

# Package ‘TraitStats’

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**Title** Statistical Data Analysis for Randomized Block Design Experiments

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**Maintainer** Nitesh Shirur Devaraja <mail@niteshgpb.in>

**Description** Functions for analysis of bulk data generated from experiments in Randomized block design as per Panse and Sukhatme (1954) <<https://books.google.co.in/books?id=Efo9AAAYAAJ>>. Computes analysis of variance; Descriptive statistics parameter like Mean, Minimum, Maximum, CV, Standard error of mean, Standard Error of deviation, CD; Genetic parameter statistics Genotypic Coefficient of Variation, Phenotypic Coefficient of Variation, Heritability in broad sense, Genetic Advance and Genetic Advance per cent mean; Variance and Co-variance matrix of genotypic, phenotypic and environmental; Correlation of genotypic, phenotypic and environmental. Further includes directly publication ready tables.

**URL** <https://www.niteshgpb.in/TraitStats.pdf>

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**Imports** utils, stats, lattice, rlist, grid, gridExtra, qpdf

**Depends** R (>= 3.5.0)

**NeedsCompilation** no

**Author** Nitesh Shirur Devaraja [aut, cre],  
Parashuram Patroti [aut],  
Shilpa Parashuram [aut],  
Aravind J [ctb] (Reference material of augmentedRCBD),  
Sunil Kumar [ctb]

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Barley	<i>Barley data (1973)</i>
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### Description

Sample data on ear per plant, ear length (cms), 100-grain weight (g), and grain yield per plant (kg) from 1973 Barley performance trial, comprising of eight varieties in four replication (Chaudhary, 1973).

### Usage

```
data("Barley")
```

### Format

A data frame with 32 observations on the following 4 variables - EPR, EL,GW,and GY.

### Source

Chaudhary BD. (1973). Estimation of genetic parameters in barley (*Hordeum vulgare* L.) by diallel analysis and its modifications. Unpublished Ph.D. Thesis, Haryana Agricultural University, Hisar.

### Examples

```
data(Barley)
```

---

traitstats.envcor1      *Environmental Correlation Analysis*

---

**Description**

An extract of environment correlation coefficient for between traits

**Usage**

```
traitstats.envcor1(Treatment, Replication, DataFile)
```

**Arguments**

Treatment	Treatment column in the DataFile
Replication	Replication column in the DataFile
DataFile	Input Data file name

**Details**

Environmental Correlation coefficient is calculated according to the Al-Jibouri et al., (1958).

**Value**

Environmental correlation coefficient matrix.

**Author(s)**

Nitesh, S.D., Parashuram Patroti, and Shilpa Parashuram.

**References**

Al-Jibour HA, Miller PA and Robinson HP. 1958. Genotypic and environmental variance in upland cotton cross of interspecific origin. *Agronomy Journal*, 50:633-637.

**Examples**

```
data("Barley")
traitstats.envcor1(Treatment=Barley$trt,
                  Replication=Barley$rep,
                  DataFile=Barley)
```

---

traitstats.envcov      *Environmental Variance and Covariance*

---

**Description**

Computation of environment variance and covariance matrix.

**Usage**

```
traitstats.envcov(Treatment, Replication, DataFile)
```

**Arguments**

Treatment	Treatment column in the DataFile
Replication	Replication column in the DataFile
DataFile	Input Data file name

**Details**

Environmental variance and covariance matrix is computed as per the methodology given by Al-Jibour et al., (1958).

**Value**

Environment variance and co-variance matrix. Diagonal value indicating the environmental variance and upper and lower half of the matrix indicating the environmental covariance.

**Author(s)**

Nitesh, S.D., Parashuram Patroti and Shilpa Parashuram

**References**

Al-Jibour HA, Miller PA and Robinson HP. 1958. Genotypic and environmental variance in upland cotton cross of interspecific origin. *Agronomy Journal*, 50:633-637.

**Examples**

```
data("Barley")
traitstats.envcov(Treatment=Barley$trt,
                  Replication=Barley$rep,
                  DataFile=Barley)
```

---

traitstats.genocor1     *Genotypic Correlation Analysis*

---

**Description**

An extract of genotypic correlation coefficient for between traits

**Usage**

```
traitstats.genocor1(Treatment, Replication, DataFile)
```

**Arguments**

Treatment	Treatment column in the DataFile
Replication	Replication column in the DataFile
DataFile	Input Data file name

**Details**

Genotypic Correlation coefficient is calculated according to the Al-Jibouri et al., (1958).

