

Department of Animal Breeding
 Department of Computer Sciences

Selection Index Program (SIP)

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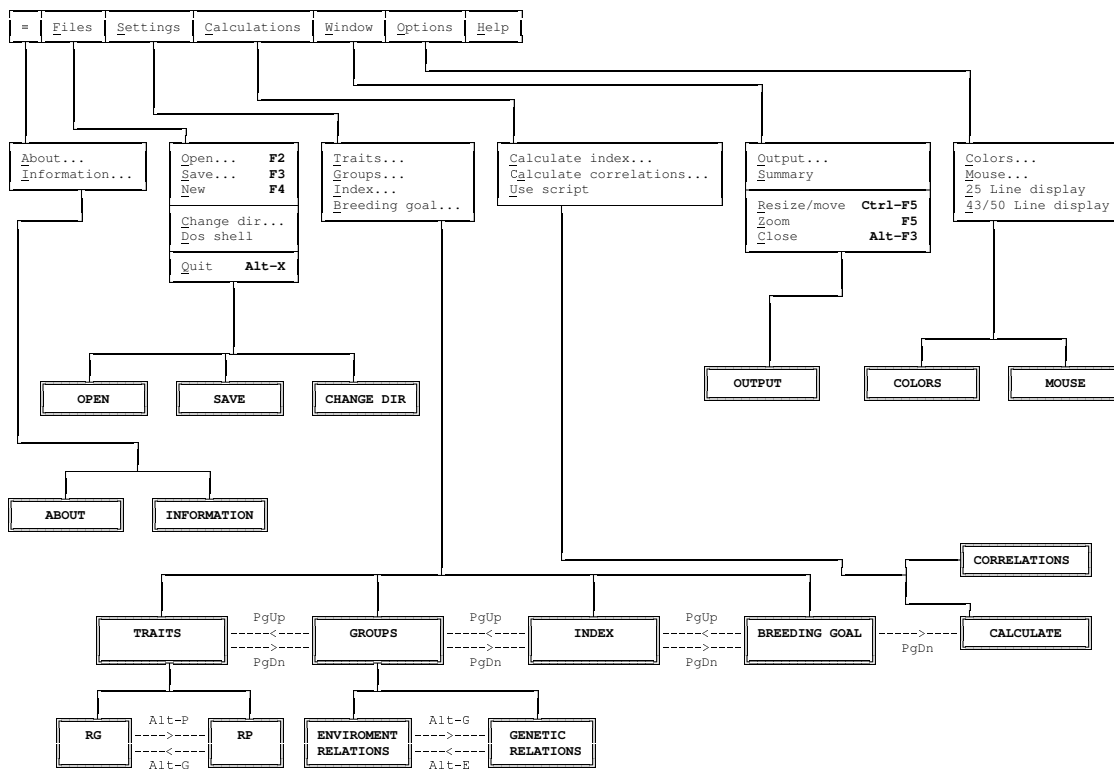


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The program SIP can calculate many selection indexes. These selection indexes may be based on economic values (type 1), on desired gains (type 2) or on a combination of both (type 3).

Pulldown menu (overview)



Reference:

TEXT - TEXT Dialog Box

Note:

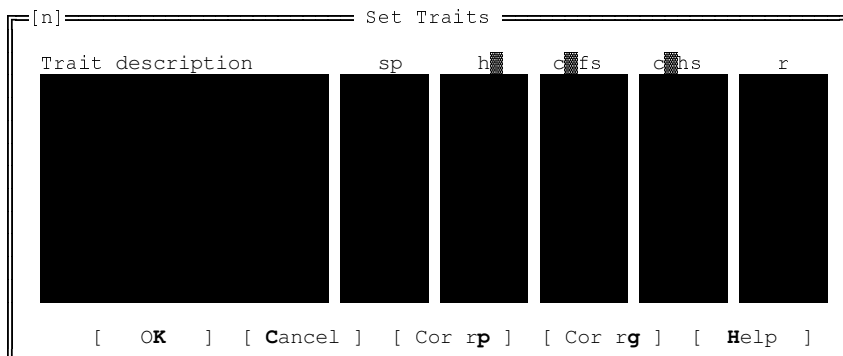
Alt-key = open dialog box
 Esc = close dialog box (cmCancel)

