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)
Set traits dialog box

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

Set r_g dialog box & r_p dialog box

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

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.
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.

Set common environment dialog box

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

Set index sources

In this dialog you can pick up to 20 index sources you want to use in your selection index.
**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 dialog box](image)

- **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.

![Calculate index dialog box](image)

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

**Remark:** e-value only by type 3 visible