

SelAction

Manual



WAGENINGEN UNIVERSITY
ANIMAL SCIENCES

in cooperation with the



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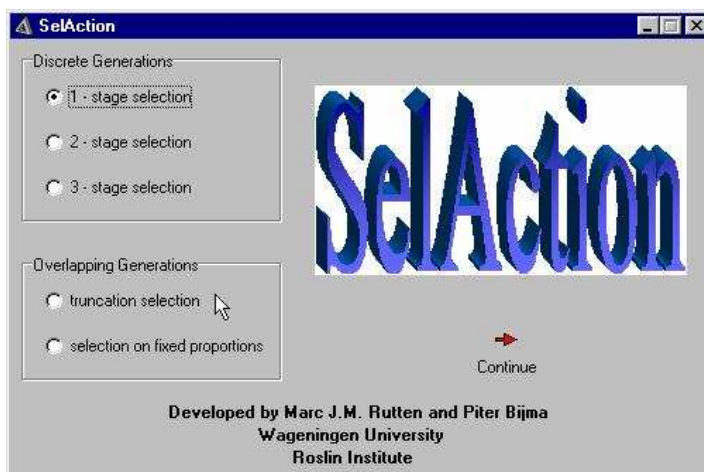
1. Starting SelAction

To start SelAction, you can either: *i)* open Windows Explorer, go the directory where the file "SelAction.exe" is located and double click the file, *ii)* include a link to SelAction in the Windows Start menu and click the link, or *iii)* you can create a link to SelAction on your desktop and click the link. The files borland.dll and reg.dll have to be in the same directory as the selaction.exe file. This manual is a step wise guide through SelAction. When using SelAction for the first time it is advised to start with a simple breeding scheme, for example a population with discrete generations, selection in a single step and a limited number of traits.

Note: To work with SelAction you need to have at least a basic understanding of livestock improvement and quantitative genetics. The program cannot be used as a black box tool. Please make sure that the input values you are entering are meaningful.

2. The start window

After starting SelAction, the following window appears on your screen:



In this window you can click five different options for the type of breeding scheme that you want to use, three options for discrete generations and two options for overlapping generations. (A detailed description of the meaning of the different options is in the general description of SelAction.) The options are:

Discrete generations

- 1 -stage selection; Selection takes place in a single step.
- 2 -stage selection; Selection takes place in two steps, individuals that are not selected in the first step are not candidates in the second step.
- 3 -stage selection; Selection takes place in three steps, individuals that are not selected in a certain step are not candidates in the next step.

Overlapping generations

- Truncation selection; Animals are selected by truncation on an index value across age classes, all animals with an index value above the truncation point are selected as parents of

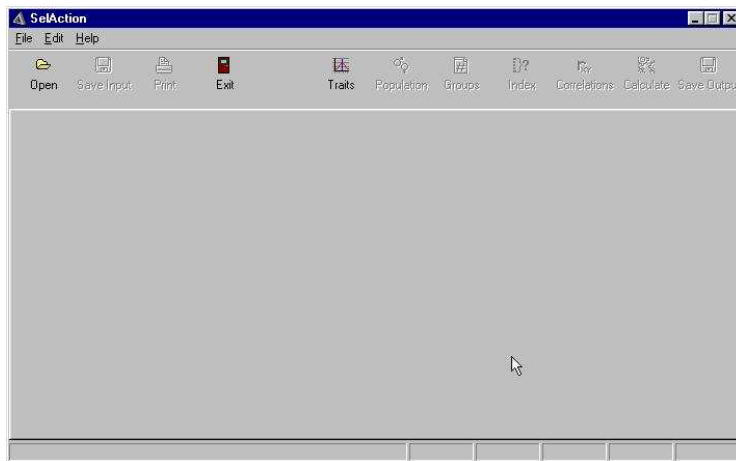
the next generation, animals with an index value below the truncation point are not selected. The program calculates the truncation point so that the number of selected individuals equals the desired number of parents of each sex. For each sex-age class, the user should enter the number of selection candidates available.

- Selection on fixed proportions; when choosing this option, the user has to specify (later on) the selected proportions in each age class, they are not determined by the program.

After clicking one of the five options, the program will proceed to the main window. If after working with one of the five population structures you want to work with another type of population, please close the program by clicking the "Exit" button and restart the program. This will only take a second.

3. The main window

The main window of SelAction looks as follows



The menu lists the following options: Open, Save Input, Print, Exit, Traits, Population, Groups, Index, Correlations, Calculate and Save Output.

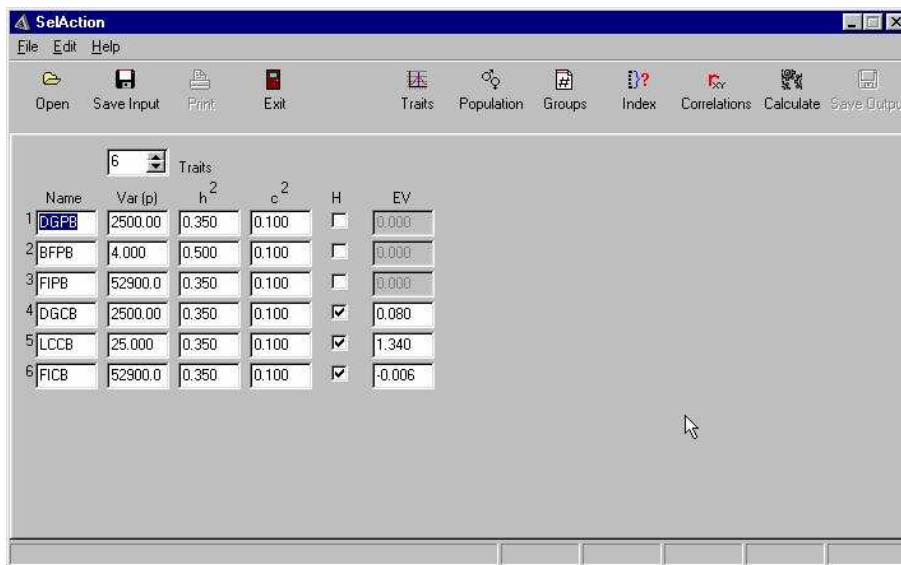
- Open; This option allows you to open a preexisting SelAction input file.
- Save Input; This option allows you to save an SelAction input file
- Exit; This option allows you to exit SelAction.
- Traits; When clicking this option, you proceed to the window where you can enter traits and trait information.
- Population; When clicking this option, you proceed to the window where you can enter population parameters such as the number of parents, selected proportions etc.
- Groups; When clicking this option, you proceed to the window where you can enter the characteristics of the groups of animals that provide information for the selection index of selection candidates.
- Index; When clicking this option, you proceed to the window where you can enter the information sources that are included in the selection index.
- Correlations; When clicking this option, you proceed to the window where you can enter genetic, phenotypic and common environmental correlations between all traits.

- Calculate; This is the "run" button, when clicking it the program starts the calculations and subsequently shows the results.
- Save output; When clicking this option the program saves the results.

The options in the main menu must be dealt with in order, from left to right. At this moment, you can only click the options Open, Exit, and Traits. To proceed, click the option "Traits", which opens the traits window.

4. The traits window.

After clicking the option "Traits" in the main menu, the following window appears (excluding the example values).



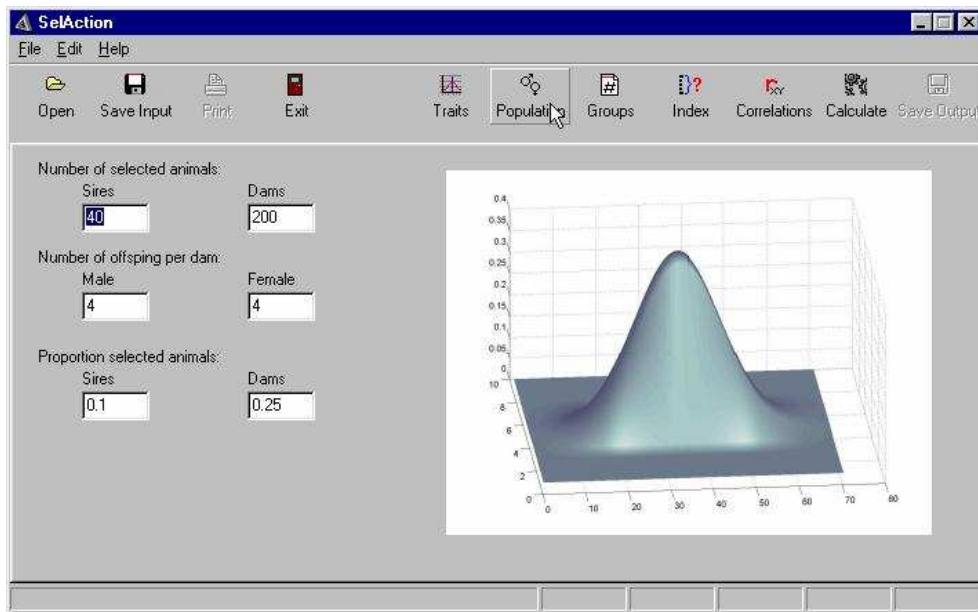
In the Traits box you can enter the number of traits. The default value is a single trait. When you increase the number of traits, the program adds a row for each trait. You can move through the fields by using the TAB-key or by using the mouse. After entering the number of traits, the window contains a row for each trait with the fields Name, Var(p), h^2 , c^2 , H and EV. The meaning of those fields is the following:

- Name; name of this trait.
- Var(p); phenotypic variance of this trait.
- h^2 ; heritability of this trait, $h^2 = \text{add. genetic variance}/\text{phenotypic variance}$.
- c^2 ; common environmental variance between full sibs for this trait as a proportion of the phenotypic variance, $c^2 = \text{comm. environmental variance of FS}/\text{phenotypic variance}$.
- H; By clicking this box (use either the mouse or the space bar) you include the trait in the breeding goal, meaning that improvement of this trait is desired. When you do not click the trait, then SelAction can use this trait only as an information source to predict breeding values for other traits. For example, when interest is in increasing lean% in pigs but backfat is the trait that is recorded on the animals, then you should click the H-box for lean% and not for backfat.
- EV; you can only enter values in this box for traits that are included in the breeding goal. For those traits, you have to specify the (economic) value of the trait in this field.

After you have entered the field for all traits, please proceed by clicking the option "Population" of the main menu, which will open the population window.

5. The population window

After clicking the option "Population", the following window appears (excluding the example values).



The window differs slightly between single stage and multi stage selection and between discrete and overlapping generations. With overlapping generations there are no fields for selected proportions, whereas with multi stage selection there are multiple fields for selected proportions. The meaning of the fields is the following:

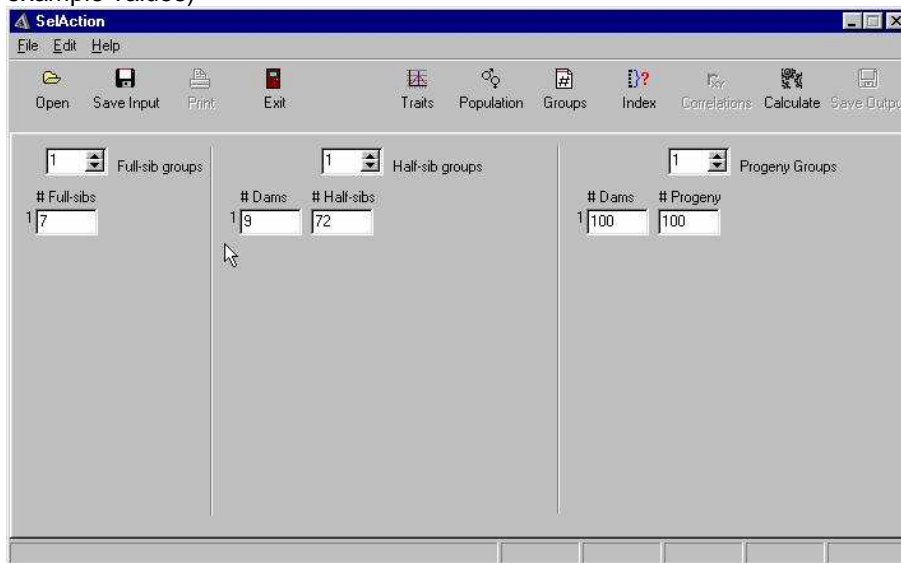
- Number of selected animals; the number of male and female parents of the next generation selected in the breeding program. With multistage selection it is the number of selected animals after the final stage of selection. With overlapping generations it is the total number of selected parents per "unit of time", summed over all age classes. With overlapping generations, the "unit of time" is equal to the time interval between two consecutive age classes. For example, in dairy cattle, age classes are typically equal to one year. Hence, the number of parents to be entered in SelAction is the number selected each year.
- Number of offspring per dam; The number of male and female offspring (selection candidates) born per dam. (This information is needed to calculate selection intensities adjusted for correlations of index values of relatives using the method of Meuwissen, see general description of SelAction)
- Proportion selected animals (not with overlapping generations); The selected proportions among male and female candidates. Thus the values are the number of selected animals divided by the number of candidates. With single stage selection, there is only a single selected proportion for each sex, thus in total there are two values to be entered. With multi stage selection, selected proportions have to be entered for each stage of selection and in addition the total selected proportion has to be entered. The default value for the total selected proportion is $p_t = p_1 \times p_2 (\times p_3)$ and is suggested automatically by SelAction.