**Value**

Genotypic correlation coefficient matrix.

**Author(s)**

Nitesh, S.D., Parashuram Patroti, and Shilpa Parashuram.

**References**

Al-Jibour HA, Miller PA and Robinson HP. 1958. Genotypic and environmental variance in upland cotton cross of interspecific origin. *Agronomy Journal*, 50:633-637.

**Examples**

```
data("Barley")
traitstats.genocor1(Treatment=Barley$trt,
                    Replication=Barley$rep,
                    DataFile=Barley)
```

---

traitstats.genocov      *Genotypic Variance and Covariance*

---

### **Description**

Computation of genotypic variance and covariance matrix.

### **Usage**

```
traitstats.genocov(Treatment, Replication, DataFile)
```

### **Arguments**

Treatment	Treatment column in the DataFile
Replication	Replication column in the DataFile
DataFile	Input Data file name

### **Details**

Genotypic variance and covariance matrix is computed as per the methodology given by Al-Jibour et al., (1958).

### **Value**

Genotypic variance and co-variance matrix. Diagonal value indicating the genetic variance and upper and lower half of the matrix indicating the genotypic covariance.

### **Author(s)**

Nitesh, S.D., Parashuram Patroti and Shilpa Parashuram

### **References**

Al-Jibour HA, Miller PA and Robinson HP. 1958. Genotypic and environmental variance in upland cotton cross of interspecific origin. *Agronomy Journal*, 50:633-637.

### **Examples**

```
data("Barley")
traitstats.genocov(Treatment=Barley$trt,
                  Replication=Barley$rep,
                  DataFile=Barley)
```

---

 traitstats.genpar      *Genetic Parameter Analysis*


---

### Description

traitstats.genpar performs genetic variability analysis for all the traits in the DataFile.

### Usage

```
traitstats.genpar(Treatment, Replication, DataFile)
```

### Arguments

Treatment	Treatment column in the DataFile
Replication	Replication column in the DataFile
DataFile	Input Data file name

### Details

traitstats.genpar performs genetic parameter analysis from the input values extracted from the ANOVA analysis for individual traits and computes several variability estimates. .

The phenotypic, genotypic and environmental variance ( $\sigma_p^2$ ,  $\sigma_g^2$  and  $\sigma_e^2$ ) are obtained from the ANOVA tables according to the expected value of mean square described by Federer and Searle (1976) as follows:

$$\sigma_p^2 = \text{Mean sum of squares of test treatments}$$

$$\sigma_e^2 = \text{Mean sum of squares of residuals}$$

$$\sigma_g^2 = \sigma_p^2 - \sigma_e^2$$

Phenotypic and genotypic coefficients of variation (*PCV* and *GCV*) are estimated according to Burton (1951, 1952) as follows:

$$PCV = \frac{\sigma_p^2}{\sqrt{\bar{x}}} \times 100$$

$$GCV = \frac{\sigma_g^2}{\sqrt{\bar{x}}} \times 100$$

Where  $\bar{x}$  is the mean.

The estimates of *PCV* and *GCV* are categorised according to Sivasubramanian and Madhavanmenon (1978) as follows:

<b>CV (%)</b>	<b>Category</b>
$x < 10$	Low
$10 \leq x < 20$	Medium
$\geq 20$	High

The broad-sense heritability ( $H^2$ ) is calculated according to method of Lush (1940) as follows:

$$H^2 = \frac{\sigma_g^2}{\sigma_p^2}$$

The estimates of broad-sense heritability ( $H^2$ ) are categorised according to Robinson (1966) as follows:

$H^2$	Category
$x < 30$	Low
$30 \leq x < 60$	Medium
$\geq 60$	High

Genetic advance ( $GA$ ) is estimated and categorised according to Johnson et al., (1955) as follows:

$$GA = k \times \sigma_g \times \frac{H^2}{100}$$

Where the constant  $k$  is the standardized selection differential or selection intensity. The value of  $k$  at 5% proportion selected is 2.063. Values of  $k$  at other selected proportions are available in Appendix Table A of Falconer and Mackay (1996).

### Value

Genotypic Coefficient of Variation and GCV Category  
 Phenotypic Coefficient of Variation and PCV Category  
 Heritability (broad sense) and  $h^2$  Category  
 Genetic Advance and GA Category  
 Genetic Advance percent Mean and GAM Category

### Note

Genetic parameter analysis need to be performed only if the sum of squares of treatment: Test is significant Negative estimates of variance components is computed are not abnormal. Ref. Dudley and Moll (1969).

