Package ‘gpbStat’

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Type Package

Title Comprehensive Statistical Analysis of Plant Breeding Experiments

Version 0.4.4

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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`>.

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Encoding UTF-8

LazyData true

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URL `https://github.com/nandp1/gpbStat/`

BugReports `https://github.com/nandp1/gpbStat/issues`

RoxygenNote 7.3.2

Imports tidyr, purrr, tibble, magrittr, dplyr

Suggests testthat, knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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Contents

`alphaltc` *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(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 intrest

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 intrest

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

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

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 ANVOA 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 Errror for comining ability effects.
`Critical Difference`	Critical Difference at 5 pecent 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)

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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

`ltcchk`, `ltc`

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.
`SSP`	Stress Susceptibility Index.

Note

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

Author(s)

Nandan Patil <`tryanother609@gmail.com`>

References

Pour-Aboughadareh, A., Yousefian, M., Moradkhani, H., Moghaddam Vahed, M., Poczai, P., & Siddique, K. H. (2019). ipastic: An online toolkit to estimate plant abiotic stress indices. Applications in Plant Sciences, 7(7). https://doi.org/10.1002/aps3.11278 Sabouri, A., Dadras, A.R., Singh V., Azar, M., Kouchesfahani, A. S., Taslimi, M. and Jalalifar, R. (2022). Screening of rice drought-tolerantlines by introducing a new composite selection index and competitive with multivariate methods. Scientific Reports, 12. https://doi.org/10.1038/s41598-022-06123-9 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`	Propotional 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 pecent 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

`ltcchk`, `dm2`, `ltcmt`

Examples

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

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

## End(Not run)
```

`ltcchk` *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

```
ltcchk(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`	Propotional 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

`ltc`, `dm2`, `ltcmt`

Examples

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

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

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

Description

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

Usage

```
ltcmt(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 trais 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`	Coefficent of Variation.
`Genetic.Variance.Covariance`	Genetic component Variance and covariance.
`Std.Error`	Standard error for combining ability effects.
`C.D.`	Critical Difference at 5 pecent 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)

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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

`ltcchk`

Examples

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

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

## End(Not run)
```

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

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`	Coefficent of Variation.

`Std.Error`	Standard error for combining ability effects.
`C.D.`	Critical Difference at 5 pecent 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)

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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. 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(rcbdltcs)
result1 = ltcs(rcbdltcs, 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 intrest

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 intrest

See Also

`rcbdltc` ,`alphaltc` ,`alphaltcchk`

Examples

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

`rcbdltcmt` *Line x Tester data (only Crosses) in Randomized Complete Block design.*

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])
```

`rcbdltcs` *Line x Tester data (only Crosses) with single plant observations laid in RCBD design.*

Description

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

Usage

```
data(rcbdltcs)
```

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

`rcbdltcs` ,`alphaltcchk` ,`rcbdltcchk` ,`rcbdltcmt`

Examples

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

Index