Package ‘variability’

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Type Package

Title Genetic Variability Analysis for Plant Breeding Research

Version 0.1.0

Description Performs analysis of various genetic parameters like genotypic and phenotypic coefficient of variance, heritability, genetic advance, genetic advance as a percentage of mean. The package also has functions for genotypic and phenotypic covariance, correlation and path analysis. Dataset has been added to facilitate example. For more information refer Singh, R.K. and Chaudhary, B.D. (1977, ISBN:81766330709788176633079).

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Encoding UTF-8

LazyData true

Imports stats

RoxygenNote 7.1.1

Depends R (>= 2.10)

NeedsCompilation no

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R topics documented:

`ancova` *Analysis of Covariance*

Description

Analysis of Covariance

Usage

```
ancova(data, genotypes, replication)
```

Arguments

`data`	traits to be analyzed
`genotypes`	vector containing genotypes
`replication`	vector containing replications

Value

ANCOVA, genotypic and phenotypic covariance

Examples

```
data(vardata)
ancova(vardata[3:11],vardata$Genotypes,vardata$Replication)
```

`gen.var` *Estimation of Genetic Parameters*

Description

Estimation of Genetic Parameters

Usage

```
gen.var(data, genotypevector, replicationvector)
```

Arguments

`data`	traits to be analyzed
`genotypevector`	vector containing genotypes
`replicationvector`	vector containig replications

Value

ANOVA, genotypic and phenotypic coefficient of variance, heritability, genetic advance and genetic advance as percentage of mean.

Examples

```
data(vardata)
gen.var(vardata[3:11],vardata$Genotypes,vardata$Replication)
```

`geno.corr` *Genotypic Correlation Analysis*

Description

Genotypic Correlation Analysis

Usage

```
geno.corr(data, genotypes, replication)
```

Arguments

`data`	traits to be analyzed
`genotypes`	vector containing genotypes
`replication`	vector containing replications

Value

Genotypic correlation matrix

Examples

```
data(vardata)
geno.corr(vardata[3:11],vardata$Genotypes,vardata$Replication)
```

`geno.path` *Genotypic Path Analysis*

Description

Genotypic Path Analysis

Usage

```
geno.path(dependent.var, independent.var, genotypes, replication)
```

Arguments

`dependent.var`	trait to be used a dependent variable
`independent.var`	traits to be used as an indpendent variables
`genotypes`	vector containing genotpes
`replication`	vector containing replications

Value

Direct effects, indirect effects and residual

Examples

```
data(vardata)
# Grain yield is considered as a dependent variable
geno.path(vardata[11],vardata[3:10],vardata$Genotypes,vardata$Replication)
```

`pheno.corr` *Phenotypic Correlation Analysis*

Description

Phenotypic Correlation Analysis

Usage

```
pheno.corr(data, genotypes, replication)
```

Arguments

`data`	traits to be analyzed
`genotypes`	vector containing genotypes
`replication`	vector containing replications

Value

Phenotypic correlation

Examples

```
data(vardata)
pheno.corr(vardata[3:11],vardata$Genotypes,vardata$Replication)
```

`pheno.path` *Phenotypic Path Analysis*

Description

Phenotypic Path Analysis

Usage

```
pheno.path(dependent.var, independent.var, genotypes, replication)
```

Arguments

`dependent.var`	trait to be considered as a dependent variable
`independent.var`	traits to be connsidered as an independent variables
`genotypes`	vector containing genotypes
`replication`	vector containing replicatons

Value

Direct effects, indirect effects and residual

Examples

```
data(vardata)
pheno.path(vardata[11],vardata[3:10],vardata$Genotypes,vardata$Replication)
```

`vardata` *Variability Data*

Description

The data consists of genotypes, replications and nine traits

Usage

```
vardata
```

Format

The data has 11 columns and 120 rows

Genotypes 40 genotypes

Replication 3 replications

DFF Days to 50 per cent flowering

PH Plant height

PL Panicle length

PW Panicle weight

HI Harvest index

TW Test weight

MILL Milling percentage

HRR Head rice recovery

GY Grain Yield

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