(Selected proportions are used to calculate the selection intensities for each sex. In principle, selected proportions could be calculated from the numbers of sires and dams and the number of offspring born per dam, however, the program allows the user to deviate from values obtained in that way.) Note that p is a proportion, $0 < p < 1$, not a percentage.

After values in the population window are entered, please click the option "Groups" on the main menu to proceed to the groups window.

6. The groups window.

When clicking the groups option in the main menu, the following window appears (excluding the example values)



In the groups window you can enter which groups of animals (relatives of the selection candidate) are available to provide information for the selection index (or the breeding value estimation) of candidates. SelAction distinguishes three types of groups; groups of full sibs, groups of half sibs and groups of progeny. For example, a group of full sibs is a group of individuals that are full sibs of the selection candidate. The meaning of the field is:

- Full-sib groups; Here you can enter the number of different full sib groups. When doing so, SelAction creates input fields for the number of individuals within each full sib group. Note that individuals in different groups are distinct individuals. For example, if litter size is 8, then selection candidates in a pig-breeding program have 7 full sibs. Suppose that male candidates have records on growth and feed intake and that female candidates have records on growth only. Next, consider male selection candidates. Out of its 7 sibs, there are 3 males with information on growth and feed intake and 4 females with records on growth only. Therefore, you have to define two full-sib groups. One group of 3 and a group of 4 individuals. (The traits that they provide information on can be entered later in the "index window".)
- Half-sib groups; Here you can enter the number of distinct half-sib groups. When doing so, SelAction creates input fields for the number of individuals within each half-sib group and for the number of dams that produces this half-sib group. (The number of dams is required to take account of the fact that half sibs of the selection candidate may be full sibs of each other). As with full sibs, individuals in different groups are distinct individuals. Continuing the

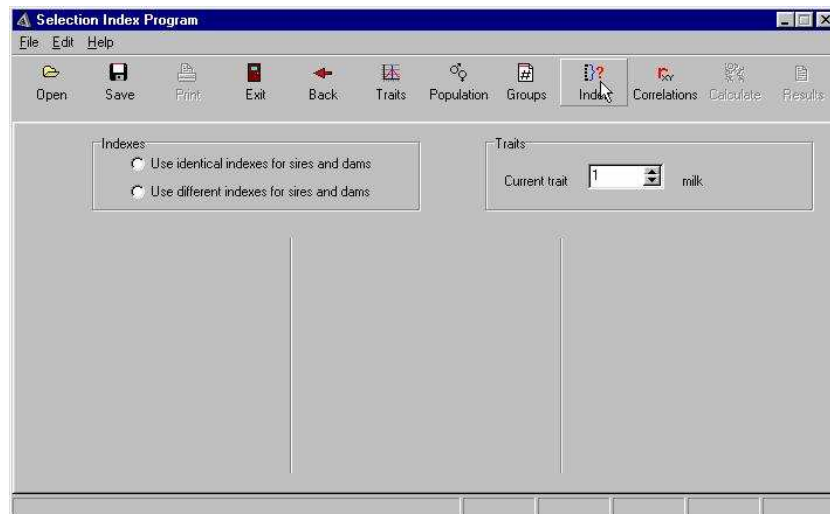
example of the pig-breeding program and assuming that each dam is mated to three sires, then there 16 half sibs in total ($3 \times 8 = 8$ FS). The 16 half sibs consist of two groups, 8 individuals providing information on growth only and 8 individuals providing information on both growth and feed intake. Thus in this case you have to specify two half sib groups, the first with 8 individuals out of 2 dams and the second with 8 individuals of 2 dams. (The information that they provide can be entered later on in the "index window".)

- Progeny groups; Here you can enter the number of different progeny groups. When doing so, SelAction creates input fields for the number of individuals within each progeny group and for the number of dams that produces this progeny group. (The number of dams is required to take account of the fact that a proportion of the progeny of male selection candidates may be full sibs of each other). Individuals in different groups are distinct individuals. In a dairy cattle breeding program, for example, production traits may be recorded on 100 daughters whereas conformation traits may be recorded on only 60 out of the 100 daughters per bull. In this case you have to specify two progeny groups, the first with 40 daughters of 40 dams (assuming there is no twinning) and the second with 60 daughters of 60 dams.

After completing the groups window, please continue to the index window by clicking the option "index" in the main menu.

7. The index window

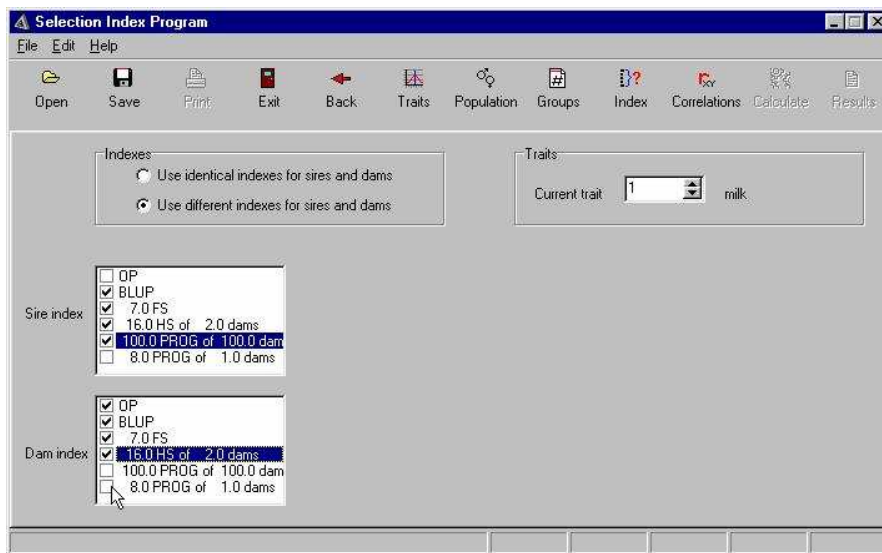
The index window allows you to enter the information sources that are available for breeding value estimation on the selection candidates. For each sex and for each trait you have to enter which information is available. The groups that you've entered in the groups window appear as clickable options in the index field.



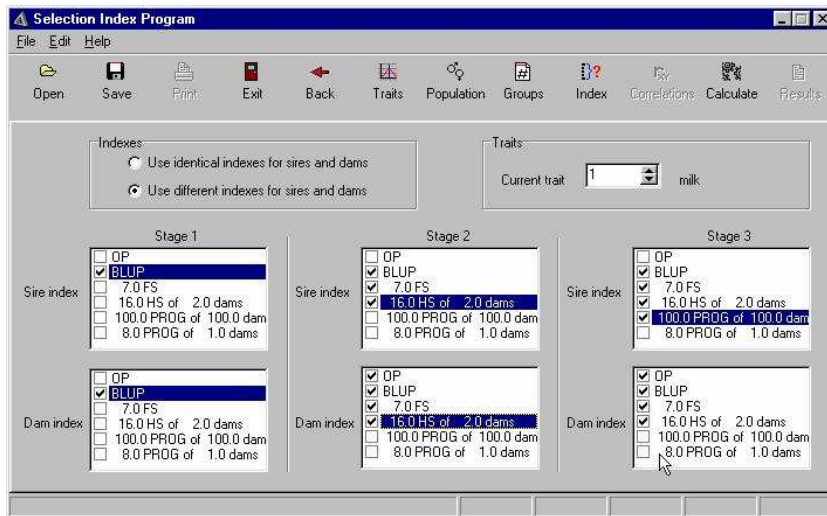
- Start with the field "Indexes". In this field you can click whether males and females have identical indexes or different indexes. When selection of males and females is based on the same information, then click the option "use identical indexes for sires and dams". If not, click the option "use different indexes for sires and dams". In dairy cattle, for example, bulls are selected based on pedigree, sib and progeny information whereas cows are selected based on pedigree, sib and own performance information. Thus in this situation bulls and cows have different indexes. (Note that with identical indexes for males and females the accuracy has to be the same for males and females.) Proceed to the field "Index".

The Index field. The set-up of the Index field depends on the type of population that you have chosen in the start window. For all types of populations, however, there are the following optional information sources: OP = own performance of the selection candidate; BLUP = breeding value estimation using BLUP with an animal model and full pedigree; #FS = the full sibs groups that were entered in the groups window, #HS of #dams = the half sib groups that were entered in the groups window, #progs of # dams = the progeny groups that were entered in the groups window. When clicking these information sources, they are included in the breeding value estimation for the selection candidates. The number of sub fields in the index field depends on the type of population entered in the start window.

For discrete generations with 1-stage selection the window looks as follows (excluding the example values).

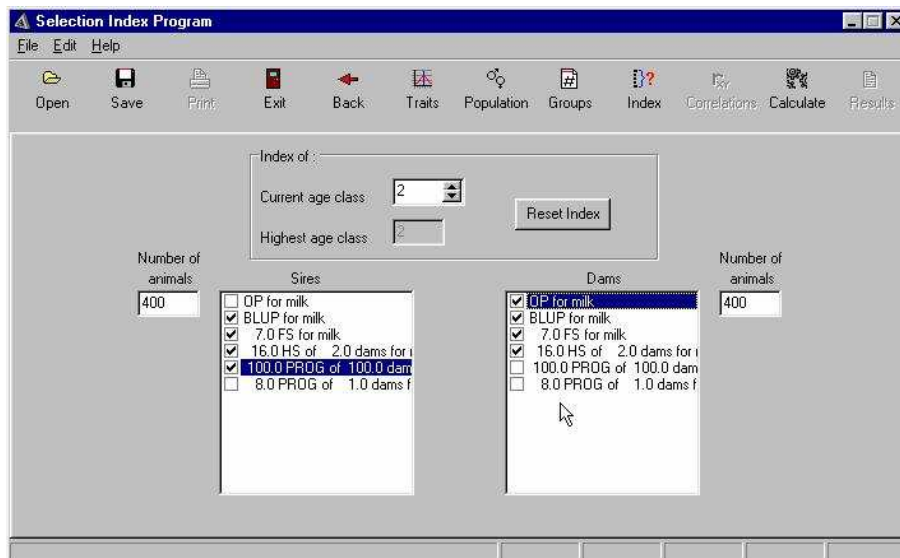


When sires and dams have different indexes then there are two sub fields in the index field, one for sires and one for dams. Otherwise there is a single field only. Please click the information sources for the first trait and subsequently go to the traits field and increase the trait number by one to go to the next trait, go back to the indexes field, etc, until the index is entered for all traits. For discrete generations with 3-stage selection the window looks as follows.



For each stage of selection there is a separate sub field where information sources can be clicked. In addition, there are separate fields for sires and dams when the index differs between the sexes. Thus there are at most six sub fields per trait. With multistage selection, information can only be added. This means that information sources available in the first stage are also available in the second and third stage, they must not be deleted. Thus a subsequent stage of selection can have more information sources but it must not have less. SelAction automatically clicks information sources in subsequent stages when they are clicked in a preceding stage. Do not remove those clicks. Please click the information sources for the first trait in all stages and in both sexes and subsequently go to the traits field, increase the trait number by one, go back to the indexes field, etc, until the index is entered for all traits.

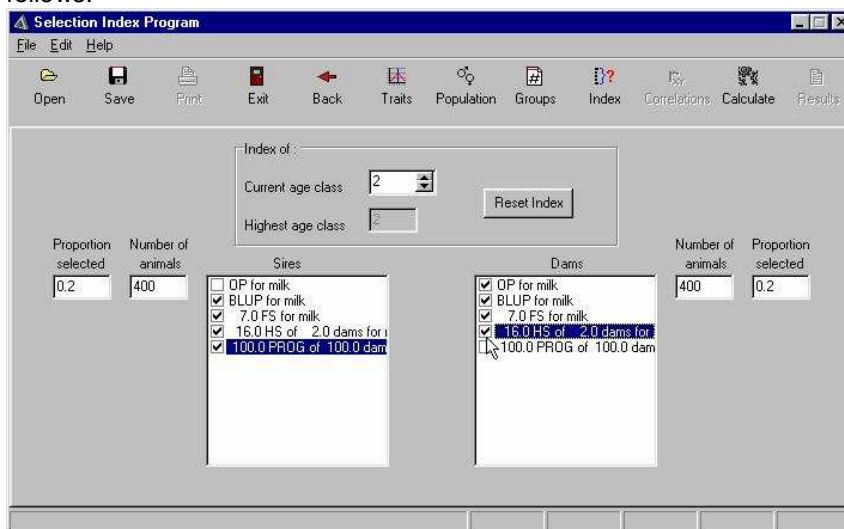
For overlapping generations with truncation selection the window looks as follows.



