Package ‘selection.index’

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Type Package

Title Analysis of Selection Index in Plant Breeding

Version 1.2.0

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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>) based on the Fisher’s (1936 <doi:10.1111/j.1469-1809.1936.tb02137.x>) “discriminant function” Dabholkar (1999 <https://books.google.co.in/books?id=m1FtumAXQ6oC&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 7.2.3

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
comb.indices

Construction of selection indices based on number of character grouping

Description

Construction of selection indices based on number of character grouping

Usage

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

Arguments

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

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

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

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)

meanPerformance        Mean performance of phenotypic data

Description

Mean performance of phenotypic data

Usage

meanPerformance(data, genotypes, replications)

Arguments

data         data for analysis
genotypes    genotypes vector
replications  replication vector

Value

Dataframe of mean performance analysis

Examples

meanPerformance(data = seldata[, 3:9], genotypes = seldata[, 2], replications = seldata[, 1])
phen.varcov

Phenotypic Variance-Covariance Analysis

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)

rcomb.indices

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

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**

```r
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**  
*Selection Index Dataset*

**Description**

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

**Usage**

```r
data(seldata)
```

**Format**

A data frame with 75 rows and 9 columns

**Details**

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