# 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 ani-
mal and plant breeding and to calculate several analytic measures around to assess its im-
pact on genetic and phenotypic progress. The methodology thereby allows to analyze ge-
netic gain of traits in the breeding goal which are not part of the actual index and automati-
cally computes several analytic measures. It further allows to retrospectively derive realized eco-
nomic weights from observed genetic trends. The framework is described in Simi-
aner, H., Heise, J., Rensing, S., Pook, T. Geibel, J. and Reimer, C. (2023) <doi:10.1186/s12711-
023-00807-0>.

**License** MIT + file LICENSE

**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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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