The "index of" field lists the age class that is displayed in the other fields. The "number of animals" field lists the number of selection candidates in this age class for each sex, and the "sires" and "dams" fields list the information sources that can be clicked for this age class. Please

enter the number of selection candidates in the "number of animals field". (The default value is zero). Next click the appropriate information sources in the "sires" and "dams" fields, go to the "index of" field, increase the number of age classes by one and go back to the "number of animals", "sires" and "dams" fields, etc, until the index is entered for all age classes. The number of age classes is equal to the highest age class for which you entered the index information sources. Note that with truncation selection the selected proportion in each age class is determined automatically by truncation across age classes, so you do not have to enter selected proportions. SelAction determines the truncation point such that the number of selected parents is equal to the desired number of parents. (Make sure that the number of candidates is entered correctly for each age class, otherwise selected proportions and intensities will be incorrect also.)

For overlapping generations with selection on fixed proportions the index window looks as follows.

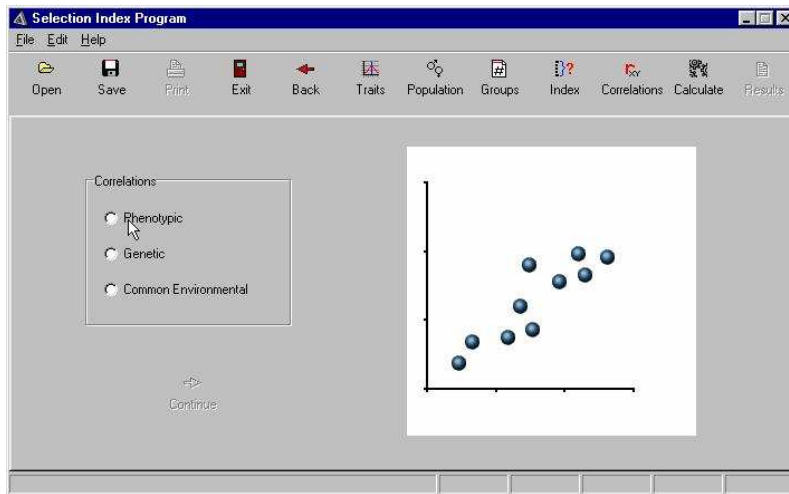


The fields are the same as with overlapping generations and truncation selection, but in addition you have to enter the selected proportion for each age class. **Make sure that, with selection on fixed proportions, the number of selected parents, which is the product of selected proportion and number of candidates summed per sex across age classes, is equal to the number of parents that you entered in the population window.**

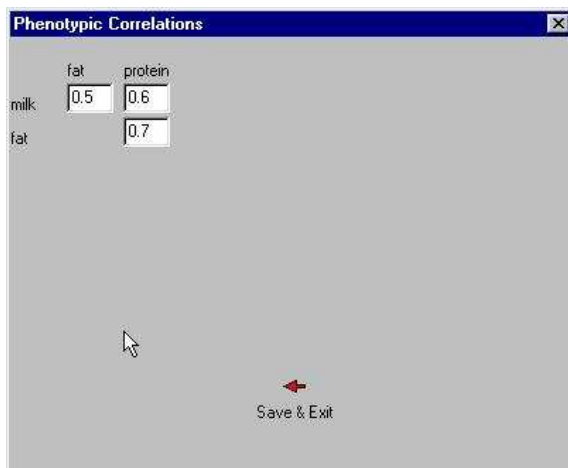
In case of multiple traits, proceed by clicking the "Correlations" option in the main menu. Otherwise click the "Save Input" option of the main menu and proceed to the "Calculate" option.

8. The correlations window

The correlations window allows you to enter phenotypic, genetic and common environmental correlations between all traits. When clicking the option "Correlations" in the main menu, the following window appears.



In this window, click the option "Phenotypic" and subsequently the "continue" arrow. The following window appears where you can enter the phenotypic correlations between all trait.



After entering the phenotypic correlations click "Save and Exit" to go back to the main correlations window and click the option "Genetic". Enter the genetic correlations, click "Save and Exit" and finally click the option "Common Environmental" and enter the common environmental correlations. SelAction does not check whether the correlation matrixes are positive definite. Please check this by yourselves. If the correlation matrixes are not positive definite then errors may occur on execution. Click the "Save Input" option in the main menu and proceed to the "Calculate" Command.

9. The calculate command

At this stage you (should) have entered all the required information to run the program. **Before clicking the option "calculate" in the main menu, please save your input by clicking the option "Save Input" in the main menu.** In case there is a typo in the input, the calculations may crash. By saving your input you prevent losing them.

To run the program, click the option "Calculate" in the main menu. For complex breeding schemes with many traits and many age classes calculation of the results may take some time. Next the results appear on the screen. Note that with overlapping generations the response and generation interval presented on the output are expressed per "unit of time", where the "unit of time" is the interval between two consecutive age classes (e.g. a year). Thus response is not presented per generation. The results sheet shows the input and the corresponding output. Examples of results sheets are given with the examples below. To save the results, click the option "Save Output" in the main menu.

10. General remarks

In case the program crashes, check before starting it again whether something is still running in the background. Press Ctrl+Alt+Del to see which tasks are running. If SelAction is running, click the End Task button to close it down. This will avoid problems when restarting SelAction.

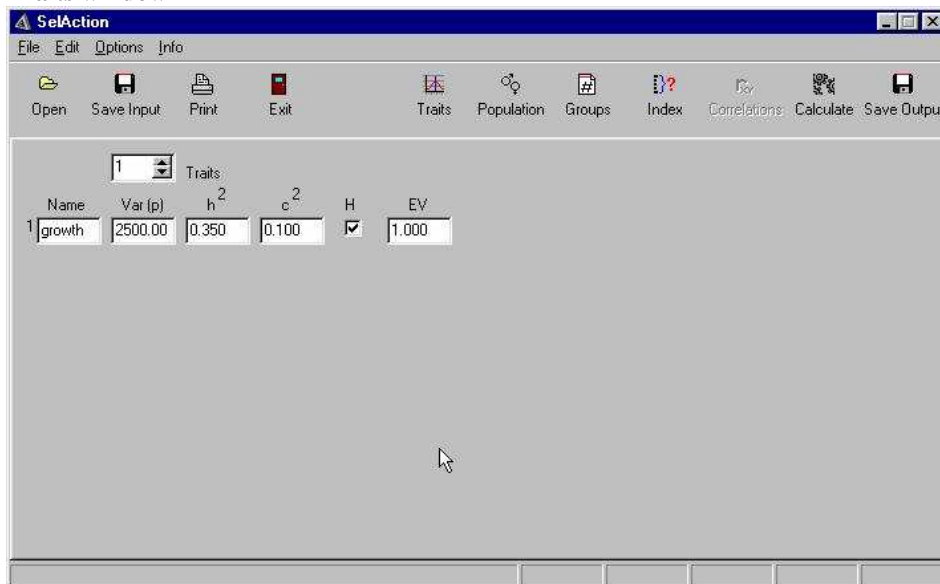
11. Examples

11.1 Getting started

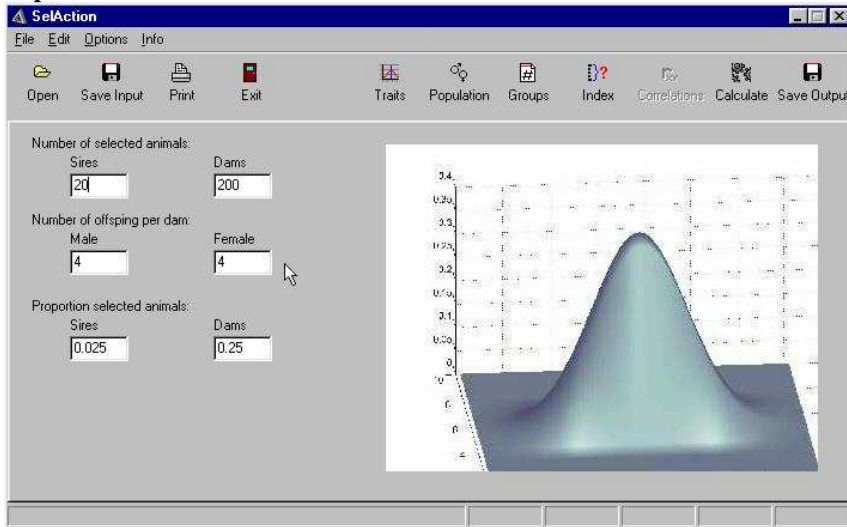
Example 1: Mass selection for growth in pigs

This is an example of discrete generations with selection in a single stage. Consider a mass selection program for growth in pigs. The heritability of growth is 0.35, the phenotypic standard deviation is 50g/day, common environment among full sibs is $c^2 = 0.1$, each generation 20 boars and 200 sows are selected and each sow produces 8 offspring, 4 of each sex. Selected proportions for boars are $p_m = 20/(200 \times 4) = 0.025$ and $p_f = 200/(200 \times 4) = 0.25$. Below are the input windows for this example and the results and an explanation thereof.

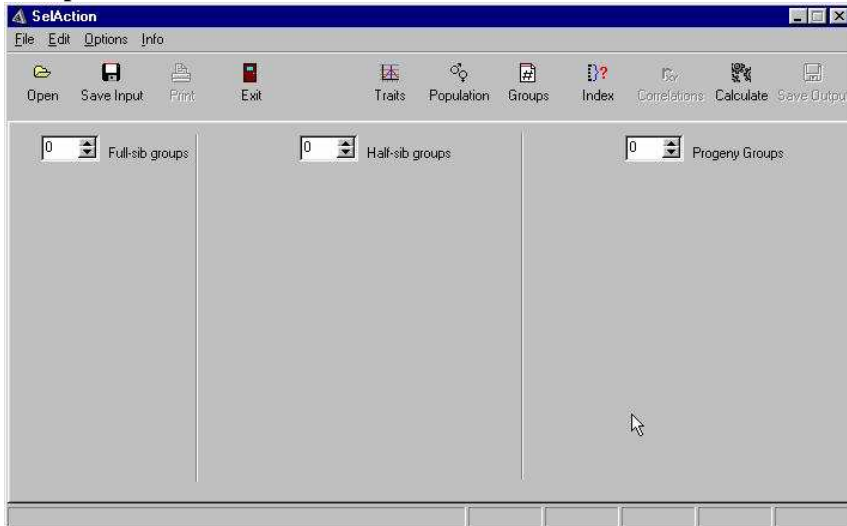
Traits window



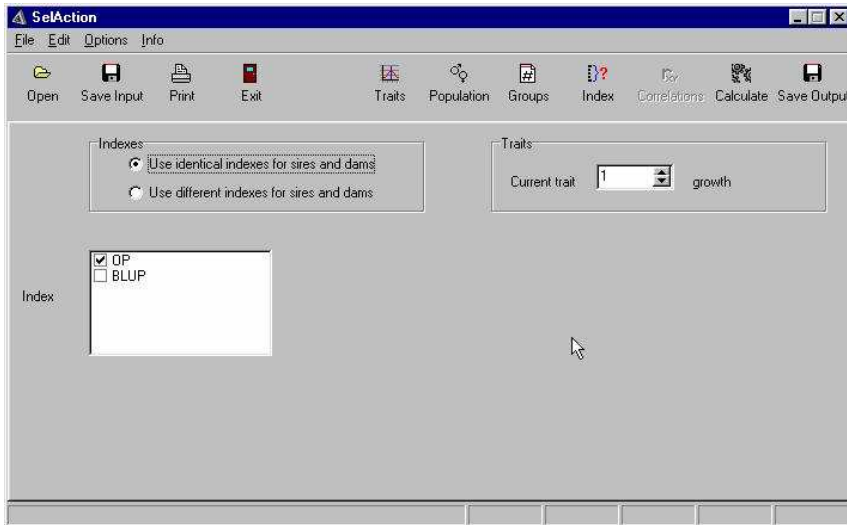
Population window



Groups window



Index window



Results

***** begin of output *****

RESULTS

TRAITS USED
growth

TRAIT PARAMETERS

	phenotypic variance	heritability	com.env.effect
growth	2,500.000	0.350	0.100

¹BREEDING GOAL INFORMATION

1.000 * growth

POPULATION SIZE

number of selected sires :	20.0
number of selected dams :	200.0
number of male selection candidates per dam :	4.0
number of female selection candidates per dam :	4.0
total selected proportion sires :	0.025
total selected proportion dams :	0.250

²INDEX INFORMATION :

Own performance of growth

***** RESULTS *****

³EQUILIBRIUM PARAMETERS

	phenotypic variance	heritability	com.env.effect
growth	2,326.823	0.302	0.107

⁴RESPONSE

	sires	dams	total
growth			
trait units:	16.898	9.220	26.118
economic units:	16.898	9.220	26.118
% of totalresponse:	64.698	35.302	100.000

⁵TOTALRESPONSE

	sires	dams	total
economic units:	16.898	9.220	26.118

⁶variance of index: 211.687 211.687⁷variance of breeding goal: 701.825⁸accuracy of index: 0.549 0.549⁹increase of inbreeding: 1.074 % per generation

***** end of output *****

Explanation of the output¹ Breeding goal; lists all traits included in the breeding goal and their economic value² Index information: lists all information sources that are used to calculate the selection index. With mass selection that is only own performance, both for sires and dams.³ Equilibrium parameters; lists the Bulmer equilibrium genetic parameters that are reached after iteration.

