

# Package ‘gpbStat’

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**Type** Package

**Title** Comprehensive Statistical Analysis of Plant Breeding Experiments

**Version** 0.4.2

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**Description** Performs statistical data analysis of various Plant Breeding experiments. Contains functions for Line by Tester analysis as per Arunachalam, V.(1974) <<http://repository.ias.ac.in/89299/>> and Diallel analysis as per Griffing, B. (1956) <<https://www.publish.csiro.au/bi/pdf/BI9560463>>.

**License** GPL-2

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**VignetteBuilder** knitr

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alphaltc	<i>Line x Tester data (only Crosses) in Alpha Lattice design.</i>
----------	---

---

**Description**

The Line x Tester data of containing only crosses laid out in Alpha Lattice design.

**Usage**

```
data(alphaltc)
```

**Format**

A data frame of five variables of 15 crosses derived from five lines and three testers.

**replication** four replications

**block** five blocks

**line** five inbred genotype

**tester** three inbred genotype

**yield** trait of interest

**See Also**

[rcbdltc](#), [alphaltcchk](#), [rcbdltcchk](#)

**Examples**

```
result = ltc(alphaltc, replication, line, tester, yield, block)
```

---

alphaltcchk

*Line x Tester data (Crosses and Checks) in Alpha Lattice*

---

**Description**

The sample Line x Tester data of containing crosses and checks laid out in Alpha Lattice design. The data is composed of five lines, three testers and three checks.

**Usage**

```
data(alphaltcchk)
```

**Format**

A dataframe of six variables.

**replication** three replications

**block** six blocks

**line** five lines

**tester** three testers

**check** three check

**yield** trait of interest

**See Also**

[rcbdltc](#), [alphaltc](#), [rcbdltcchk](#)

**Examples**

```
result = ltcchk(alphaltcchk, replication, line, tester, check, yield, block)
```

---

`alphaltcmt`*Line x Tester data (only Crosses) in Alpha Lattice design.*

---

**Description**

The Line x Tester data of containing only crosses laid out in Alpha Lattice design.

**Usage**

```
data(alphaltcmt)
```

**Format**

A data frame of 15 crosses derived from five lines and three testers.

**replication** four replications

**block** five blocks

**line** five inbred genotype

**tester** three inbred genotype

**hsw** hundred seed weight

**sh** shelling per cent

**gy** grain yield

**See Also**

[rcbdltc](#), [alphaltcchk](#), [rcbdltcchk](#), [rcbdltcmt](#)

**Examples**

```
result = ltcmt(alphaltcmt, replication, line, tester, alphaltcmt[,5:7], block)
```

---

`alphaltcs`*Line x Tester data (only Crosses) with single plant observations laid in Alpha Lattice design.*

---

**Description**

The Line x Tester data containing single plant observations of only crosses laid out in Alpha Lattice design.

**Usage**

```
data(alphaltcs)
```

**Format**

A data frame of 15 crosses derived from five lines and three testers.

**replication** four replications

**block** five blocks

**line** five inbred genotype

**tester** three inbred genotype

**obs** four single plant observations

**yield** yield as a dependent trait

**See Also**

[rcbdlts](#), [alphaltcchk](#), [rcbdltcchk](#), [rcbdltcmt](#)

**Examples**

```
result = ltcs(alphaltcs, replication, line, tester, obs, yield, block)
```

---

datdti

*Data of estimating drought tolerance indices without replication*

---

**Description**

The sample data containing 15 genotypes evaluated under non-stress and stress conditions without replications

**Usage**

```
data(datdti)
```

**Format**

A dataframe of eight variables.

**ENV** two environment

**GEN** fifteen genotypes

**CL** trait cob length

**CG** trait cob girth

**NKR** trait number of kernel rows

**NKPR** trait number of kernels per row

**HSW** trait hundred seed weight

**GY** trait grain yield

**See Also**

[datrdti](#), [alphaltc](#), [rcbdltc](#)

**Examples**

```
result = dti(datdti, environment = ENV, genotype = GEN, datdti[,3:8], ns = 'NS-DWR', st = 'ST-DWR')
```

---

datrdti

*Data of estimating drought tolerance indices with replication*

---

**Description**

The sample data containing 15 genotypes evaluated under non-stress and stress conditions with replications

**Usage**

```
data(datrdti)
```

**Format**

A dataframe of nine variables.

