Package ‘gpbStat’

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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)
```
**datdti**

**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**

```r
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**

```r
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
datrdti

See Also
datrddi, alphaltc, rcdlrtc

Examples
result = dti(datrddi, environment = ENV, genotype = GEN, datrdti[,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(datrddi)

Format
A dataframe of nine variables.

<table>
<thead>
<tr>
<th>ENV</th>
<th>two environment</th>
</tr>
</thead>
<tbody>
<tr>
<td>GEN</td>
<td>fifteen genotypes</td>
</tr>
<tr>
<td>REP</td>
<td>two replications</td>
</tr>
<tr>
<td>CL</td>
<td>trait cob length</td>
</tr>
<tr>
<td>CG</td>
<td>trait cob girth</td>
</tr>
<tr>
<td>NKR</td>
<td>trait number of kernel rows</td>
</tr>
<tr>
<td>NKPR</td>
<td>trait number of kernels per row</td>
</tr>
<tr>
<td>HSW</td>
<td>trait hundred seed weight</td>
</tr>
<tr>
<td>GY</td>
<td>trait grain yield</td>
</tr>
</tbody>
</table>

See Also
datrddi, alphaltc, rcdlrtc

Examples
result = dti(datrddi, 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 variance.
Combining ability effects Two way table containing Combining ability effects of parents and crosses
Standard Error Standard Error for combining 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


See Also

ltcchk, ltc

Examples

```r
## 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, rcdldtcchk, dm2rcbd

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

---

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

Usage
```r
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, rcdldtcchk, dm2alpha

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


See Also

ltc, ltcchk, ltcmt

Examples

```r
## 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

\text{ltc}(\text{data}, \text{replication}, \text{line}, \text{tester}, y, \text{block})

Arguments

- \text{data} \quad \text{dataframe containing following variables}
- \text{replication} \quad \text{replication}
- \text{line} \quad \text{line}
- \text{tester} \quad \text{tester}
- \text{y} \quad \text{trait of interest}
- \text{block} \quad \text{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 \quad \text{ANOVA with all the factors.}
- Coefficient of Variation \quad \text{ANOVA with all the factors.}
- Genetic Variance \quad \text{Phenotypic and Genotypic variance for the given trait.}
- Genetic Variability \quad \text{Phenotypic coefficient of variability and Genotypic coefficient of variability and Environmental coefficient of Variation.}
- Proportional Contribution \quad \text{Propotional contribution of Lines, Tester and Line x Tester interaction.}
- GCA lines \quad \text{Combining ability effects of lines.}
- GCA testers \quad \text{Combining ability effects of testers.}
- SCA crosses \quad \text{Combining ability effects of crosses}
- Line x Tester ANOVA \quad \text{ANOVA with all the factors.}
- GV Singh & Chaudhary \quad \text{Genetic component of Variance as per Singh and Chaudhary, 1977.}
- Standard Errors \quad \text{Standard error for combining ability effects.}
- Critical Difference \quad \text{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.
ltcchk

Author(s)
Nandan Patil <tryanother609@gmail.com>

References

See Also
ltcchk, dm2, ltcmt

Examples
```r
## 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 Variance  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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ltcmt

References


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 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.
- **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


See Also

- ltcchk

Examples

```r
# 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
```
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 Coefficient of Variation.
Std.Error Standard error for combining ability effects.
C.D. 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 L Patil <tryanother609@gmail.com>

References

See Also
ltc, ltcmnt

Examples
```r
## 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 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**

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

Description

The Line x Tester data 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

```r
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)
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)
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