⁴ Response; lists the response per generation separately for each trait and each sex, in trait units, in economic units and as a percentage of the total economic response. (In this example there is only a single trait with an economic weight of 1.0, so response in trait units, in economic units and total response are the same.)

⁵ Total response; lists the total response in economic units, separately for sires and dams.

⁶ Variance of index: Bulmer equilibrium variance of the index. Separate values are given for sires and dams because their index may differ.

⁷ Variance of breeding goal: In this case it is equal to the equilibrium additive genetic variance of growth because there is only a single trait with a weight of 1. The breeding goal is always the same for both sexes, thus only a single value is printed.

⁸ Accuracy of index: Bulmer equilibrium accuracy of selection. Because the index may differ between sires and dams, a value is printed for each sex. In this case it is equal to the square root of the equilibrium heritability because it is a mass selection scheme.

⁹ Rate of inbreeding. The rate of inbreeding per generation that this selection program results in. Thus a value of 1.074% means that $\Delta F = 0.01074/\text{generation}$.

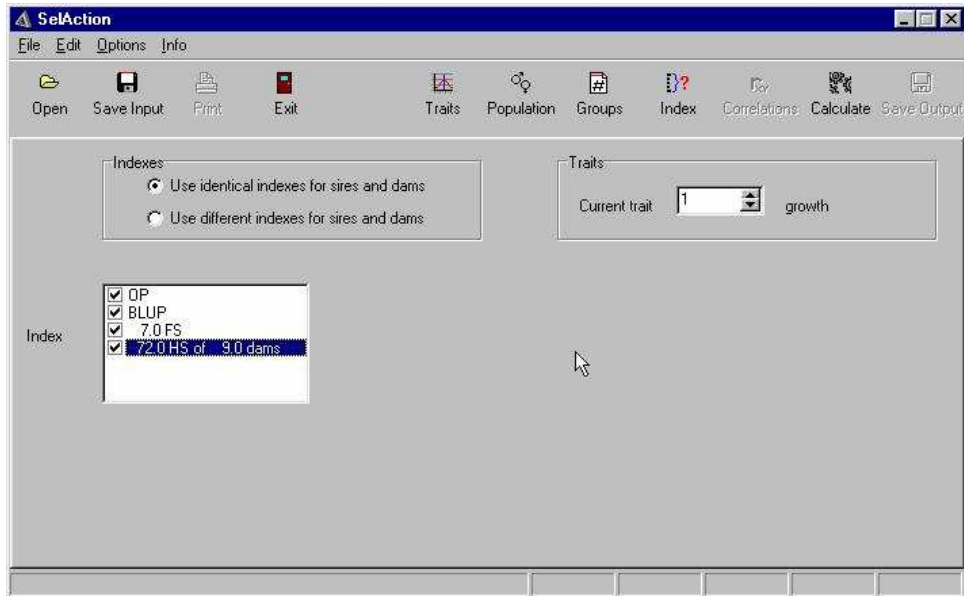
Example 2: Selection for growth in pigs using BLUP with an animal model

This is an example of discrete generations with selection in a single stage on estimated breeding values obtained with BLUP and an animal model. The heritability of growth is 0.35, the phenotypic standard deviation is 50g/day, common environment among full sibs is $c^2 = 0.1$, each generation 20 boars and 200 sows are selected and each sow produces 8 offspring, 4 of each sex. Selected proportions for boars are $p_m = 20/(200 \times 4) = 0.025$ and $p_f = 200/(200 \times 4) = 0.25$. Since litter size is 8, each selection candidate has 7 full sibs that also have a record on growth. Sire family size is $10 \times 8 = 80$ individuals, thus there are $80 - 8\text{FS} = 72$ half sibs produced by 9 dams. Below are the groups and index window and the results.

Groups window

The screenshot shows the 'Groups window' in the SelAction software. The window title is 'SelAction' and it has a menu bar with 'File', 'Edit', 'Options', and 'Info'. The toolbar includes icons for 'Open', 'Save Input', 'Print', 'Exit', 'Traits', 'Population', 'Groups', 'Index', 'Correlations', 'Calculate', and 'Save Output'. The main area contains three columns of input fields:

Full-sib groups	Half-sib groups		Progeny Groups
# Full-sibs 1 7	# Dams 1 9	# Half-sibs 72	0

Index window**Results**

***** begin of output *****

RESULTS

TRAITS USED
growth

TRAIT PARAMETERS

	phenotypic variance	heritability	com.env.effect
growth	2,500.000	0.350	0.100

BREEDING GOAL INFORMATION
1.000 * growth

POPULATION SIZE

number of selected sires :	20.0
number of selected dams :	200.0
number of male selection candidates per dam :	4.0
number of female selection candidates per dam :	4.0
total selected proportion sires :	0.025
total selected proportion dams :	0.250

CHARACTERISTICS OF THE USED GROUPS

full-sib group 1 with	7.0 animals	
half-sib group 1 with	9.0 dams, producing	72.0 animals

¹INDEX INFORMATION :

- Own performance of growth
- Dam BLUP breeding value of growth
- Sire BLUP breeding value of growth
- Observations on full-Sib group 1 on growth
- Observations on half-sib group 1 on growth
- Mean EBV of the dams of hs-group 1 on growth

```

***** RESULTS *****
EQUILIBRIUM PARAMETERS
  phenotypic variance  heritability  com.env.effect
  growth              2,298.360      0.293          0.109

RESPONSE
  sires              dams              total
  growth
    trait units:      18.011          9.874          27.885
    economic units:  18.011          9.874          27.885
    % of totalresponse: 64.590          35.410          100.000

TOTALRESPONSE
  sires              dams              total
  economic units:    18.011          9.874          27.885
  variance of index: 246.479          246.479
  variance of breeding goal: 673.361
  accuracy of index:  0.605          0.605
  increase of inbreeding: 2.124 % per generation

***** end of output *****

```

Explanation of the output

Most elements of the output are the same as in example 1 and are therefore not explained.

¹ Index information. Lists the information sources included in the index. Breeding value estimation using BLUP is accounted for by including the dam BLUP breeding value, the sire BLUP breeding value and the mean EBV of the dams of the half sibs (see general description of SelAction).

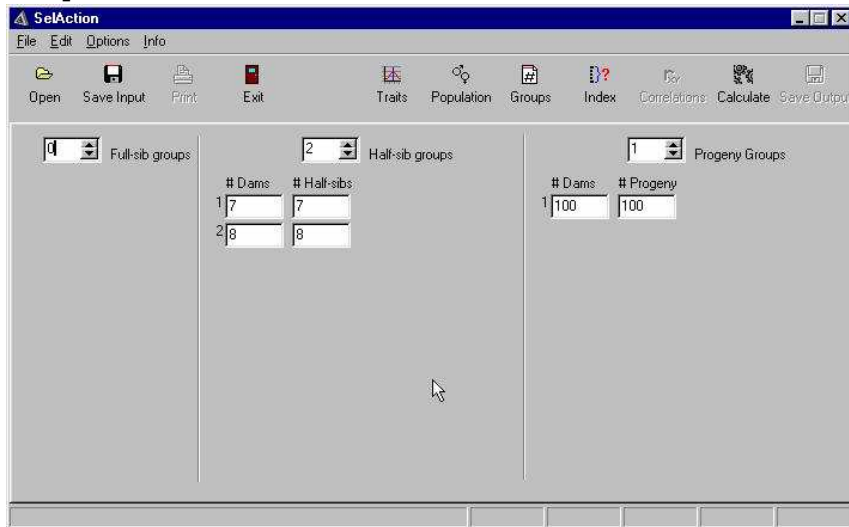
Notice the increased response to selection but also the increased rate of inbreeding compared to the mass selection scheme (Example 1). The increase in selection response compared to mass selection may seem surprisingly small, i.e. the extra information available with BLUP has only limited benefits. The reasons are the following. First, BLUP yields a higher accuracy, but differences in response are not proportional to differences in accuracy because higher accuracy results in lower equilibrium values of the breeding goal variance (Bulmer effect). Second, with selection on BLUP EBV the correlation between EBV of full and half sibs is higher than with mass selection. The selection intensity with BLUP is therefore a little bit lower than that with mass selection. (Note that BLUP is important with respect to the estimation of fixed effects, which is problematic with mass selection. Thus BLUP is to be preferred but restriction of the rate of inbreeding deserves attention).

Example 3: Single trait selection for milk yield in dairy cattle

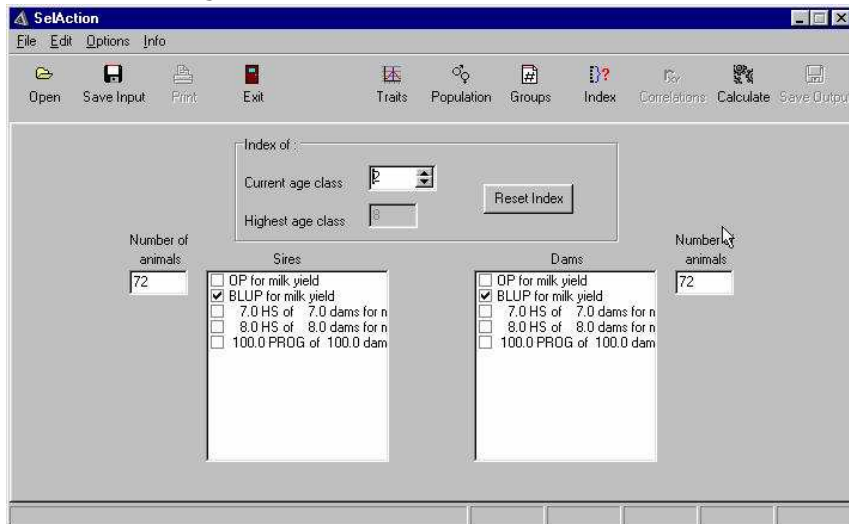
This is an example for overlapping generations with truncation selection. Annual milk yield has a heritability of 0.3 and a phenotypic standard deviation of 1000kg. The population consists of overlapping generations with a maximum age for both cows and bulls of eight years. The age class interval is one year, thus there are 8 age classes. Cows and bulls are at least two-years-old when their first offspring are born, thus parents cannot be selected from age class one because those individuals are not yet reproductive. Annually there is 10% culling among selection candidates for reasons of health and survival. Each year, 10 sires and 200 cows are selected as parents of the newborn year class. Fertility of the selected dams is 80%, thus a single selected cow is expected to produce 0.4 male and 0.4 female offspring on average. When bulls are five years of age, information on milk yield of 100 progeny becomes available.

Below are the groups window, the index windows for ageclass 2 and 5 and the results. Note that in the output, response is given per year.

