

Package ‘selection.index’

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Type Package

Title Analysis of Selection Index in Plant Breeding

Version 1.1.3

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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 7.1.1

Depends R (>= 2.10)

Imports utils, stats

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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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)
```

gen.advance

Genetic Advance for PRE

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])
```

`gen.varcov`*Genotypic Variance-Covariance Analysis*

Description

Genotypic Variance-Covariance Analysis

Usage

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

Arguments

<code>data</code>	traits to be analyzed
<code>genotypes</code>	vector containing genotypes/treatments
<code>replication</code>	vector containing replication

Value

A Genotypic Variance-Covariance Matrix

Examples

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

`phen.varcov`*Phenotypic Variance-Covariance Analysis*

Description

Phenotypic Variance-Covariance Analysis

Usage

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

Arguments

<code>data</code>	traits to be analyzed
<code>genotypes</code>	vector containing genotypes/treatments
<code>replication</code>	vector containing replication

Value

A Phenotypic Variance-Covariance Matrix

Examples

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

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)
```

sel.index	<i>Construction of Selection Index</i>
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Description

Construction of Selection Index

Usage

```
sel.index(ID, phen_mat, gen_mat, weight_mat, GAY)
```

Arguments

ID	Name of Selection Index
phen_mat	Phenotypic Variance-Covariance Matrix
gen_mat	Genotypic Variance-Covariance Matrix
weight_mat	Weight Matrix
GAY	Genetic Advance of Yield

Value

List of Selection Index Components

Examples

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

sel.score.rank	<i>Analysis of selection score and Genotype/Progeny ranking based on selection score</i>
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Description

Analysis of selection score and Genotype/Progeny ranking based on selection score

Usage

```
sel.score.rank(data, bmat, genotype)
```

Arguments

data	traits to be analyzed
bmat	Selection/discriminant coefficient matrix
genotype	Vector containing Genotypes/Treatments

Value

A data frame containing the genotypes with selection score

Examples

```
sel.score.rank(data = seldata[,3], bmat = 0.6455, genotype = seldata[,2])
```

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
- ddf. Days to 50
- rpp. Racemes per Plant
- ppr. Pods per Raceme
- ppp. Pods per Plant
- spp. Seeds per Pod
- pw. Pods Weight

weight *Weight dataset*

Description

A dataset containing the data of 2 different weights namely euqal 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
-

weight.mat *Convert dataframe to matrix*

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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