### Elston Index

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#### 1 Definition

The Elston index (Elston, 1963) is a weight free index. Given p traits, for each genotype the Elston index is computed as

$$I_E = \prod_{i=1}^p (x_i - k_i)$$

where  $x_i$  is the value of the genotype for trait i and  $k_i$  is some lower bound. Before computing the index it could be a good idea to standardize x by subtracting the mean and dividing by the standard deviation over all the genotypes, so that all the traits were comparable. If some traits are of a negative selection direction, such as a disease measure, then the negative values must be used. If the main purpose is to select some genotypes, then the lower bounds  $k_i$  can be the minima of the traits. If the main purpose is to produce a ranking for all the genotypes, making  $k_i = \min x_i$  has the disadvantage that will give the value of 0 to all the genotypes with the lowest value for at least one trait, producing many ties on the lowest rank. This can be avoided by letting

$$k_i = \frac{n \min x_i - \max x_i}{n - 1}$$

where n is the number of genotypes. This is justified on the assumption that the n values come from a rectangular distribution. Under this assumption the above value of k is the minimum variance unbiased estimate of the point at which the distribution starts.

## 2 Computation

The computation of this index has been implemented in the R function Eslton that is available in the Elston.R file. The usage of the function is:

Elston <- function(..., geno, k=1)</pre>

where

- ... is a list of traits,
- geno is the index for genotypes,
- 1b is the lower bound. 1 for  $k = \min(x)$  and 2 for  $k = (n * \min(x) \max(x))/(n-1)$ , 1 by default.

The function returns the following elements:

- Elston.Index: The Elston index value.
- Sorted.Elston.Index: The Elston index value sorted in descending order.

# 3 References

• Elston, R. C. (1963). A weight-free index for the purpose of ranking or selection with respect to several traits at a time. *Biometrics*. 19(1): 85-97.