Standard statusline:

F1 Help F10 Menu Use the F10 key for popup menus

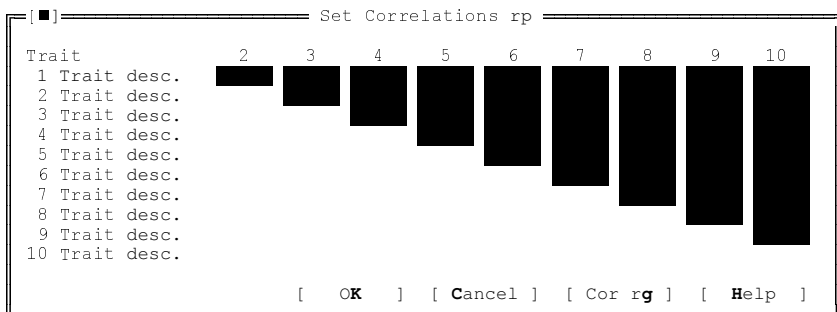
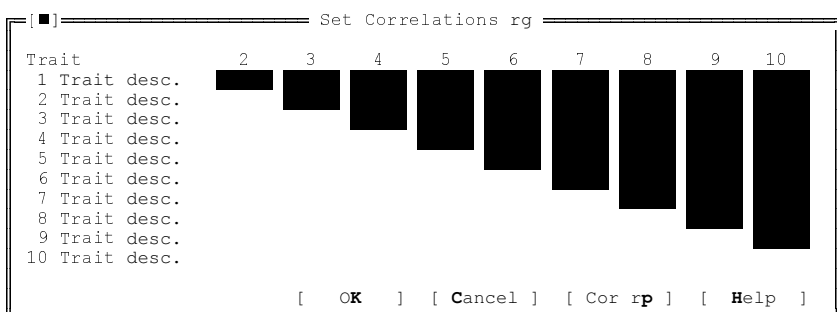
note: visible when no dialog box is opened.

Set traits dialog box



- Trait description = name of trait
 - σp = phenotypic SD
 - h² = heritability
 - c²fs = c² full sibs
 - c²hs = c² half sibs
 - r = repeatability
- OK** = close dialog box (keep changes)
 - Cancel** = close dialog box (don't keep changes)
 - Cor rp** = open phenotypic correlations dialog box
 - Cor rg** = open genetic correlations dialog box
 - [■]** = close dialog box (don't keep changes)

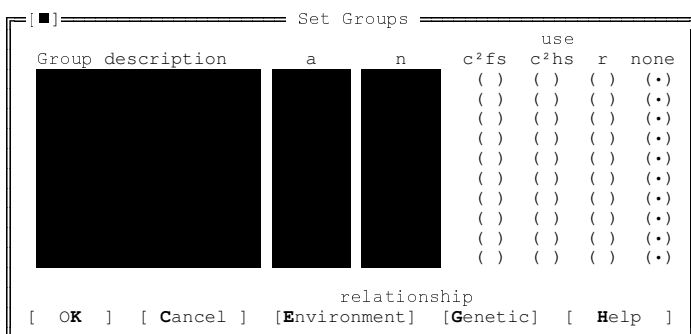
Set r_g dialog box & r_p dialog box



- OK** = close dialog box (keep changes)
- Cancel** = close dialog box (don't keep changes)
- Cor rg** = open genetic correlations dialog box and close this box (keep changes)
- Cor rp** = open phenotypic correlations dialog box and close this box (keep changes)
- [■]** = close dialog box with mouse (don't keep changes)

Set groups dialog box

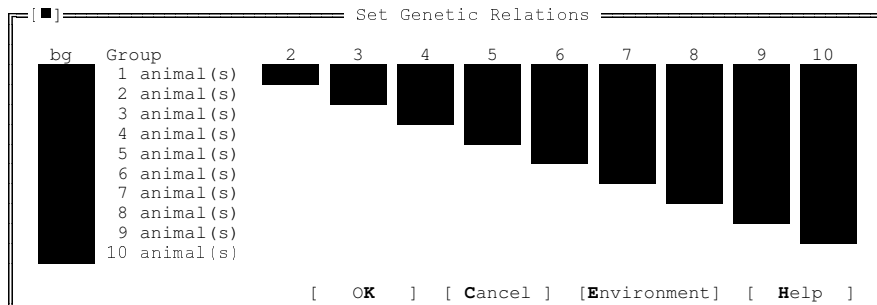
In this box you name all the groups of animals you will use as an information source to calculate the index.



