

Package ‘variability’

September 29, 2020

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

Author Raj Popat [aut, cre],
Rumit Patel [aut],
Dinesh Parmar [aut]

Maintainer Raj Popat <popatrajc@gmail.com>

Repository CRAN

Date/Publication 2020-09-29 08:30:02 UTC

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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 independent variables
genotypes vector containing genotypes
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 considered 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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