' and *RunBlup* 1 in namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* or *FemaleSelCrit* 'genomicblup' and *MaleRunBlup* and/or *FemaleRunBlup* 1 in namelist &EVA, variable *EvaSelection*, and (iii) and phenotypes and/or genotypes realised since breeding values last predicted

#### ***dmu.lst***

Description: Log-file from DMU when predicting genomic-breeding values

Criteria for output: (i) *selection\_criterion* 'polyblup', 'genomicblup', or 'gas' and *RunBlup* 1 in namelist &SELECTION, variable *selection\_scheme*, or (ii) *MaleSelCrit* and/or *FemaleSelCrit* 'polyblup', 'genomicblup', or 'gas' and *MaleRunBlup* and/or *FemaleRunBlup* 1 in namelist &EVA, variable *EvaSelection*, and (iii) and phenotypes and/or genotypes realised since breeding values last predicted

[LD\_Hayes]

#### ***ldSummary.r***

Description: R-script used to generate summary data and plots from LD-analysis

Criteria for output: (i) *printLdHayesFiles* 'yes' in namelist &REPORT and (ii) *GeneticModel* 'genomic' in namelist &CONTROLPARAMETERS and *UseStoredHaplotypes* 'no' in namelist &LD or *GeneticModel* 'ld\_Only' in namelist &CONTROLPARAMETERS

#### ***ldSummary.rLog***

Description: Log-file from execution of *ldSummary.r* by R

Criteria for output: (i) *printLdHayesFiles* 'yes' in namelist &REPORT and (ii) *GeneticModel* 'genomic' in namelist &CONTROLPARAMETERS and *UseStoredHaplotypes* 'no' in namelist &LD or *GeneticModel* 'ld\_Only' in namelist &CONTROLPARAMETERS

[Report]

#### ***geneticTrendsPlots.r***

Description: R-script used to generate output file, *geneticTrends.pdf*, plots of genetic trends as functions of time

Criteria for output: R-script always generated

#### ***geneticTrendsPlots.rLog***

Description: Log-file from execution of *geneticTrendsPlots.r* by R

Criteria for output: Log-file always generated

#### ***biasAccuracyMeans.r***

Description: R-script used to generate output file, *biasAccuracyMeans.res*, mean biases and accuracies for each trait at each time step, selection stage, and sex

Criteria for output: *printBiasAccuracy* 'yes' in namelist &REPORT

#### ***biasAccuracyMeans.rLog***

Description: Log-file from execution of *biasAccuracyMeans.r* by R

Criteria for output: *printBiasAccuracy* 'yes' in namelist &REPORT

#### ***biasAccuracyPlots.r***

Description: R-script used to generate output file, *biasAccuracyPlots.pdf*, plots of biases and accuracies as functions of time

Criteria for output: *printBiasAccuracy* 'yes' in namelist &REPORT

#### ***biasAccuracyPlots.rLog***

Description: Log-file from execution of *biasAccuracyPlots.r* by R

Criteria for output: *printBiasAccuracy* 'yes' in namelist &REPORT

[genomicInbreedingCoefficients]

#### ***map.gimatrix***

Description: Input-data file with marker loci. The file is used as input for Guosheng's program, *invmatrix*, to construct genomic-relationship matrix with markers

Criteria for output: *GeneticModel* 'genomic' in namelist &CONTROLPARAMETERS. New data files replace older files written to output directory.

***marker.gimatrix***

Description: Input-data file with genotypes of all plants. The file is used as input to Guosheng's program, *invmatrix*, to construct genomic-relationship matrix with markers

Criteria for output: *GeneticModel* 'genomic' in namelist &CONTROLPARAMETERS. New data files replace older files written to output directory.

***par.gimatrix***

Description: Parameter file used by Guosheng's program, *invmatrix*, to construct genomic-relationship matrix with markers

Criteria for output: *GeneticModel* 'genomic' in namelist &CONTROLPARAMETERS. New data files replace older files written to output directory.

***giMatrix.dat***

Description: G-matrix; genomic-relationship matrix constructed with markers. The matrix is output from Guosheng's program, *invmatrix*. It is used by ADAM to calculate breeding coefficients for all plants in the population.

Criteria for output: *GeneticModel* 'genomic' in namelist &CONTROLPARAMETERS. New data files replace older files written to output directory.

***giMatrix.lst***

Description: Log-file from Guosheng's program, *invmatrix*, when constructing genomic-relationship matrix with markers.

Criteria for output: *GeneticModel* 'genomic' in namelist &CONTROLPARAMETERS. New data files replace older files written to output directory.

*giMatrix.dat* \*.lst par.  
*giBlendedHMatrix.dat* \*.lst par.

## References

Goddard 2009

Grundy et al. 1999. JABG 115:39-51

Henryon et al. (2010)

Jannink 2010 GSE 42:35

Meuwissen 2000

Meuwissen 2001

Wu & Schaeffer 2000. JABG 117:361-374

See Grundy et al. (1998) JABG 115:39-51 and Wu & Schaeffer (2000) JABG 117:361-374 for details