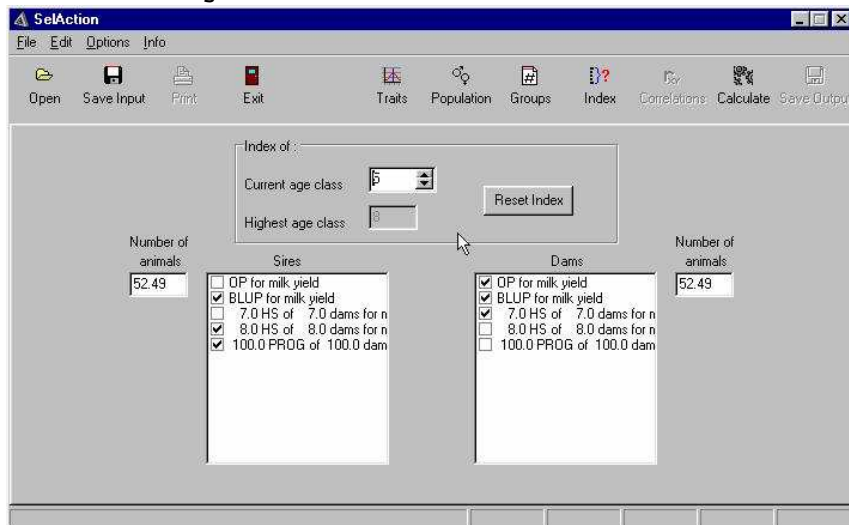
Groupswindow



Index window ageclass 2



Index window ageclass 5



Results

*****output file*****

RESULTS

TRAITS USED

milk yield

TRAIT PARAMETERS

phenotypic variance heritability
 milk yield 1,000,000.000 0.300

BREEDING GOAL INFORMATION

1.000 * milk yield

POPULATION SIZE

number of selected sires : 10.0
 number of selected dams : 200.0
 number of male selection candidates per dam : 0.4
 number of female selection candidates per dam : 0.4

selected proportion sires in age class 1 : 0.067 x 0.000 = 0.000
 selected proportion sires in age class 2 : 0.008 x 72.000 = 0.550
 selected proportion sires in age class 3 : 0.001 x 64.800 = 0.038
 selected proportion sires in age class 4 : 0.000 x 58.320 = 0.001
 selected proportion sires in age class 5 : 0.088 x 52.490 = 4.634
 selected proportion sires in age class 6 : 0.056 x 47.240 = 2.629
 selected proportion sires in age class 7 : 0.033 x 42.520 = 1.420
 selected proportion sires in age class 8 : 0.019 x 38.260 = 0.728

selected proportion dams in age class 9 : 1.000 x 0.000 = 0.000
 selected proportion dams in age class 10 : 0.992 x 72.000 = 71.427
 selected proportion dams in age class 11 : 0.752 x 64.800 = 48.754
 selected proportion dams in age class 12 : 0.600 x 58.320 = 35.014
 selected proportion dams in age class 13 : 0.431 x 52.490 = 22.632
 selected proportion dams in age class 14 : 0.274 x 47.240 = 12.939
 selected proportion dams in age class 15 : 0.152 x 42.520 = 6.454
 selected proportion dams in age class 16 : 0.073 x 38.260 = 2.779

generation interval : 4.515 cohort intervals

CHARACTERISTICS OF THE USED GROUPS

half-sib group 1 with	7.0 dams, producing	7.0 animals
half-sib group 2 with	8.0 dams, producing	8.0 animals
progeny group information		
progeny group 1 with	100.0 dams, producing	100.0 progeny

INDEX INFORMATION :

sire class : 1
 Dam BLUP breeding value of milk yield
 Sire BLUP breeding value of milk yield

sire class : 2
 Dam BLUP breeding value of milk yield
 Sire BLUP breeding value of milk yield

sire class : 3
 Dam BLUP breeding value of milk yield
 Sire BLUP breeding value of milk yield
 Observations on half-sib group 2 on milk yield
 Mean EBV of the dams of hs-group 2 on milk yield

```
sire class : 4
    Dam BLUP breeding value of milk yield
    Sire BLUP breeding value of milk yield
    Observations on half-sib group 2 on milk yield
Mean EBV of the dams of hs-group 2 on milk yield

sire class : 5
    Dam BLUP breeding value of milk yield
    Sire BLUP breeding value of milk yield
    Observations on half-sib group 2 on milk yield
Mean EBV of the dams of hs-group 2 on milk yield
    Observations on progeny group 1 on milk yield

sire class : 6
    Dam BLUP breeding value of milk yield
    Sire BLUP breeding value of milk yield
    Observations on half-sib group 2 on milk yield
Mean EBV of the dams of hs-group 2 on milk yield
    Observations on progeny group 1 on milk yield

sire class : 7
    Dam BLUP breeding value of milk yield
    Sire BLUP breeding value of milk yield
    Observations on half-sib group 2 on milk yield
Mean EBV of the dams of hs-group 2 on milk yield
    Observations on progeny group 1 on milk yield

sire class : 8
    Dam BLUP breeding value of milk yield
    Sire BLUP breeding value of milk yield
    Observations on half-sib group 2 on milk yield
Mean EBV of the dams of hs-group 2 on milk yield
    Observations on progeny group 1 on milk yield

dam class : 1 (= age class 9)
    Dam BLUP breeding value of milk yield
    Sire BLUP breeding value of milk yield

dam class : 2 (= age class 10)
    Dam BLUP breeding value of milk yield
    Sire BLUP breeding value of milk yield

dam class : 3 (= age class 11)
    Own performance of milk yield
    Dam BLUP breeding value of milk yield
    Sire BLUP breeding value of milk yield
    Observations on half-sib group 1 on milk yield
Mean EBV of the dams of hs-group 1 on milk yield

dam class : 4 (= age class 12)
    Own performance of milk yield
    Dam BLUP breeding value of milk yield
    Sire BLUP breeding value of milk yield
    Observations on half-sib group 1 on milk yield
Mean EBV of the dams of hs-group 1 on milk yield

dam class : 5 (= age class 13)
    Own performance of milk yield
    Dam BLUP breeding value of milk yield
    Sire BLUP breeding value of milk yield
    Observations on half-sib group 1 on milk yield
Mean EBV of the dams of hs-group 1 on milk yield
```

dam class : 6 (= age class 14)
 Own performance of milk yield
 Dam BLUP breeding value of milk yield
 Sire BLUP breeding value of milk yield
 Observations on half-sib group 1 on milk yield
 Mean EBV of the dams of hs-group 1 on milk yield

dam class : 7 (= age class 15)
 Own performance of milk yield
 Dam BLUP breeding value of milk yield
 Sire BLUP breeding value of milk yield
 Observations on half-sib group 1 on milk yield
 Mean EBV of the dams of hs-group 1 on milk yield

dam class : 8 (= age class 16)
 Own performance of milk yield
 Dam BLUP breeding value of milk yield
 Sire BLUP breeding value of milk yield
 Observations on half-sib group 1 on milk yield
 Mean EBV of the dams of hs-group 1 on milk yield

***** RESULTS *****

EQUILIBRIUM PARAMETERS

phenotypic variance heritability
 milk yield 916,151.131 0.236

RESPONSE

	sires	dams	total
milk yield			
trait units:	90.922	12.810	103.732
economic units:	90.922	12.810	103.732
% of totalresponse:	87.651	12.349	100.000

TOTALRESPONSE

	sires	dams	total
economic units:	90.922	12.810	103.732

sire class 1 variance of index:	12,460.481
accuracy of index:	0.240
sire class 2 variance of index:	12,460.481
accuracy of index:	0.240
sire class 3 variance of index:	13,317.017
accuracy of index:	0.248
sire class 4 variance of index:	13,317.017
accuracy of index:	0.248
sire class 5 variance of index:	185,459.586
accuracy of index:	0.926
sire class 6 variance of index:	185,459.586
accuracy of index:	0.926
sire class 7 variance of index:	185,459.586
accuracy of index:	0.926

```

sire class 8 variance of index:    185,459.586
              accuracy of index:      0.926

dam class 1 variance of index:     12,460.481
              accuracy of index:      0.240

dam class 2 variance of index:     12,460.481
              accuracy of index:      0.240

dam class 3 variance of index:     58,826.215
              accuracy of index:      0.522

dam class 4 variance of index:     58,826.215
              accuracy of index:      0.522

dam class 5 variance of index:     58,826.215
              accuracy of index:      0.522

dam class 6 variance of index:     58,826.215
              accuracy of index:      0.522

dam class 7 variance of index:     58,826.215
              accuracy of index:      0.522

dam class 8 variance of index:     58,826.215
              accuracy of index:      0.522

variance of breeding goal:        216,149.591

```

***** end of output *****

11.2 More advanced breeding programs

Example 4: combined crossbred purebred selection in pigs

The previous examples have considered simple breeding schemes, considerably simpler than practical breeding schemes. However, the power of SelAction is that it can deal with complex breeding schemes that occur in practice. This example considers a more complicated breeding scheme in pigs where information on crossbred relatives is used to increase selection response in the purebred lines.

Consider a pig-breeding program that aims to improve three traits, daily gain (DG, g/day), carcass lean content (LC, %) and feed intake (FI, g/day). It is a 3-way breeding program with a single sire line and two dam lines. This example concerns genetic improvement of the sire line. Because the crossbreds are the final products, the breeding goal is defined at the crossbred level, meaning that crossbred traits have an economic value whereas purebred traits do not.

The purebred line consists of 40 boars and 200 sows per generation. Each sow produces 8 offspring, 4 males and 4 females. Traits recorded in the purebred line are DG, FI and back fat thickness (BF, mm) which is used as an indicator trait for carcass lean content. Carcass lean content itself is not recorded in the purebred lines. All 8 offspring of each of the 200 litters have records on DG and BF. FI is recorded only on 2 males out of each litter. Only males that have a record on feed intake are selection candidates, thus there are $200 \times 2 = 400$ male selection candidates, so that $p_m = 0.1$. All female offspring per litter are selection candidates, thus there are 800 female selection candidates, so that $p_f = 0.25$.

Carcass lean content is measured on the crossbred fattening pigs in the slaughterhouses. It is assumed that the sires of the purebred selection candidates are also used as sires of crossbred fattening pigs. Purebred selection candidates therefore have crossbred half sibs with a record on carcass lean content. It is assumed that each purebred sire has 64 crossbred fattening pigs with a record for LC which are born out of 8 sows. Thus each purebred selection candidate has information on LC of 64 crossbred half sibs out of 8 dams.

The correlation between the same trait in a purebred and in a crossbred may deviate from 1 due to dominance and genotype by environment interaction. This correlation is commonly called the "purebred-crossbred correlation", r_{pc} . Here it is assumed that $r_{pc} = 0.8$. Thus purebred and crossbred performance are different traits. Hence, we have to make a distinction between DG in purebreds and crossbreds, giving two traits, DGPB and DGCB; the same holds for the other traits. In total there are six traits; DGPB, BFPB, FIPB, DGCB, LCCB and FICB. It is not needed to include LCPB and BFCB because those traits are not recorded and have no economic importance.

The traits

Genetic parameters and economic values for the traits are taken from the Ph.D.-theses of Alfred de Vries and Jacco Eissen.

trait	phen. var.	h^2	c^2	EV
DGPB	2,500.000	0.350	0.100	-
BFPB	4.000	0.500	0.100	-
FIPB	52,900.000	0.350	0.100	-
DGCB	2,500.000	0.350	0.100	0.08 €/g/day
LCCB	25.000	0.350	0.100	1.34 €/%
FICB	52,900.000	0.350	0.100	-0.006 €/g/day

The population

40 males 200 females
 2 male offsp. 4 female offsp.
 $p_m = 0.1$ $p_f = 0.25$

The groups

Within each litter, all 8 individuals have records for DG and BF and 2 males have records for FI. Thus for males there are two full sib groups:

FS-group 1 with 1 individuals with records on DGPB, BFPB and FIPB.

FS-group 2 with 6 individuals with records on DGPB and BFPB.

Note that individuals in different groups are different individuals, so that in total there are 7 full sibs.

For females there are also two full sib groups:

FS-group 3 with 2 individuals with records on DGPB, BFPB and FIPB.

FS-group 4 with 5 individuals with records on DGPB and BFPB.

Each sire is mated to 5 dams and each dam produces 8 offspring. Thus in total there are $(5-1) \times 8 = 32$ purebred half sibs, and within each litter 2 out of the 8 individuals have a record for feed intake. In addition there are 64 crossbred half sibs. Thus there are three half sib groups, they are the same for sires and dams.

HS-group 1 with 8 individuals out of 4 dams with records on DGPB, BFPB and FIPB.

HS-group 2 with 24 individuals out of 4 dams with records on DGPB and BFPB.

HS-group 3 with 64 individuals out of 8 dams with records on LCCB.

The index

There is BLUP breeding value estimation for all traits, thus the box BLUP should be clicked for all traits. For males, own performance information is available on DGPB, BFPB and FIPB. For females, own performance information is available on DGPB and BFPB. For the full and half sibs groups, for a particular trait the box for a group should be clicked if that group provides information for the trait (see groups above, the results file printed below shows which index information sources were included for which traits).

