Package ‘IndexWizard’

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Type Package

Title Constructing and Analyzing Complex Selection Indices

Version 0.2.1.0

Description Allows the construction selection indices based on estimated breeding values in animal and plant breeding and to calculate several analytic measures around to assess its impact on genetic and phenotypic progress. The methodology thereby allows to analyze genetic gain of traits in the breeding goal which are not part of the actual index and automatically computes several analytic measures. It further allows to retrospectively derive realized economic weights from observed genetic trends. The framework is described in Simianer, H., Heise, J., Rensing, S., Pook, T. Geibel, J. and Reimer, C. (2023) <doi:10.1186/s12711-023-00807-0>.

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Encoding UTF-8

RoxygenNote 7.2.3

Suggests knitr, rmarkdown

VignetteBuilder knitr

URL `https://github.com/johannesgeibel/IndexWizard`

BugReports `https://github.com/johannesgeibel/IndexWizard/issues`

NeedsCompilation no

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Repository CRAN

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Contents

`print.SelInd` *Function to nicely print a SelInd object*

Description

Function to nicely print a SelInd object

Usage

```
## S3 method for class 'SelInd'
print(x, ...)
```

Arguments

`x`	An object of class SelInd
`...`	does nothing, only for compatibility with the generic function

Value

No return value, only prints formatted output.

Examples

```
tn <- c("RZM", "RZN", "RZEo")
G <- matrix(
    c(1.0,0.13,0.13,
    0.13,1.0,0.23,
    0.13,0.23,1.0),
    3, 3, dimnames = list(tn,tn)
    ) * 144
w <- c(0.7, 0.3, 0)
names(w) <- tn
r2 <- c(0.743, 0.673)
names(r2) <- tn[1:2]
res <- SelInd(
  w = w,
  G = G,
  r2 = r2
)
print(res)
```

`SelInd` *Function to calculate selection index*

Description

Function to calculate selection index

Usage

```
SelInd(
  w,
  G,
  r2,
  H = NULL,
  i = NULL,
  h2 = NULL,
  d_G_obs = NULL,
  delta = 1e-04,
  verbose = TRUE
)
```

Arguments

`w`	Numeric vector of n economic weights. Traits present in G, but not part of the index need to be coded as 0. If traits of G are missing, they will be added automatically with zero weight. Required.
`G`	Named n*n genetic variance- covariance matrix. Dimnames of G need to match w to ensure correct sorting. Required.
`r2`	Named numeric vector of reliabilities with length m. Required.
`H`	Named m*m variance-covariance matrix of estimated breeding to internally derive the residual variance-covariance matrix. If H contains more traits than r2, it will be subsetted.
`i`	Selection intensity
`h2`	named numeric vector of length n containing heritabilities for the traits
`d_G_obs`	named numeric vector of length n containing the observed composition of the genetic gain scaled in genetic standard deviations. If sum(d_G_obs) != 1, it will be rescaled.
`delta`	small increment to calculate approximate first derivative
`verbose`	Shall information be printed?

Details

The framework allows to have less traits in the selection index than in the breeding goal (m < n). Calculation of realized economic weights, however, requires m == n.

Value

A list of class SelInd

Examples

```
tn <- c("RZM", "RZN", "RZEo")
G <- matrix(
    c(1.0,0.13,0.13,
    0.13,1.0,0.23,
    0.13,0.23,1.0),
    3, 3, dimnames = list(tn,tn)
    ) * 144
w <- c(0.7, 0.3, 0)
names(w) <- tn
r2 <- c(0.743, 0.673)
names(r2) <- tn[1:2]
SelInd(
  w = w,
  G = G,
  r2 = r2
)
```

`summary.SelInd` *Function to summarize the content of a SelInd object.*

Description

Function to summarize the content of a SelInd object.

Usage

```
## S3 method for class 'SelInd'
summary(object, ...)
```

Arguments

`object`	An object of class SelInd
`...`	does nothing, only for compatibility with the generic function

Value

No return value, only prints a summary of the SelInd object.

Examples

```
tn <- c("RZM", "RZN", "RZEo")
G <- matrix(
    c(1.0,0.13,0.13,
    0.13,1.0,0.23,
    0.13,0.23,1.0),
    3, 3, dimnames = list(tn,tn)
    ) * 144
w <- c(0.7, 0.3, 0)
names(w) <- tn
r2 <- c(0.743, 0.673)
names(r2) <- tn[1:2]
res <- SelInd(
  w = w,
  G = G,
  r2 = r2
)
summary(res)
```

Index