**ENV** two environment

**GEN** fifteen genotypes

**REP** two replications

**CL** trait cob length

**CG** trait cob girth

**NKR** trait number of kernel rows

**NKPR** trait number of kernels per row

**HSW** trait hundred seed weight

**GY** trait grain yield

**See Also**

[datdti](#), [alphaltc](#), [rcbdltc](#)

**Examples**

```
result = dti(datrdti, environment = ENV, genotype = GEN, datrdti[,4:9],  
             ns = 'NS-DWR', st = 'ST-DWR')
```

---

dm2	<i>Analysis of Diallel Method 2 data containing only Crosses laid out in RCBD or Alpha Lattice design.</i>
-----	--

---

**Description**

Analysis of Diallel Method 2 data containing only Crosses laid out in RCBD or Alpha Lattice design.

**Usage**

```
dm2(data, rep, parent1, parent2, var, block)
```

**Arguments**

data	dataframe containing following variables
rep	replication
parent1	parent 1
parent2	parent 2
var	trait of interest
block	block (for alpha lattice only)

**Details**

Analyzing the Diallel Method 2 data containing only crosses which are evaluated in RCBD & Alpha lattice design. All the factors are considered as fixed.

**Value**

Means	Two way mean table.
ANOVA	ANOVA for the given variable.
Coefficient of Variation	Coefficient of Variation of the variable.
Diallel ANOVA	Diallel ANOVA for the given trait.
Genetic Variance	GCA & SCA varaince.
Combining ability effects	Two way table containing Combining ability effects of parents and crosses
Standard Error	Standard Error for comining ability effects.
Critical Difference	Critical Difference at 5 percent for combining ability effects.

**Note**

The blocks are mentioned at end of the function if the experimental design is Alpha Lattice. For RCBD no need mention the blocks.

**Author(s)**

Nandan Patil <tryanother609@gmail.com>

**References**

Griffing, B. (1956) Concept of General and Specific Combining Ability in relation to Diallel Crossing Systems. Australian Journal of Biological Sciences, 9(4), 463-493.

Dabholkar, A. R. (1999). Elements of Bio Metrical Genetics. Concept Publishing Company, New Delhi.

Singh, R. K. and Chaudhary, B. D. (1977). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi.

**See Also**

[lrcchk](#), [lrc](#)

**Examples**

```
## Not run: #Diallel Method 2 analysis containing only crosses in RCBD.
library(gpbStat)
data(dm2rcbd)
result1 = dm2(dm2rcbd, rep, parent1, parent2, DTP)
result1

#Diallel Method 2 analysis containing only crosses in Alpha Lattice
library(gpbStat)
data(dm2alpha)
result2 = dm2(dm2alpha, replication, parent1, parent2, TW, block)
result2

# Save results to csv file
lapply(result2, function(x) write.table(data.frame(x), 'result2.csv' , append= T, sep=','))

## End(Not run)
```

---

dm2alpha

*Diallel Method 2 data in Alpha Lattice.*

---

**Description**

The Diallel Method 2 data laid out in Alpha Lattice Design.

**Usage**

```
data(dm2alpha)
```



**Format**

A data frame for Diallel analysis Method 2 containing 105 crosses and 15 parents.

**replication** two replications

**block** twelve blocks

**parent1** fifteen inbred genotype

**parent2** fifteen inbred genotype

**TW** data for test weight

**See Also**

[alphaltcchk](#), [alphaltc](#), [rcbdltcchk](#), [dm2rcbd](#)

**Examples**

```
result2 = dm2(dm2alpha, replication, parent1, parent2, TW, block)
```

---

dm2rcbd

*Diallel Method 2 data in RCBD*

---

**Description**

The Diallel Method 2 data laid out in Randomized Complete Block Design (RCBD).

**Usage**

```
data(rcbdltc)
```

**Format**

A data frame for Diallel analysis Method 2 containing four variables of 105 crosses and 15 parents.

**rep** four replications

**parent1** five inbred genotype

**parent2** three inbred genotype

**DTP** data for days to pollen shed

**See Also**

[alphaltcchk](#), [alphaltc](#), [rcbdltcchk](#), [dm2alpha](#)

**Examples**

```
result2 = dm2(dm2rcbd, rep, parent1, parent2, DTP)
```

---

dti *Estimation of Drought Tolerance Indices.*

---

### Description

Estimation of Drought Tolerance Indices.

### Usage

```
dti(data, environment, genotype, traits, ns, st)
```

### Arguments

data	dataframe containing following variables
environment	column with two levels i.e., non-stress and stress conditions
genotype	genotypes evaluated
traits	trait of interest
ns	name of level indicating evaluation under non-stress (irrigated) conditions
st	name of level indicating evaluation under stress conditions

### Details

Estimation various Drought Tolerance Indices of genotypes evaluated under stress and non-stress conditions of both replicated and non-replicated data.

