**Package PBTools**

**Technical Documents**

Biometrics and Breeding Informatics

Plant Breeding, Genetics and Biotechnology Division

INTERNATIONAL RICE RESEARCH INSTITUTE

**Package “PBTools”**

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**Type** Package

**Title** Plant Breeding Tools

**Depends** R (>= 3.0.2)

**Description** Statistical Analysis for Plant Breeding

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**License** GPL (>= 2)

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## PBTools package *Plant Breeding Tools*

**Description**

**Details**

Package PBTools

Version 1.5

Date August 2014

Depends

Suggests

LazyLoad

License

**Requirements**

**Future Direction**

**License**

The release of this package is licensed under GPL version 2 or newer.

**Warning**

Classes and methods are considered either to be in its beta or alpha (pre-beta) stage.

**Author(s)**

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**Reference(s)**

## checkGenoError

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## *checkMarkerOrder*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## *checkQTLdata*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## *class.information*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## *compareGenotypes*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## *contrastAnalysis* Contrast Analysis

**Description**

This function determines the variables in the data frame and the type of the variable.

**Usage**

contrastAnalysis (model, contrastOpt = c("control", "user"), controlLevel = NULL, contrast = NULL, alpha = 0.05)

**Arguments**

Model

contrastOpt = c("control", "user")

controlLevel = NULL

contrast = NULL

alpha = 0.05

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## *contrastAnalysisUtil* Contrast Analysis Utilities

**Description**

Utilities for contrast analysis.

**Usage**

compareControlContrast(model, control, alpha = 0.05)

contrastCompute(model, contrast, alpha)

userDefContrast(model, contrast, alpha = 0.05)

**Arguments**

model

controlLevel

contrast

alpha = 0.05

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## *createQTLdata*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## DataAttribute *Data Attributes*

**Description**

This function determines the variables in the data frame and the type of the variable.

**Usage**

DataAttribute(data)

**Arguments**

data a data frame or a character string indicating the name of the data frame that will be used

**Details**

**Value**

A data frame containing the following columns:

VAR NAME all the variable names in the data frame

TYPE type of the variable e.g. (factor, integer, numeric, logical, etc)

NLEVELS if the variable is a factor, how many categories the variable has

LEVELS if the variable is a factor, contains the list of the levels of the factor

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

GERUA <- read.csv(file = 'E:gerua\_split.csv')

DataAttributes(GERUA)

## DescriptiveStatistics *Numerical Descriptive Statistics*

**Description**

It displays univariate summary statistics for several variables per levels of a grouping variable in a single table.

**Usage**

DescriptiveStatistics(data, var, grp = NULL, statistics = c(“nnmiss”, “mean”, “sd”))

**Arguments**

data a non-null character string which indicates the name of the data frame containing the variables specified in var and grp

var a non-empty character vector which indicates the name of the variable(s) where summary statistics will be computed

grp NULL (default) or a character vector which indicates the name of the variable(s) whose value define the subgroup for generating the descriptive statistic

statistics a non-empty character vector which indicates the statistics to be computed. Must be at least one of the following: “n”, “nnmiss”, “nmiss”, “sum”, “css”, “ucss”, “se.skew”, “se.kurtosis”, “range”, “iqr”, “var”, “sd”, “se.mean”, “cv”, “mean”, “median”, “mode”, “min”, “max”, “q1”, “q3”, “skew” and/or “kurtosis”.

**Details**

The elements of var should correspond to numeric variable in the data frame.

**Value**

A data frame.

**Author(s)**

Alaine A. Gulles

**Reference(s)**

**See Also**

**Examples**

## read the data set

Gerua <- read.csv(file = 'E:/gerua\_split.csv')

## compute the default statistics for variables DFF, PLHT, PNCLE and GRNYLD

DescriptiveStatistics(data = “Gerua”, var = c(“DFF”, “PLHT”, “PNCLE”, “GRNYLD”))

## compute the mean, standard deviation and skewness for variables DFF, PLHT, PNCLE and GRNYLD per level of TPL

DescriptiveStatistics(data = “Gerua”, var = c(“DFF”, “PLHT”, “PNCLE”, “GRNYLD”), grp = “TPL”, statistics = c(“mean”, “sd”, “skew”))

## designAlphaLattice *Alpha Lattice Design*

**Description**

Generate randomization for alpha lattice design using the 4 series formulated by Patterson and Williams.