The correlations

Phenotypic	DGPB	BFPB	FIPB	DGCB	LCCB	FICB
DGPB	1.000					
BFPB	0.150	1.000				
FIPB	0.700	0.500	1.000			
DGCB	0.280	0.050	0.200	1.000		
LCCB	-0.030	-0.270	-0.080	-0.100	1.000	

FICB 0.200 0.170 0.280 0.700 -0.300 1.000

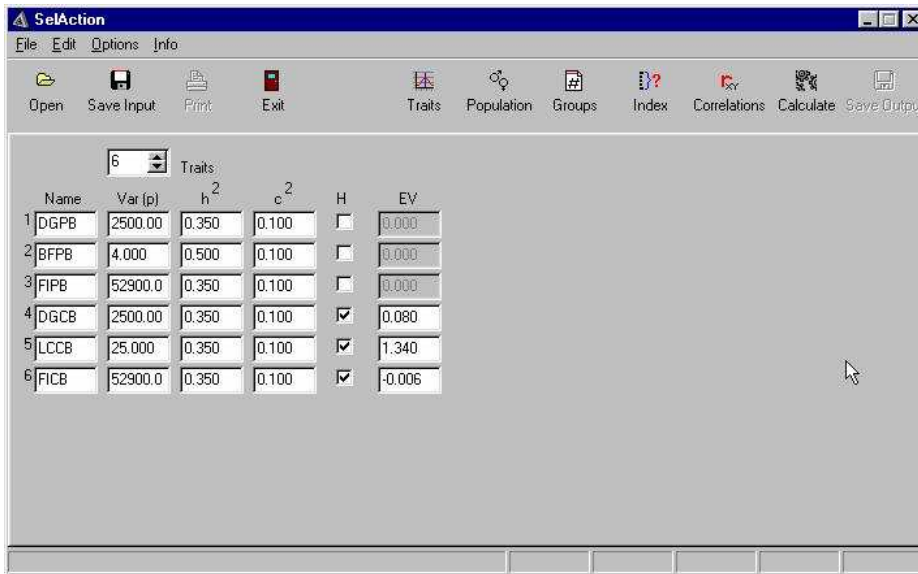
Genetic

	DGPB	BFPB	FIPB	DGCB	LCCB	FICB
DGPB	1.000					
BFPB	0.150	1.000				
FIPB	0.700	0.500	1.000			
DGCB	0.800	0.120	0.560	1.000		
LCCB	-0.080	-0.640	-0.240	-0.100	1.000	
FICB	0.560	0.400	0.800	0.700	-0.300	1.000

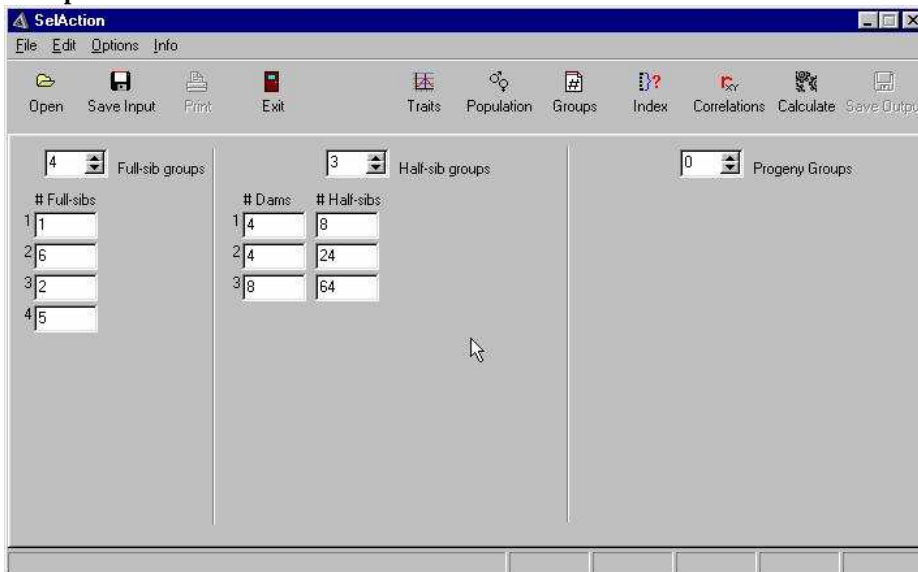
Common environmental

All common environmental correlations were assumed to be zero.

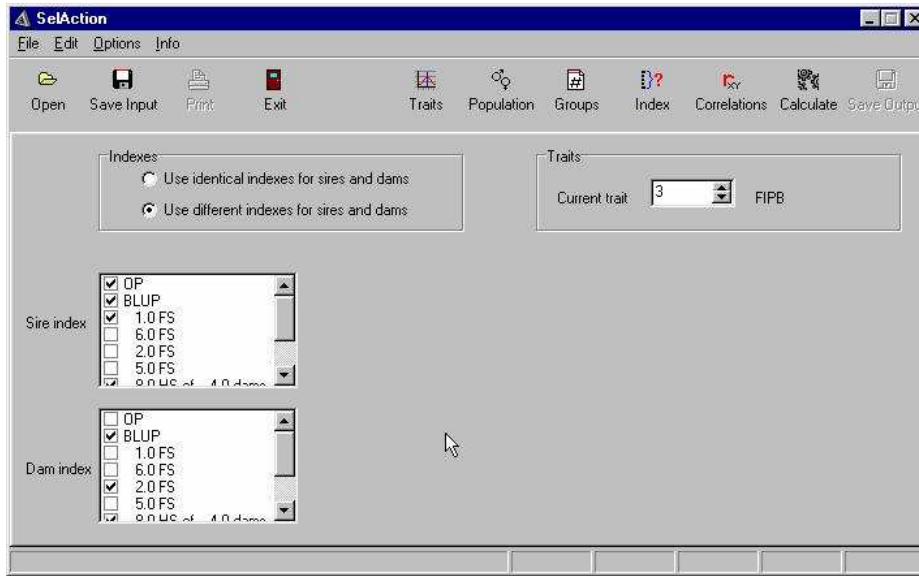
Traits window



Groups window



Index window for FIPB



Results

***** begin of output *****

RESULTS

TRAITS USED

DGPB
BFPB
FIPB
DGCB
LCCB
FICB

TRAIT PARAMETERS

	phenotypic variance	heritability	com.env.effect
DGPB	2,500.000	0.350	0.100
BFPB	4.000	0.500	0.100
FIPB	52,900.000	0.350	0.100
DGCB	2,500.000	0.350	0.100
LCCB	25.000	0.350	0.100
FICB	52,900.000	0.350	0.100

PHENOTYPIC CORRELATIONS

	DGPB	BFPB	FIPB	DGCB	LCCB	FICB
DGPB	1.000					
BFPB	0.150	1.000				
FIPB	0.700	0.500	1.000			
DGCB	0.280	0.050	0.200	1.000		
LCCB	-0.030	-0.270	-0.080	-0.100	1.000	
FICB	0.200	0.170	0.280	0.700	-0.300	1.000

GENETIC CORRELATIONS

	DGPB	BFPB	FIPB	DGCB	LCCB	FICB
DGPB	1.000					
BFPB	0.150	1.000				
FIPB	0.700	0.500	1.000			
DGCB	0.800	0.120	0.560	1.000		
LCCB	-0.080	-0.640	-0.240	-0.100	1.000	
FICB	0.560	0.400	0.800	0.700	-0.300	1.000

COMMON ENVIRONMENTAL CORRELATIONS

	DGPB	BFPB	FIPB	DGCB	LCCB	FICB
DGPB	1.000					
BFPB	0.000	1.000				
FIPB	0.000	0.000	1.000			
DGCB	0.000	0.000	0.000	1.000		
LCCB	0.000	0.000	0.000	0.000	1.000	
FICB	0.000	0.000	0.000	0.000	0.000	1.000

BREEDING GOAL INFORMATION

0.080 * DGCB
 1.340 * LCCB
 -0.006 * FICB

POPULATION SIZE

number of selected sires : 40.0
 number of selected dams : 200.0
 number of male selection candidates per dam : 2.0
 number of female selection candidates per dam : 4.0

 total selected proportion sires : 0.100
 total selected proportion dams : 0.250

CHARACTERISTICS OF THE USED GROUPS

full-sib group 1 with 1.0 animals
 full-sib group 2 with 6.0 animals
 full-sib group 3 with 2.0 animals
 full-sib group 4 with 5.0 animals
 half-sib group 1 with 4.0 dams, producing 8.0 animals
 half-sib group 2 with 4.0 dams, producing 24.0 animals
 half-sib group 3 with 8.0 dams, producing 64.0 animals

INDEX INFORMATION FOR SIRE :

Own performance of DGPB
 Dam BLUP breeding value of DGPB
 Sire BLUP breeding value of DGPB
 Observations on full-Sib group 1 on DGPB
 Observations on full-Sib group 2 on DGPB
 Observations on half-sib group 1 on DGPB
 Observations on half-sib group 2 on DGPB
 Mean EBV of the dams of hs-group 1 on DGPB
 Mean EBV of the dams of hs-group 2 on DGPB

Own performance of BFPB
 Dam BLUP breeding value of BFPB
 Sire BLUP breeding value of BFPB
 Observations on full-Sib group 1 on BFPB
 Observations on full-Sib group 2 on BFPB
 Observations on half-sib group 1 on BFPB
 Observations on half-sib group 2 on BFPB
 Mean EBV of the dams of hs-group 1 on BFPB
 Mean EBV of the dams of hs-group 2 on BFPB

Own performance of FIPB
 Dam BLUP breeding value of FIPB
 Sire BLUP breeding value of FIPB
 Observations on full-Sib group 1 on FIPB
 Observations on half-sib group 1 on FIPB
 Mean EBV of the dams of hs-group 1 on FIPB

Dam BLUP breeding value of DGCB
 Sire BLUP breeding value of DGCB

Dam BLUP breeding value of LCCB
 Sire BLUP breeding value of LCCB
 Observations on half-sib group 3 on LCCB
 Mean EBV of the dams of hs-group 3 on LCCB

Dam BLUP breeding value of FICB
 Sire BLUP breeding value of FICB

INDEX INFORMATION FOR DAMS :

Own performance of DGPB
 Dam BLUP breeding value of DGPB
 Sire BLUP breeding value of DGPB
 Observations on full-Sib group 3 on DGPB
 Observations on full-Sib group 4 on DGPB
 Observations on half-sib group 1 on DGPB
 Observations on half-sib group 2 on DGPB
 Mean EBV of the dams of hs-group 1 on DGPB
 Mean EBV of the dams of hs-group 2 on DGPB

Own performance of BFPB
 Dam BLUP breeding value of BFPB
 Sire BLUP breeding value of BFPB
 Observations on full-Sib group 3 on BFPB
 Observations on full-Sib group 4 on BFPB
 Observations on half-sib group 1 on BFPB
 Observations on half-sib group 2 on BFPB
 Mean EBV of the dams of hs-group 1 on BFPB
 Mean EBV of the dams of hs-group 2 on BFPB

Dam BLUP breeding value of FIPB
 Sire BLUP breeding value of FIPB
 Observations on full-Sib group 3 on FIPB
 Observations on half-sib group 1 on FIPB
 Mean EBV of the dams of hs-group 1 on FIPB

Dam BLUP breeding value of DGCB
 Sire BLUP breeding value of DGCB

Dam BLUP breeding value of LCCB
 Sire BLUP breeding value of LCCB
 Observations on half-sib group 3 on LCCB
 Mean EBV of the dams of hs-group 3 on LCCB

Dam BLUP breeding value of FICB
 Sire BLUP breeding value of FICB

***** RESULTS *****

EQUILIBRIUM PARAMETERS

	phenotypic variance	heritability	com.env.effect
DGPB	2,485.566	0.346	0.101
BFPB	3.679	0.456	0.109
FIPB	52,825.614	0.349	0.100
DGCB	2,491.939	0.348	0.100
LCCB	23.701	0.314	0.105
FICB	52,801.438	0.349	0.100

PHENOTYPIC CORRELATIONS

	DGPB	BFPB	FIPB	DGCB	LCCB	FICB
DGPB	1.000					
BFPB	0.179	1.000				
FIPB	0.705	0.511	1.000			
DGCB	0.277	0.069	0.203	1.000		
LCCB	-0.049	-0.220	-0.074	-0.116	1.000	

FICB 0.204 0.165 0.279 0.704 -0.298 1.000

GENETIC CORRELATIONS

	DGPB	BFPB	FIPB	DGCB	LCCB	FICB
DGPB	1.000					
BFPB	0.222	1.000				
FIPB	0.715	0.520	1.000			
DGCB	0.798	0.174	0.570	1.000		
LCCB	-0.141	-0.574	-0.235	-0.149	1.000	
FICB	0.576	0.406	0.799	0.712	-0.296	1.000

COMMON ENVIRONMENTAL CORRELATIONS

	DGPB	BFPB	FIPB	DGCB	LCCB	FICB
DGPB	1.000					
BFPB	0.000	1.000				
FIPB	0.000	0.000	1.000			
DGCB	0.000	0.000	0.000	1.000		
LCCB	0.000	0.000	0.000	0.000	1.000	
FICB	0.000	0.000	0.000	0.000	0.000	1.000

RESPONSE

	sires	dams	total
DGCB			
trait units:	2.686	2.039	4.725
economic units:	0.215	0.163	0.378
% of totalresponse:	7.041	5.344	12.385
LCCB			
trait units:	1.127	0.796	1.923
economic units:	1.510	1.067	2.576
% of totalresponse:	49.460	34.942	84.403
FICB			
trait units:	-8.286	-8.057	-16.343
economic units:	0.050	0.048	0.098
% of totalresponse:	1.629	1.584	3.213

CORRELATED RESPONSE

	sires	dams	total
DGPB			
trait units:	3.632	2.749	6.381
BFPB			
trait units:	-0.558	-0.397	-0.955
FIPB			
trait units:	-6.574	-7.299	-13.873

TOTALRESPONSE

	sires	dams	total
economic units:	1.774	1.278	3.052
variance of index:	4.165	4.098	
variance of breeding goal:	16.048		
accuracy of index:	0.509	0.505	
increase of inbreeding:	1.017 % per generation		

***** end of output *****

Example 5: Two stage selection for growth and feed intake in pigs

This example considers a two stage breeding program for growth and feed intake in pigs. Because recording of feed intake is expensive, it is recorded on males only and after preselection on growth. Preselection takes place half way through the growth period and is based on growth in the first part of the growth period and full pedigree information. The final stage of selection takes place at the end of the growth period and is based on full pedigree, growth over the full growth period and feed intake for males. Growth during the first part of the growth period is considered to be a different trait than growth over the full period, a genetic and phenotypic correlation of 0.7 is assumed.

