

# Package: variability (via r-universe)

August 30, 2024

**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

**Author** Raj Popat [aut, cre], Runit Patel [aut], Dinesh Parmar [aut]

**Maintainer** Raj Popat <popatrajc@gmail.com>

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**Repository** <https://popatraj.r-universe.dev>

**RemoteUrl** <https://github.com/cran/variability>

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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                      *Genotypic Correlation Analysis*

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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)
```

---

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)
```

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pheno.corr                      *Phenotypic Correlation Analysis*

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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**

- 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)
```

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vardata

*Variability Data*

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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

**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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