### Author(s)

Nitesh, S.D., Parashuram Patroti and Shilpa Parashuram

### References

- Lush JH. (1940). Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics. Proceedings of the American Society of Animal Nutrition, 1940(1):293-301.
- Burtone GW and De Vane GM. (1953). Estimating heritability in tall Fescus (*Festuca arundinaceae*) from replicated clonal material. Agronomy Journal, 45:478-481.



Johnson HW, Robinson HF and Comstock RE. (1955). Estimates of genetic and environmental variability in soybeans. *Agronomy Journal*, 47:314-318.

Robinson HF. (1966). Quantitative genetics in relation to breeding on centennial of Mendelism. *Indian Journal of Genetics and Plant Breeding*, 171.

Dudley JW and Moll RH. (1969). Interpretation and Use of estimates of heritability of genetics variance in Plant Breeding. *Crop Science*, 9:257-262.

Sivasubramaniam S and Madhavamenon P. (1973). Genotypic and Phenotypic variability in rice. *The Madras Agricultural Journal*, 60:1093-1096.

## Examples

```
data("Barley")
traitstats.genpar(Treatment=Barley$trt,
                 Replication=Barley$rep,
                 DataFile=Barley)
```

---

traitstats.phenocor1 *Phenotypic Correlation Analysis*

---

## Description

An extract of phenotypic correlation coefficient for between traits

## Usage

```
traitstats.phenocor1(Treatment, Replication, DataFile)
```

## Arguments

Treatment	Treatment column in the DataFile
Replication	Replication column in the DataFile
DataFile	Input Data file name

## Details

Phenotypic Correlation coefficient is calculated according to the Al-Jibouri et al., (1958).

## Value

Phenotypic correlation coefficient matrix.

## Author(s)

Nitesh, S.D., Parashuram Patroti, and Shilpa Parashuram.

## References

Al-Jibour HA, Miller PA and Robinson HP. 1958. Genotypic and environmental variance in upland cotton cross of interspecific origin. *Agronomy Journal*, 50:633-637.

## Examples

```
data("Barley")
traitstats.phenocov1(Treatment=Barley$str,
                    Replication=Barley$rep,
                    DataFile=Barley)
```

---

traitstats.phenocov    *Phenotypic Variance and Covariance*

---

## Description

Computation of phenotypic variance and covariance matrix.

## Usage

```
traitstats.phenocov(Treatment, Replication, DataFile)
```

## Arguments

Treatment	Treatment column in the DataFile
Replication	Replication column in the DataFile
DataFile	Input Data file name

## Details

Phenotypic variance and covariance matrix is computed as per the methodology given by Al-Jibour et al., (1958).

## Value

Phenotypic variance and co-variance matrix. Diagonal value indicating the phenotypic variance and upper and lower half of the matrix indicating the phenotypic covariance.

## Author(s)

Nitesh, S.D., Parashuram Patroti and Shilpa Parashuram

## References

Al-Jibour HA, Miller PA and Robinson HP. 1958. Genotypic and environmental variance in upland cotton cross of interspecific origin. *Agronomy Journal*, 50:633-637.

**Examples**

```
data("Barley")
traitstats.phenocov(Treatment=Barley$str,
                    Replication=Barley$rep,
                    DataFile=Barley)
```

---

traitstats.rbd	<i>RCBD Bulk Data Analysis</i>
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---

**Description**

Bulk RCBD data analysis for ANOVA and Descriptive statistics

**Usage**

```
traitstats.rbd(Treatment, Replication, DataFile)
```

**Arguments**

Treatment	Treatment column in the DataFile
Replication	Replication column in the DataFile
DataFile	Input Data file name

**Details**

traitstats.rbd function analysis the input DataFile according to the methodology given by Panse and Sukhatme (1984). Futhermore, it also represent the analysis results along with descriptive statistics parameters like Trait mean, Minimum, Maximum, CV, StdError(m) and StdError(d) in the tabular representation of the publication ready format.

**Value**

Number of Replication  
Number of Treatment  
Treatment Mean Sum of Square along with Test of Significance  
Replication Mean Sum of Square along with Test of Significance  
Error Mean Sum of Square  
Trait Mean  
Minimum  
Maximum  
CV  
StdError(m)  
StdError(d)

**Author(s)**

Nitesh, S.D., Parashuram Patroti and Shilpa Parashuram

## References

Panse and Sukhatme. 1984. Statistical Methods for Agricultural Workers. ICAR, New Delhi.

