

# Package ‘selection.index’

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**Type** Package

**Title** Analysis of Selection Index in Plant Breeding

**Version** 1.1.4

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**Description** The aim of most plant breeding programmes is simultaneous improvement of several characters. An objective method involving simultaneous selection for several attributes then becomes necessary. It has been recognised that most rapid improvements in the economic value is expected from selection applied simultaneously to all the characters which determine the economic value of a plant, and appropriate assigned weights to each character according to their economic importance, heritability and correlations between characters. So the selection for economic value is a complex matter. If the component characters are combined together into an index in such a way that when selection is applied to the index, as if index is the character to be improved, most rapid improvement of economic value is expected. Such an index was first proposed by Smith (1937 <[doi:10.1111/j.1469-1809.1936.tb02143.x](https://doi.org/10.1111/j.1469-1809.1936.tb02143.x)>) based on the Fisher's (1936 <[doi:10.1111/j.1469-1809.1936.tb02137.x](https://doi.org/10.1111/j.1469-1809.1936.tb02137.x)>) ``discriminant function" Dabholkar (1999 <<https://books.google.co.in/books?id=mLFtumAXQ0oC&lpg=PA4&ots=Xgxp1qLuxS&dq=elements%20of%20biometrical%20genetics&lr&pg=PP1#v=onepage&q&f=false>>). In this package selection index is calculated based on the Smith (1937) selection index method.

**License** GPL (>= 3)

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.2.0

**Depends** R (>= 2.10)

**Imports** utils

**URL** <https://github.com/zankrut20/selection.index>

**BugReports** <https://github.com/zankrut20/selection.index/issues>

**Suggests** rmarkdown, markdown, knitr, testthat (>= 3.0.0)

**VignetteBuilder** knitr

**Config/testthat/edition** 3

**NeedsCompilation** no

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**Repository** CRAN

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comb.indices	<i>Construction of selection indices based on number of character grouping</i>
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## Description

Construction of selection indices based on number of character grouping

## Usage

```
comb.indices(ncomb, pmat, gmat, wmat, wcol = 1, GAY)
```

## Arguments

ncomb	Number of Characters/Traits group
pmat	Phenotypic Variance-Covariance Matrix
gmat	Genotypic Variance-Covariance Matrix
wmat	Weight Matrix
wcol	Weight column number incase more than one weights, by default its 1
GAY	Genetic Advance of comparative Character/Trait i.e. Yield (Optional argument)

## Value

Data frame of all possible selection indices

**Examples**

```

gmat<- gen.varcov(seldata[,3:9], seldata[,2], seldata[,1])
pmat<- phen.varcov(seldata[,3:9], seldata[,2], seldata[,1])
wmat<- weight.mat(weight)
comb.indices(ncomb = 1, pmat = pmat, gmat = gmat, wmat = wmat, wcol = 1, GAY = 1.075)

```

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gen.advance

*Genetic Advance for PRE*


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**Description**

Genetic Advance for PRE

**Usage**

```
gen.advance(phen_mat, gen_mat, weight_mat)
```

**Arguments**

phen_mat	phenotypic matrix value of desired characters
gen_mat	genotypic matrix value of desired characters
weight_mat	weight matrix value of desired characters

**Value**

Genetic advance of character or character combinations

**Examples**

```

gmat<- gen.varcov(seldata[,3:9], seldata[,2], seldata[,1])
pmat<- phen.varcov(seldata[,3:9], seldata[,2], seldata[,1])
gen.advance(phen_mat = pmat[1,1], gen_mat = gmat[1,1], weight_mat = weight[1,2])

```

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gen.varcov

*Genotypic Variance-Covariance Analysis*


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**Description**

Genotypic Variance-Covariance Analysis

**Usage**

```
gen.varcov(data, genotypes, replication)
```

**Arguments**

data	traits to be analyzed
genotypes	vector containing genotypes/treatments
replication	vector containing replication

**Value**

A Genotypic Variance-Covariance Matrix

**Examples**

```
gen.varcov(data=seldata[,3:9], genotypes=seldata$treat,replication=seldata$rep)
```

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phen.varcov	<i>Phenotypic Variance-Covariance Analysis</i>
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**Description**

Phenotypic Variance-Covariance Analysis

**Usage**

```
phen.varcov(data, genotypes, replication)
```

**Arguments**

data	traits to be analyzed
genotypes	vector containing genotypes/treatments
replication	vector containing replication

**Value**

A Phenotypic Variance-Covariance Matrix

**Examples**

```
phen.varcov(data=seldata[,3:9], genotypes=seldata$treat,replication=seldata$rep)
```

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rcomb.indices	<i>Remove trait or trait combination from possible trait combinations of possible Trait combinations</i>
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**Description**

Remove trait or trait combination from possible trait combinations of possible Trait combinations

**Usage**

```
rcomb.indices(ncomb, i, pmat, gmat, wmat, wcol = 1, GAY)
```

**Arguments**

ncomb	Number of character combination
i	remove trait or trait combination
pmat	Phenotypic Variance Covariance Matrix
gmat	Genotypic Variance Covariance Matrix
wmat	Weight Matrix
wcol	Respective weight column number of Weight Matrix
GAY	Genetic Advance/Genetic Gain of base selection index

**Value**

Data frame of possible selection indices with per cent relative efficiency and ranking

**Examples**

```
gmat<- gen.varcov(seldata[,3:9], seldata[,2], seldata[,1])
pmat<- phen.varcov(seldata[,3:9], seldata[,2], seldata[,1])
rcomb.indices(ncomb = 2, i = 1, pmat = pmat, gmat = gmat, wmat = weight[,2:3], wcol = 1)
```

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seldata	<i>Selection Index DataSet</i>
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**Description**

A dataset containing the data of three replications and 48 progenies with 7 different traits.

**Usage**

```
data(seldata)
```

**Format**

A data frame with 144 rows and 9 columns

**Details**

- rep. Replications
- treat. Treatments/Genotypes
- sypp. Seed Yield per Plant
- dff. Days to 50
- rpp. Racemes per Plant
- ppr. Pods per Raceme
- ppp. Pods per Plant
- spp. Seeds per Pod
- pw. Pods Weight

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weight

*Weight dataset*

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**Description**

A dataset containing the data of 2 different weights namely equal weight and broad sense heritability

**Usage**

```
data(weight)
```

**Format**

A data frame with 7 rows and 3 columns

**Details**

- EW. Equal Weight
- h2. Broad Sense Heritability

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`weight.mat`

*Convert dataframe to matrix*

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**Description**

Convert dataframe to matrix

**Usage**

```
weight.mat(data)
```

**Arguments**

`data`            dataframe of weight

**Value**

A matrix

**Examples**

```
weight.mat(data = weight)
```

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