### Value

TOL	Stress tolerance.
STI	Stress tolerance index.
SSPI	Stress susceptibility percentage index.
YI	Yield index.
YSI	Yield stability index.
RSI	Relative stress index.
MP	Mean productivity.
GMP	Geometric mean productivity
HM	Harmonic mean.
MRP	Mean relative performance.
PYR	Percent yield Reduction.
PYR	Drought Susceptibility Index.

### Note

The function can handle both replicated and non-replicated data refer the examples.

**Author(s)**

Nandan Patil <tryanother609@gmail.com>

**References**

Lamba, K., Kumar M., Singh V., Chaudhary L., Sharma R., Yashveer S. and Dalal, M. S. (2023). Heat stress tolerance indices for identification of the heat tolerant wheat genotypes. *Scientific Reports*, 13(1). <https://doi.org/10.1038/s41598-023-37634-8> Fischer, R. and Maurer, R. (1978) Drought Resistance in Spring Wheat Cultivars. I. Grain Yield Responses. *Australian Journal of Agricultural Research*, 29, 897-912. <https://doi.org/10.1071/AR9780897>

**See Also**

[ltc](#), [ltcchk](#), [ltcmt](#)

**Examples**

```
## Not run: # Estimating drought tolerance indices
library(gpbStat)

data(datdti)
result1 = dti(datdti, environment = ENV, genotype = GEN, datdti[,3:8],
             ns = 'NS-DWR', st = 'ST-DWR')
result1

data(datrdti)
result2 = dti(datrdti, environment = ENV, genotype = GEN, datrdti[,4:9],
             ns = 'NS-DWR', st = 'ST-DWR')
result2

## End(Not run)
```

---

ltc

*Analysis of Line x Tester data containing only Crosses laid out in RCBD or Alpha Lattice design.*

---

**Description**

Analysis of Line x Tester data containing only Crosses laid out in RCBD or Alpha Lattice design.

**Usage**

```
ltc(data, replication, line, tester, y, block)
```

**Arguments**

data	dataframe containing following variables
replication	replication
line	line
tester	tester
y	trait of interest
block	block (for alpha lattice design only)

**Details**

Analyzing the line by tester data only using the data from crosses which are evaluated in alpha lattice design. All the factors are considered as fixed.

**Value**

Overall ANOVA	ANOVA with all the factors.
Coefficient of Variation	ANOVA with all the factors.
Genetic Variance	Phenotypic and Genotypic variance for the given trait.
Genetic Variability	Phenotypic coefficient of variability and Genotypic coefficient of variability and Environmental coefficient of Variation.
Proportional Contribution	Proportional contribution of Lines, Tester and Line x Tester interaction.
GCA lines	Combining ability effects of lines.
GCA testers	Combining ability effects of testers.
SCA crosses	Combining ability effects of crosses
Line x Tester ANOVA	ANOVA with all the factors.
GV Singh & Chaudhary	Genetic component of Variance as per Singh and Chaudhary, 1977.
Standard Errors	Standard error for combining ability effects.
Critical Difference	Critical Difference at 5 percent for combining ability effects.

**Note**

The block variable is inserted at the last if the experimental design is Alpha Lattice. For RCBD no need to have block factor.

**Author(s)**

Nandan Patil <tryanother609@gmail.com>

**References**

Kempthorne, O. (1957), Introduction to Genetic Statistics. John Wiley and Sons, New York. , 468-472. Singh, R. K. and Chaudhary, B. D. (1977). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi.

**See Also**

[lrcchk](#), [dm2](#), [lrcmt](#)

**Examples**

```
## Not run: #Line Tester analysis data with only crosses in RCBD
library(gpbStat)
data(rcbdlrc)
result1 = lrc(rcbdlrc, replication, line, tester, yield)
result1

#Line Tester analysis data with only crosses in Alpha Lattice
library(gpbStat)
data(alphalrc)
result2 = lrc(alphalrc, replication, line, tester, yield, block)
result2

## End(Not run)
```

---

lrcchk

*Analysis of Line x Tester data containing crosses and checks laid out in RCBD or Alpha Lattice experimental design.*

---

**Description**

Analysis of Line x Tester data containing crosses and checks laid out in RCBD or Alpha Lattice experimental design.

**Usage**

```
lrcchk(data, replication, line, tester, check, y, block)
```

**Arguments**

data	dataframe containing following variables
replication	replication variable
line	line variable
tester	tester variable
check	check variable
y	trait of interest
block	block variable (for alpha lattice design only)

**Details**

Analyzing the line by tester data only using the data from crosses which are evaluated in alpha lattice design. All the factors are considered as fixed.