## See Also

[traitstats.rbdmeantable](#), [traitstats.rbdstats](#), [traitstats.rbdsummary](#)

## Examples

```
data("Barley")
traitstats.rbd (Barley$trt,
               Barley$rep,
               Barley)
```

---

```
traitstats.rbdmeantable
```

*RCBD Mean Table*

---

## Description

Individual treatment mean table along with Grand trait mean, CV, SE(m) and CD.

## Usage

```
traitstats.rbdmeantable(Treatment, Replication, DataFile)
```

## Arguments

Treatment	Treatment column in the DataFile
Replication	Replication column in the DataFile
DataFile	Input Data file name

## Details

traitstats.rbdmeantable function analysis the input DataFile according to the methodology given by Panse and Sukhatme (1984) and generates the data frame consisting of the treatment mean over replication. Furthermore, it also represent the descriptive statistics parameter – Trait mean, StdError(m), CV and CD at 5 percent level of significance in the tabular representation of the publication ready format.

## Value

Individual Treatment mean  
Trait Mean  
SE(m)  
CV  
CD

**Author(s)**

Nitesh, S.D, Parashuram Patroti and Shilpa Parashuram

**References**

Panse and Sukhatme. 1984. Statistical Methods for Agricultural Workers. ICAR, New Delhi.

**See Also**

[traitstats.rbd](#), [traitstats.rbdstats](#), [traitstats.rbdsummary](#),

**Examples**

```
data("Barley")
traitstats.rbdmeantable(Barley$str,
                        Barley$rep,
                        Barley)
```

---

traitstats.rbdstats    *RCBD Descriptive Statistics*

---

**Description**

Descriptive Statistics for Trait Mean, Minimum, Maximum, SE(m), SE(d) and CV.

**Usage**

```
traitstats.rbdstats(Treatment, Replication, DataFile)
```

**Arguments**

Treatment	Treatment column in the DataFile
Replication	Replication column in the DataFile
DataFile	Input Data file name

**Details**

traitstats.rbdstats function analysis the input DataFile according to the methodology given by Panse and Sukhatme (1984) and generates the RBD descriptive statistics for Trait Mean, Minimum, Maximum, Standard Error(mean), Standard Error(deviation) and Coefficient of Variation.

**Value**

Trait Mean  
Minimum  
Maximum  
StdError(m)  
StdError(d)  
CV

**Author(s)**

Nitesh, S.D, Parashuram Patroti and Shilpa Parashuram

**References**

Panse and Sukhatme. 1984. Statistical Methods for Agricultural Workers. ICAR, New Delhi.

**See Also**

[traitstats.rbd](#), [traitstats.rbdmeantable](#), [traitstats.rbdsummary](#)

**Examples**

```
data("Barley")
traitstats.rbdstats(Barley$trt,
                   Barley$rep,
                   Barley)
```

---

traitstats.rbdsummary *RCBD Data Analysis Report*

---

**Description**

RCBD data analysis report in PDF formate compiling the ANOVA, Descriptive Statistics and Genetic Parameter along with Data distribution graph.

**Usage**

```
traitstats.rbdsummary(Treatment, Replication, DataFile)
```

**Arguments**

Treatment	Treatment column in the DataFile
Replication	Replication column in the DataFile
DataFile	Input Data file name

**Details**

`traitstats.rbdsummary` function analysis the input `DataFile` according to the methodology given by Panse and Sukhatme (1984) and generates the RCBD data analysis results comprising of Data point distribution, ANOVA table, Descriptive statistics and Genetic parameter arranged in the PDF format output file.

**Value**

Data distribution graph  
ANOVA table : Rep, Trt, MStrt, MSrep and MSerror along the test of significance  
Descriptive statistics table : Trait Mean, Min, Max, SE(m), SE(d), CV and CD.  
Genetic Parameter : GCV, PCV, h<sup>2</sup>, GA and GAM along with the category

**Author(s)**

Nitesh, S.D., Parashuram Patroti and Shilpa Prashuram

**References**

Panse and Sukhatme. 1984. Statistical Methods for Agricultural Workers. ICAR, New Delhi.

**See Also**

[traitstats.rbd](#), [traitstats.rbdmeantable](#), [traitstats.rbdstats](#)

**Examples**

```
data("Barley")
traitstats.rbd (Barley$trt,
               Barley$rep,
               Barley)
```

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