- a = additive genetic relationship within group
 - n = number of observations in the group
 - c²fs = c² full sibs
 - c²hs = c² half sibs
 - r = repeatability
 - none = none of the others
- Environment** = open environmental relations dialog box
 - Genetic** = open genetic relations dialog box
 - [■]** = close dialog box with mouse (don't keep changes)

Set genetic relations dialog box

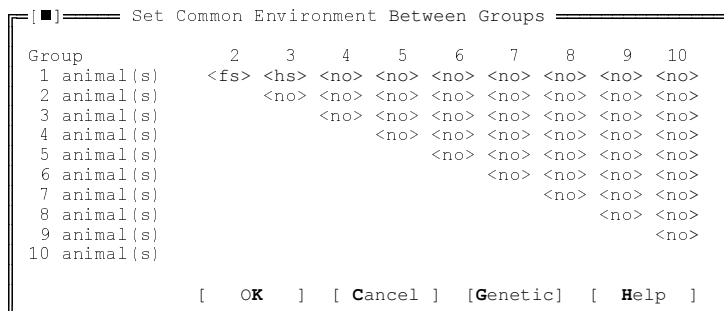
In this box you set additive genetic correlations between groups and additive genetic relations between the group and the animal (in column bg) for whom we're calculating the index



Group = group from groups dialog box
 bg = additive genetic relation of the group with the animal in breeding goal
 Environment = open environmental relations dialog box

Set common environment dialog box

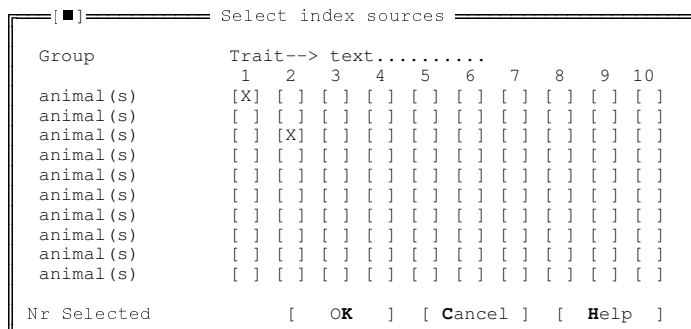
Decide which type of common environment component to use between groups for the same trait.



Group = a group from groups dialog box
 options: no - use c²=0
 fs - use c²fs (from traits dialog box)
 hs - use c²hs (from traits dialog box)
 Genetic = open genetic relations dialog box

Set index sources

In this dialog you can pick up to 20 index sources you want to use in your selection index.



Group = name of a group from groups dialog box
 Trait--> text... = name of the trait - from traits dialog box
 [] = not selected item
 [X] = selected item

Set breeding goal

In this dialog box you can set which traits are in the breeding goal what kind of trait (economic or desired gain) and you can insert a value for each trait.

```

[■] Set breeding goal
Trait      skip  v   d   value
description ( ) (•) ( )
description ( ) (•) ( )
description ( ) (•) ( )
description ( ) (•) ( )
description ( ) (•) ( )
description ( ) (•) ( )
description ( ) (•) ( )
description ( ) (•) ( )
description ( ) (•) ( )
description ( ) (•) ( )
[ OK ] [ Cancel ] [ Help ]

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- skip = don't put this trait in breeding goal
- v = economic trait
- d = desired gain trait
- value = economic value or relative change
- () = not selected item
- (•) = selected item

Calculation box

In this box you can start the calculations; when it is an index of type 3 you must give an e-value.

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[■] Calculate index
index type (1,2 or 3)      e-value
Action: text
=====
Matrix:On [ Start ] [ Cancel ] [ Help ]

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- index type (1,2 or 3) used during calculation
- Matrix:On/Off = Matrices written (or not)
- Start = start index calculation

Remark:e-value only by type 3 visible