Thus there are three traits:

- DG1, daily gain during the first part of the growth period (g/day)
- DG, daily gain over the full growth period (g/day)
- FI, feed intake (g/day)

Genetic parameters are given in the results below. Note that DG1 has no economic importance in itself, it is an index trait providing information on DG.

The breeding program has 40 boars and 200 sows with litter size of 8, 4 males and 4 females. Information sources available at the preselection are:

- full pedigree for all traits (meaning, EBVs of the previous generation for all traits).
- own performance for DG1
- 7 full sibs with records on DG1
- 32 half sibs out of 4 dams with records on DG1

Selected proportions in the preselection are $p_{1,m} = 0.25$ and $p_{1,f} = 0.5$.

The preselection halves the number of selection candidates, thus in the final stage of selection there are fewer. When halving the family size there would be 3.5 FS which we round down to 3 FS with records on DG. Only males have records for FI, thus females have 1.5 FS with records on FI and males have $0.5 \approx 0$ FS with records on FI. In addition there are 16HS, 8 with records on both FI and DG and 8 with records only on DG. Thus additional (compared to preselection) information sources in the final stage are, for males:

- own performance for DG and FI
- 3 FS with records on DG
- 8 HS with records on DG
- 8 HS with records on DG and FI

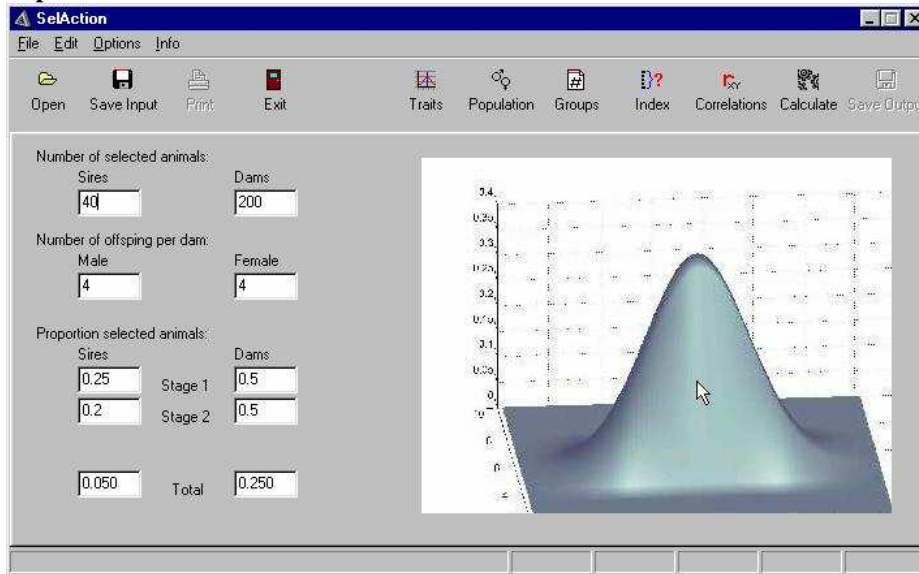
and for females

- own performance for DG
- 1.5 FS with records on DG
- 1.5 FS with records on DG and FI
- 8 HS with records on DG
- 8 HS with records on DG and FI

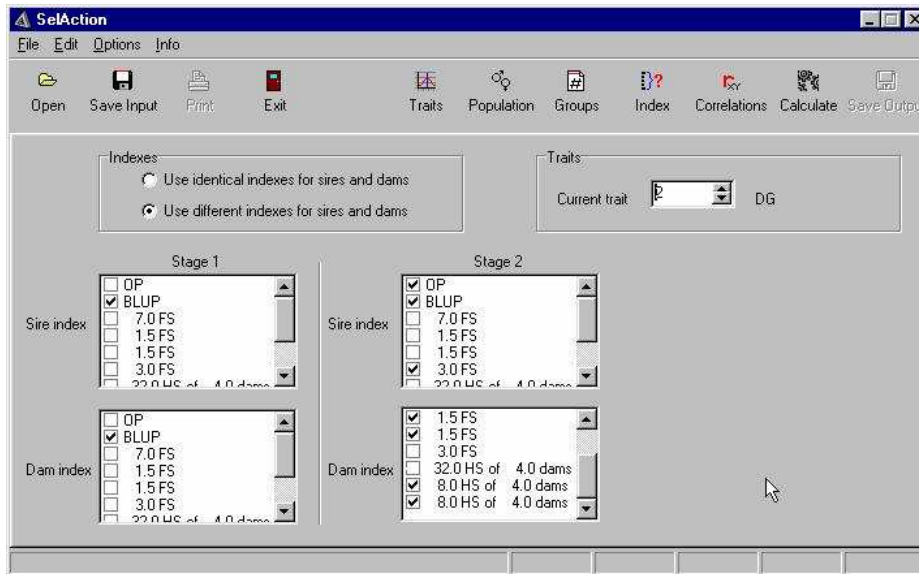
Selected proportions in the final stage are $p_{2,m} = 0.2$ and $p_{f,2} = 0.5$ so that overall selected proportions are $p_m = 0.25 \times 0.2 = 0.05 = 40/(200 \times 4)$ and $p_f = 0.5 \times 0.5 = 0.25 = 200/(200 \times 4)$.

The results of SelAction is given below. Notice that the first stage selection results in an (undesired) increase of FI because there is only information on DG1 available in the first stage. In the final stage, males have information on FI and the increase of FI due to the first stage is reduced in the final stage selection of boars.

Population window



Index window for trait DG



Results

***** begin of output *****

RESULTS

TRAITS USED

DG1
DG
FI

TRAIT PARAMETERS

	phenotypic variance	heritability	com.env.effect
DG1	625.000	0.350	0.100
DG	2,500.000	0.350	0.100

FI 52,900.000 0.350 0.100

PHENOTYPIC CORRELATIONS

	DG1	DG	FI
DG1	1.000		
DG	0.700	1.000	
FI	0.500	0.700	1.000

GENETIC CORRELATIONS

	DG1	DG	FI
DG1	1.000		
DG	0.700	1.000	
FI	0.500	0.700	1.000

COMMON ENVIRONMENTAL CORRELATIONS

	DG1	DG	FI
DG1	1.000		
DG	0.000	1.000	
FI	0.000	0.000	1.000

BREEDING GOAL INFORMATION

0.080 * DG
-0.012 * FI

POPULATION SIZE

number of selected sires : 40.0
 number of selected dams : 200.0
 number of male selection candidates per dam : 4.0
 number of female selection candidates per dam : 4.0

selected proportion sires in stage 1 : 0.250
 selected proportion sires in stage 2 : 0.200

selected proportion dams in stage 1 : 0.500
 selected proportion dams in stage 2 : 0.500

total selected proportion sires : 0.050
 total selected proportion dams : 0.250

CHARACTERISTICS OF THE USED GROUPS

full-sib group 1 with	7.0 animals	
full-sib group 2 with	1.5 animals	
full-sib group 3 with	1.5 animals	
full-sib group 4 with	3.0 animals	
half-sib group 1 with	4.0 dams, producing	32.0 animals
half-sib group 2 with	4.0 dams, producing	8.0 animals
half-sib group 3 with	4.0 dams, producing	8.0 animals

STAGE 1 INDEX INFORMATION FOR SIREs :

Own performance of DG1
 Dam BLUP breeding value of DG1
 Sire BLUP breeding value of DG1
 Observations on full-Sib group 1 on DG1
 Observations on half-sib group 1 on DG1
 Mean EBV of the dams of hs-group 1 on DG1
 Dam BLUP breeding value of DG
 Sire BLUP breeding value of DG
 Dam BLUP breeding value of FI
 Sire BLUP breeding value of FI

STAGE 1 INDEX INFORMATION FOR DAMS :

Own performance of DG1
 Dam BLUP breeding value on DG1
 Sire BLUP breeding value on DG1
 Observations on full-Sib group 1 on DG1
 Observations on half-sib group 1 on DG1
 Mean EBV of the dams of hs-group 1 on DG1
 Dam BLUP breeding value on DG
 Sire BLUP breeding value on DG
 Dam BLUP breeding value on FI
 Sire BLUP breeding value on FI

STAGE 2 INDEX INFORMATION FOR SIREs :

Own performance of DG1
 Dam BLUP breeding value of DG1
 Sire BLUP breeding value of DG1
 Observations on full-Sib group 1 on DG1
 Observations on half-sib group 1 on DG1
 Mean EBV of the dams of hs-group 1 on DG1
 Own performance of DG
 Dam BLUP breeding value of DG
 Sire BLUP breeding value of DG
 Observations on full-Sib group 4 on DG
 Observations on half-sib group 2 on DG
 Observations on half-sib group 3 on DG
 Mean EBV of the dams of hs-group 2 on DG
 Mean EBV of the dams of hs-group 3 on DG
 Own performance of FI
 Dam BLUP breeding value of FI
 Sire BLUP breeding value of FI
 Observations on half-sib group 2 on FI
 Mean EBV of the dams of hs-group 2 on FI

STAGE 2 INDEX INFORMATION FOR DAMS :

Own performance of DG1
 Dam BLUP breeding value on DG1
 Sire BLUP breeding value on DG1
 Observations on full-Sib group 1 on DG1
 Observations on half-sib group 1 on DG1
 Mean EBV of the dams of hs-group 1 on DG1
 Own performance of DG
 Dam BLUP breeding value on DG
 Sire BLUP breeding value on DG
 Observations on full-Sib group 2 on DG
 Observations on full-Sib group 3 on DG
 Observations on half-sib group 2 on DG
 Observations on half-sib group 3 on DG
 Mean EBV of the dams of hs-group 2 on DG
 Mean EBV of the dams of hs-group 3 on DG
 Dam BLUP breeding value on FI
 Sire BLUP breeding value on FI
 Observations on full-Sib group 2 on FI
 Observations on half-sib group 2 on FI
 Mean EBV of the dams of hs-group 2 on FI

***** RESULTS *****

EQUILIBRIUM PARAMETERS

	phenotypic variance	heritability	com.env.effect
DG1	608.967	0.333	0.103
DG	2,373.194	0.315	0.105
FI	52,529.100	0.345	0.101

PHENOTYPIC CORRELATIONS

	DG1	DG	FI
DG1	1.000		
DG	0.690	1.000	
FI	0.498	0.706	1.000

GENETIC CORRELATIONS

	DG1	DG	FI
DG1	1.000		
DG	0.671	1.000	
FI	0.493	0.720	1.000

COMMON ENVIRONMENTAL CORRELATIONS

	DG1	DG	FI
DG1	1.000		
DG	0.000	1.000	
FI	0.000	0.000	1.000

RESPONSE AFTER STAGE 1

	sires	dams	total
DG			
trait units:	6.759	4.244	11.003
economic units:	0.541	0.340	0.880
% of totalresponse:	109.418	68.704	178.122
FI			
trait units:	19.762	12.409	32.171
economic units:	-0.237	-0.149	-0.386
% of totalresponse:	-47.989	-30.133	-78.122

CORRELATED RESPONSE AFTER STAGE 1

	sires	dams	total
DG1			
trait units:	4.437	2.786	7.223

TOTALRESPONSE AFTER STAGE 1

	sires	dams	total
economic units:	0.304	0.191	0.494
variance of index:	0.231	0.231	
variance of breeding goal:	2.309		
accuracy of index:	0.316	0.316	

RESPONSE AFTER STAGE 2

	sires	dams	total
DG			
trait units:	12.339	8.599	20.938
economic units:	0.987	0.688	1.675
% of totalresponse:	76.222	53.121	129.343
FI			
trait units:	10.347	21.320	31.667
economic units:	-0.124	-0.256	-0.380
% of totalresponse:	-9.588	-19.756	-29.343

CORRELATED RESPONSE AFTER STAGE 2

	sires	dams	total
DG1			

trait units:	5.375	3.724	9.099
TOTALRESPONSE AFTER STAGE 2			
	sires	dams	total
economic units:	0.863	0.432	1.295
variance of index:	0.817	0.519	
variance of breeding goal:	2.309		
accuracy of index:	0.595	0.474	

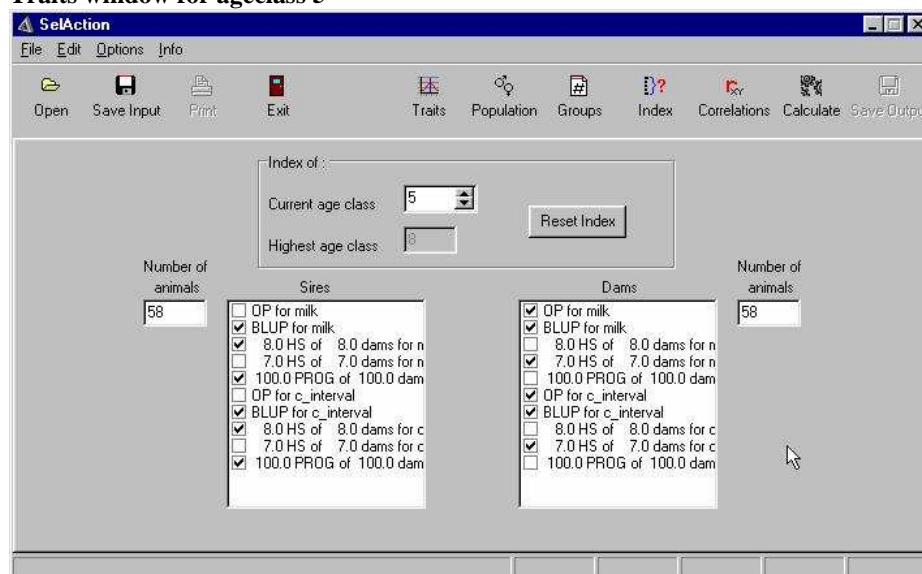
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Example 6: Maintaining the fertility level in dairy cattle

Though it is often difficult to derive exact economic values for traits, it may be possible to define desired changes or levels of traits. In dairy cattle for example, it may be difficult to derive an exact economic value for fertility. However, it may be considered desirable to maintain the present level of fertility, i.e. to avoid a continued reduction of fertility due to selection for production traits. SelAction can accommodate such situations. The program is sufficiently quick to allow the user to iterate on the economic weights until the desired gain is achieved. Below are the results of a dairy cattle-breeding program that achieves zero change in calving interval while improving protein yield. The weight on calving interval in the breeding goal is determined iteratively until genetic gain for it is zero.

