

Guideline

Practical implementation of selection indices



Excellence in Breeding Platform

This guideline provides a step-by-step approach to implement selection indices, with the objective of providing a creating a practical reference for plant breeding professionals. More in-depth knowledge can be found in links throughout the text.

Optimizing breeding schemes

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As a prerequisite to implementing selection indices, it is assumed that the breeding scheme in question can be identified as series of stages in which a reasonably limited number of traits are evaluated in order to rapidly develop new varieties for a defined target market, and that the breeding program has access to biometrics expertise.

1. Create a table to record the stages at which traits are used for selection, the surrogate for trait merit used and the number of environments in which selection takes place for each trait.
2. Identify the stage at which you would like to implement a selection index (**Figure 1**).

	Trait 1		Trait 2		Trait 3		Trait 4		Trait 5		Trait 6	
	Surrogate	#Envs	Surrogate	#Envs	Surrogate	#Envs	Surrogate	#Envs	Surrogate	#Envs	Surrogate	#Envs
Crossing Block												
Nursery	Visual	1			Visual	1						
STG1			BLUP	1	Visual	1	BLUP	2				
STG2							BLUP	4	BLUP	2		
STG3							BLUP	6			BLUP	2
On Farm							BLUP	30				

Figure 1. Example table of traits used for selection across different stages highlighting a selected stage to implement a selection index.

3. Identify the traits for no data is collected at the selection index stage. Adjust the breeding scheme so that data is collected for all traits at the selection index stage (beyond visual evaluation).
4. Once complete data is available for all traits of interest at the selection index stage, record adjusted means for all individuals and traits at that stage (one mean per trait per individual) (**Figure 2**).

	Trait 1	Trait 2	Trait 3	Trait 4	Trait 5	Trait 6
Individual 1		100	30	1.2		
Individual 2		110	32	1.4		
...			
Individual n		105	36	1.6		

Figure 2. Example table of adjusted means for traits of interest for all individuals in the stage at which the selection index is applied (for the purposes of this example, STG1).

5. Standardize the adjusted means across all traits in the table (**Figure 3**).

	Trait 1	Trait 2	Trait 3	Trait 4	Trait 5	Trait 6
Individual 1		-1.6	-1	-0.5		
Individual 2		0.6	0.1	-0.05		
...			
Individual n		0.4	0.4	0.3		

Figure 3. Example table of standardized adjusted means for in the stage at which the selection index is applied.

6. Assign weights to the traits. With standardized traits, a desired differential (d) of 1 implies that you look to select individuals that are 1 standard deviation (σ) away from the population mean, if r_g among traits is zero the weight will stay as 1, and with $r_g \neq 0$ will be $\neq 1$.

Start by assigning a differential of 1 to all traits (implying you desire 1 standard deviation (σ) progress for each trait when you select).¹ Ultimately, selection will be constrained by the genetic correlation between traits, and the selection intensity of the breeding program.

Do not attempt to interpret the weights; they lack meaning (especially with strong genetic correlations). The selection differential is the only decision of interest.

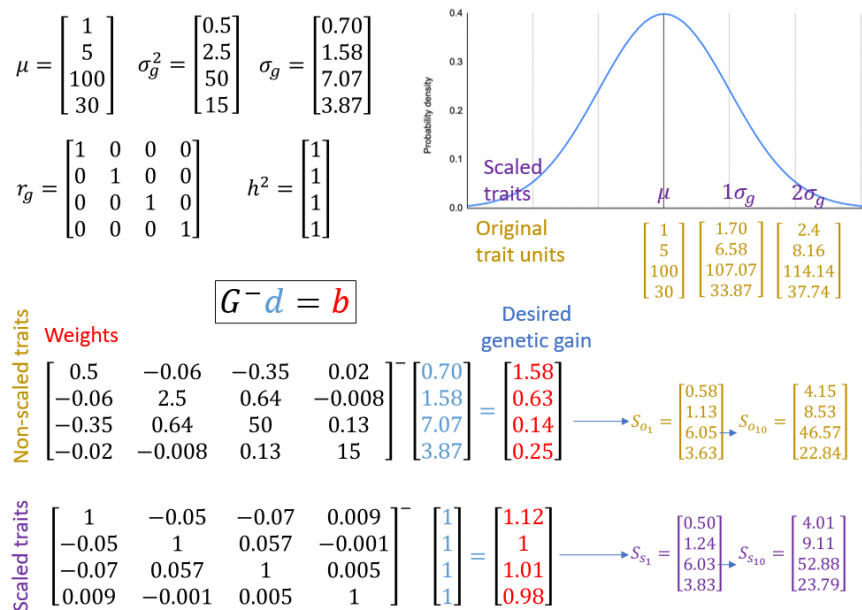


Figure 4. Graphical example of 4 traits with different scales and variance (covariance=0). Although scaled and non-scaled traits have the same effect on selection, desired differentials used with scaled traits are interpreted as desired standard deviations (σ) of genetic gain, while differentials for non-scaled traits must be specified in their original units and resulting weights are difficult to interpret. Although the weights will be different for the two approaches, both will lead to the same results with the advantage of an easier interpretation when scaled traits are used. Small differences in gain are due to the stochastic nature of the simulations.