Analyzing the line by tester data only using the data from crosses which are evaluated in alpha lattice design. All the factors are considered as fixed.

**Value**

Overall ANOVA	ANOVA with all the factors.
Coefficient of Variation	ANOVA with all the factors.
Genetic Variance	Phenotypic and Genotypic variance for the given trait.
Genetic Variability	Phenotypic coefficient of variability and Genotypic coefficient of variability and Environmental coefficient of Variation.
Proportional Contribution	Proportional contribution of Lines, Tester and Line x Tester interaction.
GCA lines	Combining ability effects of lines.
GCA testers	Combining ability effects of testers.
SCA crosses	Combining ability effects of crosses
Line x Tester ANOVA	ANOVA with all the factors.
GV Singh & Chaudhary	Genetic component of Variance as per Singh and Chaudhary, 1977.
Standard Errors	Standard error for combining ability effects.
Critical Difference	Critical Difference at 5 percent for combining ability effects.

**Note**

The block variable is inserted at the last if the experimental design is Alpha Lattice. For RCBD no need to have block factor.

**Author(s)**

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**References**

Kempthorne, O. (1957), Introduction to Genetic Statistics. John Wiley and Sons, New York. , 468-472. Singh, R. K. and Chaudhary, B. D. (1977). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi.

**See Also**

[lrc](#), [dm2](#), [lrcmt](#)

**Examples**

```
## Not run: #Line x Tester analysis with crosses and checks in RCBD
library(gpbStat)
data(rcbdlrcchk)
results = lrcchk(rcbdlrcchk, replication, line, tester, check, yield)
results

#Line X Tester analysis with crosses and checks in Alpha Lattice
library(gpbStat)
data(alphalrcchk)
results1 = lrcchk(alphalrcchk, replication, line, tester, check, yield, block)
results1
## End(Not run)
```

---

lrcmt	<i>Analysis of Line x Tester data for multiple traits containing only Crosses laid out in RCBD or Alpha Lattice design.</i>
-------	---

---

**Description**

Analysis of Line x Tester data for multiple traits containing only Crosses laid out in RCBD or Alpha Lattice design.

**Usage**

```
lrcmt(data, replication, line, tester, traits, block)
```

**Arguments**

data	dataframe containing following variables
replication	replication
line	line
tester	tester
traits	multiple traits of interest
block	block (for alpha lattice design only)

**Details**

Analyzing the line by tester data of multiple traits only using the data from crosses which are evaluated in RCBD and Alpha lattice design. All the factors are considered as fixed.

**Value**

Mean	Table of means.
ANOVA	ANOVA with all the factors.
GCA.Line	GCA effects of lines.
GCA.Tester	GCA effects of testers.
SCA	SCA effects of crosses.
CV	Coefficient of Variation.
Genetic.Variance.Covariance	Genetic component Variance and covariance.
Std.Error	Standard error for combining ability effects.
C.D.	Critical Difference at 5 percent for combining ability effects.
Add.Dom.Var	Additive and Dominance component of Variance.
Contribution.of.Line.Tester	Contribution of Lines, Testers and Line x Tester towards total variation.

**Note**

The block variable is inserted at the last if the experimental design is Alpha Lattice. For RCBD no need to have block factor.

**Author(s)**

Nandan Patil <tryanother609@gmail.com>

**References**

Kemphorne, O. (1957), Introduction to Genetic Statistics. John Wiley and Sons, New York. , 468-472. Singh, R. K. and Chaudhary, B. D. (1977). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi.

**See Also**

[lrcchk](#)

**Examples**

```
## Not run: #Line Tester analysis data with only crosses in RCBD
library(gpbStat)
data(rcbdltcmt)
result1 = lrcchk(rcbdltcmt, replication, line, tester, rcbdltcmt[,4:5])
result1

#Line Tester analysis data with only crosses in Alpha Lattice
library(gpbStat)
data(alphalrcchk)
result2 = lrcchk(alphalrcchk, replication, line, tester, alphalrcchk[,5:7], block)
result2

## End(Not run)
```



---

ltcs	<i>Analysis of Line x Tester data on single plant basis containing only Crosses laid out in RCBD or Alpha Lattice design.</i>
------	---

---

### Description

Analysis of Line x Tester data on single plant basis containing only Crosses laid out in RCBD or Alpha Lattice design.