Without a negative weight on calving interval, calving interval increased annually by an amount of 0.6 days. In that case, selection response in protein yield was +3.790 kg/yr (results not shown). To avoid an increase of calving interval, a negative economic weight was given to calving interval, and its value was increased until calving interval did not increase any longer. This required an economic value of -1.67/day (note that the weight on protein yield was arbitrarily set to 1). With change of calving interval, genetic gain in protein yield was 3.239, which is 14% less than without a restriction on calving interval. Thus the cost of avoiding a decrease in calving interval was a 14% reduction of genetic gain in protein yield.

Traits window for ageclass 5



Results

*****start of output*****

RESULTS

TRAITS USED
 milk
 c_interval

TRAIT PARAMETERS
 phenotypic variance heritability
 milk 1,225.000 0.300
 c_interval 441.000 0.100

PHENOTYPIC CORRELATIONS
 milk c_interval
 milk 1.000
 c_interval 0.500 1.000

GENETIC CORRELATIONS
 milk c_interval
 milk 1.000
 c_interval 0.500 1.000

BREEDING GOAL INFORMATION
 1.000 * milk
 -1.670 * c_interval

POPULATION SIZE
 number of selected sires : 10.0
 number of selected dams : 200.0
 number of male selection candidates per dam : 0.4
 number of female selection candidates per dam : 0.4

selected proportion sires in age class 1 : 0.063 x 0.000 = 0.000
 selected proportion sires in age class 2 : 0.006 x 80.000 = 0.447
 selected proportion sires in age class 3 : 0.000 x 72.000 = 0.023
 selected proportion sires in age class 4 : 0.000 x 65.000 = 0.000
 selected proportion sires in age class 5 : 0.083 x 58.000 = 4.805
 selected proportion sires in age class 6 : 0.051 x 52.000 = 2.641
 selected proportion sires in age class 7 : 0.030 x 47.000 = 1.387
 selected proportion sires in age class 8 : 0.016 x 43.000 = 0.697

selected proportion dams in age class 9 : 0.999 x 0.000 = 0.000
 selected proportion dams in age class 10 : 0.984 x 80.000 = 78.740
 selected proportion dams in age class 11 : 0.697 x 72.000 = 50.161
 selected proportion dams in age class 12 : 0.525 x 65.000 = 34.129
 selected proportion dams in age class 13 : 0.349 x 58.000 = 20.218
 selected proportion dams in age class 14 : 0.200 x 52.000 = 10.407
 selected proportion dams in age class 15 : 0.098 x 47.000 = 4.605
 selected proportion dams in age class 16 : 0.040 x 43.000 = 1.741

generation interval : 4.441 cohort intervals

CHARACTERISTICS OF THE USED GROUPS

half-sib group 1 with 8.0 dams, producing 8.0 animals
 half-sib group 2 with 7.0 dams, producing 7.0 animals
 progeny group information
 progeny group 1 with 100.0 dams, producing 100.0 progeny

INDEX INFORMATION :

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sire class : 1
    Dam BLUP breeding value of milk
    Sire BLUP breeding value of milk
    Dam BLUP breeding value of c_interval
    Sire BLUP breeding value of c_interval

sire class : 2
    Dam BLUP breeding value of milk
    Sire BLUP breeding value of milk
    Dam BLUP breeding value of c_interval
    Sire BLUP breeding value of c_interval

sire class : 3
    Dam BLUP breeding value of milk
    Sire BLUP breeding value of milk
    Observations on half-sib group 1 on milk
    Mean EBV of the dams of hs-group 1 on milk
    Dam BLUP breeding value of c_interval
    Sire BLUP breeding value of c_interval
    Observations on half-sib group 1 on c_interval
    Mean EBV of the dams of hs-group 1 on c_interval

sire class : 4
    Dam BLUP breeding value of milk
    Sire BLUP breeding value of milk
    Observations on half-sib group 1 on milk
    Mean EBV of the dams of hs-group 1 on milk
    Dam BLUP breeding value of c_interval
    Sire BLUP breeding value of c_interval
    Observations on half-sib group 1 on c_interval
    Mean EBV of the dams of hs-group 1 on c_interval

sire class : 5
    Dam BLUP breeding value of milk
    Sire BLUP breeding value of milk
    Observations on half-sib group 1 on milk
    Mean EBV of the dams of hs-group 1 on milk
    Observations on progeny group 1 on milk
    Dam BLUP breeding value of c_interval
    Sire BLUP breeding value of c_interval
    Observations on half-sib group 1 on c_interval
    Mean EBV of the dams of hs-group 1 on c_interval
    Observations on progeny group 1 on c_interval

sire class : 6
    Dam BLUP breeding value of milk
    Sire BLUP breeding value of milk
    Observations on half-sib group 1 on milk
    Mean EBV of the dams of hs-group 1 on milk
    Observations on progeny group 1 on milk
    Dam BLUP breeding value of c_interval
    Sire BLUP breeding value of c_interval
    Observations on half-sib group 1 on c_interval
    Mean EBV of the dams of hs-group 1 on c_interval
    Observations on progeny group 1 on c_interval

sire class : 7
    Dam BLUP breeding value of milk
    Sire BLUP breeding value of milk
    Observations on half-sib group 1 on milk
  
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Mean EBV of the dams of hs-group 1 on milk
  Observations on progeny group 1 on milk
    Dam BLUP breeding value of c_interval
    Sire BLUP breeding value of c_interval
  Observations on half-sib group 1 on c_interval
Mean EBV of the dams of hs-group 1 on c_interval
  Observations on progeny group 1 on c_interval

sire class : 8
  Dam BLUP breeding value of milk
  Sire BLUP breeding value of milk
  Observations on half-sib group 1 on milk
Mean EBV of the dams of hs-group 1 on milk
  Observations on progeny group 1 on milk
    Dam BLUP breeding value of c_interval
    Sire BLUP breeding value of c_interval
  Observations on half-sib group 1 on c_interval
Mean EBV of the dams of hs-group 1 on c_interval
  Observations on progeny group 1 on c_interval

dam class : 1 (= age class 9)
  Dam BLUP breeding value of milk
  Sire BLUP breeding value of milk
  Dam BLUP breeding value of c_interval
  Sire BLUP breeding value of c_interval

dam class : 2 (= age class 10)
  Dam BLUP breeding value of milk
  Sire BLUP breeding value of milk
  Dam BLUP breeding value of c_interval
  Sire BLUP breeding value of c_interval

dam class : 3 (= age class 11)
  Own performance of milk
  Dam BLUP breeding value of milk
  Sire BLUP breeding value of milk
  Observations on half-sib group 2 on milk
Mean EBV of the dams of hs-group 2 on milk
  Own performance of c_interval
  Dam BLUP breeding value of c_interval
  Sire BLUP breeding value of c_interval
  Observations on half-sib group 2 on c_interval
Mean EBV of the dams of hs-group 2 on c_interval

dam class : 4 (= age class 12)
  Own performance of milk
  Dam BLUP breeding value of milk
  Sire BLUP breeding value of milk
  Observations on half-sib group 2 on milk
Mean EBV of the dams of hs-group 2 on milk
  Own performance of c_interval
  Dam BLUP breeding value of c_interval
  Sire BLUP breeding value of c_interval
  Observations on half-sib group 2 on c_interval
Mean EBV of the dams of hs-group 2 on c_interval

dam class : 5 (= age class 13)
  Own performance of milk
  Dam BLUP breeding value of milk
  Sire BLUP breeding value of milk
  Observations on half-sib group 2 on milk
Mean EBV of the dams of hs-group 2 on milk
  Own performance of c_interval

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Dam BLUP breeding value of c_interval
 Sire BLUP breeding value of c_interval
 Observations on half-sib group 2 on c_interval
 Mean EBV of the dams of hs-group 2 on c_interval

dam class : 6 (= age class 14)
 Own performance of milk
 Dam BLUP breeding value of milk
 Sire BLUP breeding value of milk
 Observations on half-sib group 2 on milk
 Mean EBV of the dams of hs-group 2 on milk
 Own performance of c_interval
 Dam BLUP breeding value of c_interval
 Sire BLUP breeding value of c_interval
 Observations on half-sib group 2 on c_interval
 Mean EBV of the dams of hs-group 2 on c_interval

dam class : 7 (= age class 15)
 Own performance of milk
 Dam BLUP breeding value of milk
 Sire BLUP breeding value of milk
 Observations on half-sib group 2 on milk
 Mean EBV of the dams of hs-group 2 on milk
 Own performance of c_interval
 Dam BLUP breeding value of c_interval
 Sire BLUP breeding value of c_interval
 Observations on half-sib group 2 on c_interval
 Mean EBV of the dams of hs-group 2 on c_interval

dam class : 8 (= age class 16)
 Own performance of milk
 Dam BLUP breeding value of milk
 Sire BLUP breeding value of milk
 Observations on half-sib group 2 on milk
 Mean EBV of the dams of hs-group 2 on milk
 Own performance of c_interval
 Dam BLUP breeding value of c_interval
 Sire BLUP breeding value of c_interval
 Observations on half-sib group 2 on c_interval
 Mean EBV of the dams of hs-group 2 on c_interval

***** RESULTS *****

EQUILIBRIUM PARAMETERS

	phenotypic variance	heritability
milk	1,148.078	0.253
c_interval	440.984	0.100

PHENOTYPIC CORRELATIONS

	milk	c_interval
milk	1.000	
c_interval	0.516	1.000

GENETIC CORRELATIONS

	milk	c_interval
milk	1.000	
c_interval	0.561	1.000

RESPONSE

	sires	dams	total
milk			
trait units:	2.793	0.446	3.239

economic units:	2.793	0.446	3.239
% of totalresponse:	86.187	13.779	99.966
c_interval			
trait units:	-0.026	0.025	-0.001
economic units:	0.043	-0.042	0.001
% of totalresponse:	1.316	-1.283	0.034
TOTALRESPONSE			
	sires	dams	total
economic units:	2.835	0.405	3.240
sire class 1 variance of index:	10.386		
accuracy of index:	0.227		
sire class 2 variance of index:	10.386		
accuracy of index:	0.227		
sire class 3 variance of index:	11.147		
accuracy of index:	0.235		
sire class 4 variance of index:	11.147		
accuracy of index:	0.235		
sire class 5 variance of index:	166.683		
accuracy of index:	0.910		
sire class 6 variance of index:	166.683		
accuracy of index:	0.910		
sire class 7 variance of index:	166.683		
accuracy of index:	0.910		
sire class 8 variance of index:	166.683		
accuracy of index:	0.910		
dam class 1 variance of index:	10.386		
accuracy of index:	0.227		
dam class 2 variance of index:	10.386		
accuracy of index:	0.227		
dam class 3 variance of index:	51.393		
accuracy of index:	0.505		
dam class 4 variance of index:	51.393		
accuracy of index:	0.505		
dam class 5 variance of index:	51.393		
accuracy of index:	0.505		
dam class 6 variance of index:	51.393		
accuracy of index:	0.505		
dam class 7 variance of index:	51.393		
accuracy of index:	0.505		
dam class 8 variance of index:	51.393		
accuracy of index:	0.505		
variance of breeding goal:	201.371		
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