¹ Alternatively, you could obtain initial weights by performing a retrospective analysis where weights are obtained as $b=P^{-1}S$, with P being a phenotype variance-covariance matrix (Bernardo, 2005) and S are the selection differentials for the different traits. Take the selection differentials (S) and translate them into equivalent σ which will become your initial weights for the standardized traits.

Use programs such as DESIRE ([DESIRE - Target your genetic gains \[une.edu.au\]](http://une.edu.au)) to understand if the progress of 1 or more σ is possible given your current trait genetic correlations (r_g) and selection intensity, and experiment with potential gains that can be achieved with different traits.

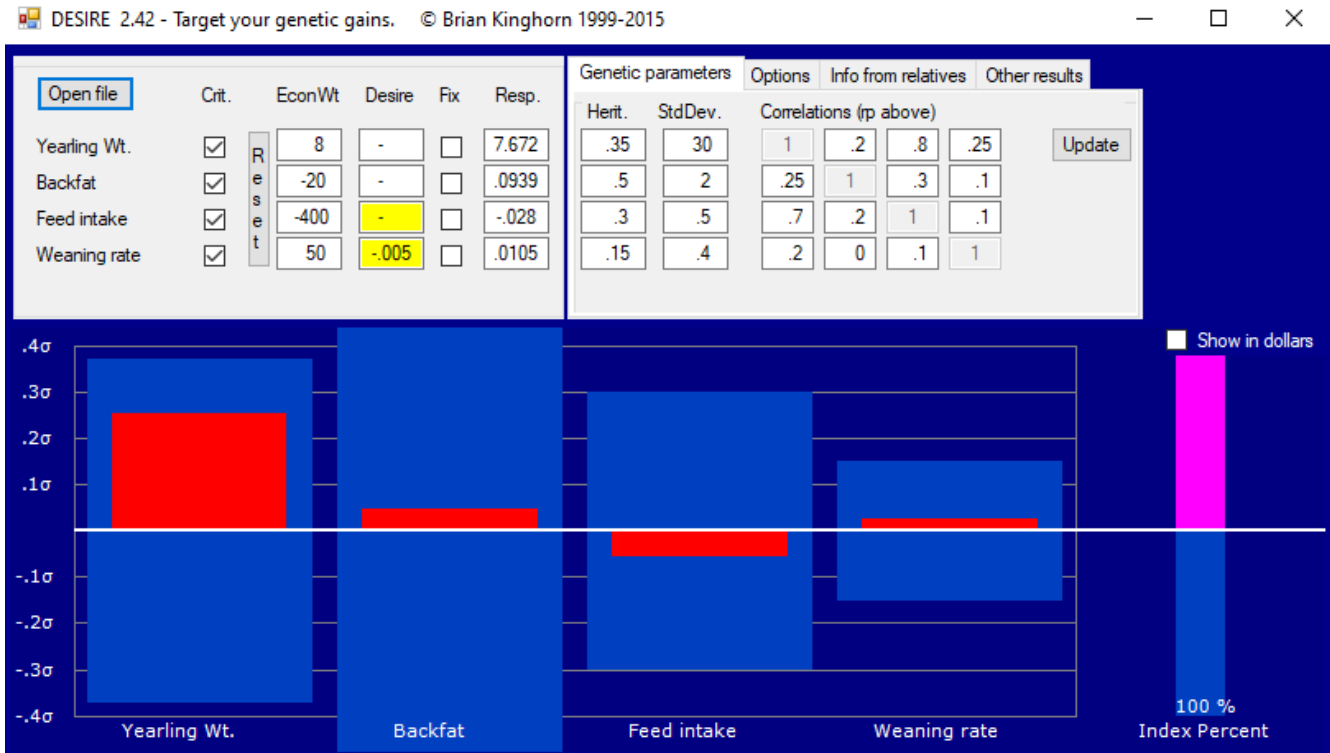


Figure 5. Example of the DESIRE interface to experiment with trait weights in a selection index. Programs like this allow the user to see the effect of weighting one trait in the correlated traits.

When adjusting the weights using the genetic correlation through the inverse of the genetic covariance (Pesek and Baker, 1969) this removes interpretability of weights for scaled traits but has an important effect in the long-term gains so needs to be done and should not be considered to use directly as weights the desired progress of standard deviations. In practice G is not known and is enough to use across-environment adjusted means by a mixed model to scale, define the desired σ of progress and use the covariance of those adjusted means as a surrogate for G .

7. Apply the weights in the index (remember the relationship between the indices and models used to obtain adjusted means to avoid repeating certain calculations) and select the best individuals for the index.
8. Repeat steps 7) and 8) every selection season, ensuring that values are fine-tuned.

References: 1) Bernardo, R. (2002). Breeding for quantitative traits in plants (Vol. 1, p. 369). Woodbury, MN: Stemma press. 2) Pešek, J., & Baker, R. J. (1969). Desired improvement in relation to selection indices. Canadian journal of plant science, 49(6), 803-804.