### Usage

```
ltcs(data, replication, line, tester, obs, y, block)
```

### Arguments

data	dataframe containing following variables
replication	replication
line	line
tester	tester
obs	single plant observations
y	dependent variable
block	block (for alpha lattice design only)

### Details

Analyzing the line by tester data single plant observations evaluated in RCBD and Alpha lattice design. All the factors are considered as fixed.

### Value

Mean	Table of means.
ANOVA	ANOVA with all the factors.
GCA.Line	GCA effects of lines.
GCA.Tester	GCA effects of testers.
SCA	SCA effects of crosses.
CV	Coefficient of Variation.
Std.Error	Standard error for combining ability effects.
C.D.	Critical Difference at 5 percent for combining ability effects.
Contribution.of.Line.Tester	Contribution of Lines, Testers and Line x Tester towards total variation.

**Note**

The block variable is inserted at the last if the experimental design is Alpha Lattice. For RCBD no need to have block factor.

**Author(s)**

Nandan L Patil <tryanother609@gmail.com>

**References**

Kempthorne, O. (1957), Introduction to Genetic Statistics. John Wiley and Sons, New York. , 468-472. Singh, R. K. and Chaudhary, B. D. (1977). Biometrical Methods in Quantitative Genetic Analysis. Kalyani Publishers, New Delhi. Arunachalam, V. (1974), The fallacy behind use of modified line x tester design. The Indian Journal of Genetics and Plant Breeding, 34: 280-287.

**See Also**

[ltc](#), [ltcmt](#)

**Examples**

```
## Not run: #Line Tester analysis data with only crosses in RCBD
library(gpbStat)
data(rcbdltc)
result1 = ltcs(rcbdltc, replication, line, tester, obs, yield)
result1

#Line Tester analysis data with only crosses in Alpha Lattice
library(gpbStat)
data(alphaltcs)
result2 = ltcs(alphaltcs, replication, line, tester, obs, yield, block)
result2

## End(Not run)
```

---

rcbdltc

*Line x Tester data in RCBD*

---

**Description**

The sample Line x Tester data containing only crosses laid out in Randomized Complete Block Design (RCBD).

**Usage**

```
data(rcbdltc)
```

**Format**

A data frame of four variables of 15 crosses derived from five lines and three testers.

**replication** four replications

**line** five inbred genotype

**tester** three inbred genotype

**yield** trait of interest

**See Also**

[alphaltcchk](#), [alphaltc](#), [rcbdltcchk](#)

**Examples**

```
result = ltc(rcbdltc, replication, line, tester, yield)
```

---

rcbdltcchk

*Line x Tester data (Crosses and Checks) in RCBD*

---

**Description**

The sample Line x Tester data of containing crosses and checks laid out in Randomized Complete Block Design (RCBD). The data is composed of five lines, three testers and three checks.

**Usage**

```
data(rcbdltcchk)
```

**Format**

A dataframe of six variables.

**replication** four replications

**line** five lines

**tester** three testers

**yield** trait of interest

**See Also**

[rcbdltc](#), [alphaltc](#), [alphaltcchk](#)

**Examples**

```
result = ltcchk(rcbdltcchk, replication, line, tester, check, yield)
```

---

rcbdltcmt	<i>Line x Tester data (only Crosses) in Randomized Complete Block design.</i>
-----------	---

---

**Description**

The Line x Tester data of containing only crosses laid out in Randomized Complete Block design.

**Usage**

```
data(rcbdltcmt)
```

**Format**

A data frame of 15 crosses derived from five lines and three testers.

**replication** four replications

**line** five inbred genotype

**tester** three inbred genotype

**ph** plant height

**eh** ear height

**See Also**

[rcbdltc](#), [alphaltcchk](#), [rcbdltcchk](#), [alphaltcmt](#)

**Examples**

```
result = ltcmt(rcbdltcmt, replication, line, tester, rcbdltcmt[,4:5])
```

---

rcbdltc	<i>Line x Tester data (only Crosses) with single plant observations laid in RCBD design.</i>
---------	--

---

**Description**

The Line x Tester data containing single plant observations of only crosses laid out in RCBD design.

**Usage**

```
data(rcbdltc)
```

**Format**

A data frame of 15 crosses derived from five lines and three testers.

**replication** four replications

**line** five inbred genotype

**tester** three inbred genotype

**obs** four single plant observations

**yield** yield as a dependent trait

**See Also**

[rcbdlts](#) [.alphaltcchk](#) [rcbdltcchk](#) [rcbdltcmt](#)

**Examples**

```
result = ltcs(rcbdlts, replication, line, tester, obs, yield)
```

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