

# Package ‘variability’

July 22, 2025

**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).

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**Imports** stats

**RoxygenNote** 7.1.1

**Depends** R (>= 2.10)

**NeedsCompilation** no

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**Repository** CRAN

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|        |                               |
|--------|-------------------------------|
| ancova | <i>Analysis of Covariance</i> |
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**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)
```

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|         |                                         |
|---------|-----------------------------------------|
| gen.var | <i>Estimation of Genetic Parameters</i> |
|---------|-----------------------------------------|

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**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)
```

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|           |                                       |
|-----------|---------------------------------------|
| geno.corr | <i>Genotypic Correlation Analysis</i> |
|-----------|---------------------------------------|

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**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)
```

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|           |                                |
|-----------|--------------------------------|
| geno.path | <i>Genotypic Path Analysis</i> |
|-----------|--------------------------------|

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**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)
```

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|            |                                        |
|------------|----------------------------------------|
| pheno.corr | <i>Phenotypic Correlation Analysis</i> |
|------------|----------------------------------------|

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**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)
```

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pheno.path

*Phenotypic Path Analysis*

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**Description**

Phenotypic Path Analysis

**Usage**

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

**Arguments**

|                              |                                                     |
|------------------------------|-----------------------------------------------------|
| <code>dependent.var</code>   | trait to be considered as a dependent variable      |
| <code>independent.var</code> | traits to be considered as an independent variables |
| <code>genotypes</code>       | vector containing genotypes                         |
| <code>replication</code>     | vector containing replicatons                       |

**Value**

Direct effects, indirect effects and residual

**Examples**

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

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|         |                         |
|---------|-------------------------|
| vardata | <i>Variability Data</i> |
|---------|-------------------------|

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**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

**DDF** 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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