**Usage**

designAlphaLattice(generate, blksize, r = 2, trial = 1, rowPerBlk, rowPerRep, numFieldRow, serpentine = FALSE, file = NULL)

**Arguments**

generate

blksize

r = 2

trial = 1

rowPerBlk

rowPerRep

numFieldRow

serpentine = FALSE

file = NULL

**Details**

This function uses the DiGGer package.

**Value**

A list with the following components:

fieldbook a data frame containing 7 columns

layout a list whose length is equivalent to the number of trials; each component is a character matrix

plotNum a character matrix

blkNum a character matrix

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## *designAugmentedLSD*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## designAugmentedRCB *Augmented design in Randomized Complete Block*

**Description**

Generate randomization for augmented design in randomized complete block.

**Usage**

designAugmentedRCB(checkTrmt, newTrmt, r = 2, trial = 1, numFieldRow = 2, serpentine = FALSE, factorName = NULL, display = TRUE, file = NULL)

**Arguments**

checkTrmt

newTrmt

r = 2

trial = 1

numFieldRow = 2

serpentine = FALSE

factorName = NULL

display = TRUE

file = NULL

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## designLSD *Randomization for Latin Square Design*

**Description**

Generate randomization for Latin Square design for any number of factors.

**Usage**

designLSD(generate, trial = 1, serpentine = FALSE, display = TRUE, file = NULL)

**Arguments**

generate a list of named object that specify the factors whose levels are to be generated. The component of should be either *i*) a single numeric value that is the number of levels or *ii*) a character vector that contains the labels of the levels of the factors

trial a single numeric value which indicates the number of trial

display logical which indicate whether an output should be displayed in the R console

file a character string indicating the labels for the factors or NULL

**Details**

**Value**

A data frame.

**Author(s)**

Alaine A. Gulles

**Reference(s)**

Package agricolae

**See Also**

designAugmented, designLattice, designCRD, designRCBD, designSplit, designStrip

**Examples**

## generate 10 levels of a factor

designLSD(list(variety = 10))

## generate a randomization for treatment combination of a 10 x 5 factorial experiment replicated 5 times for 3 trials

designLSD (generate = list(variety = 1:10, fertilizer = 5), trial = 3)

## designLatinizedAlpha *Latinized Alpha Lattice Design*

**Description**

Generate randomization for Latinized Alpha Lattice design.

**Usage**

designLatinizedAlpha(generate, blksize, r = 2, trial = 1, numFieldRow, serpentine = FALSE, file = NULL)

**Arguments**

generate

blksize

r = 2

trial = 1

numFieldRow

serpentine = FALSE

file = NULL

**Details**

This function uses the DiGGer package to generate the layout.

**Value**

A list with the following components:

fieldbook a data frame containing 7 columns

layout a list whose length is equivalent to the number of trials; each component is a character matrix

plotNum a character matrix

blkNum a character matrix

**Author(s)**

Alaine A. Gulles

**Reference(s)**

**See Also**

**Examples**

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## designRCBD *Randomization for Randomized Complete Block Design*

**Description**

Generate randomization for randomized complete block design for any number of factors.

**Usage**

designRCBD(generate, r = 2, trial = 1, display = TRUE, file = NULL)

**Arguments**

generate a list of named object that specify the factors whose levels are to be generated. The component of should be either *i*) a single numeric value that is the number of levels or *ii*) a character vector that contains the labels of the levels of the factors

r a single numeric value which indicates the number of replicates

trial a single numeric value which indicates the number of trial

display logical which indicate whether an output should be displayed in the R console

file a character string indicating the labels for the factors or NULL

**Details**

**Value**

A data frame.

**Author(s)**

Alaine A. Gulles

**Reference(s)**

Package agricolae

**See Also**

designAugmented, designLattice, designCRD, designLSD, designSplit, designStrip

**Examples**

## generate 10 levels of a factor

designRCBD(list(variety = 10))

## generate a randomization for treatment combination of a 10 x 5 factorial experiment replicated 5 times for 3 trials

designRCBD (generate = list(variety = 1:10, fertilizer = 5), r = 5, trial = 3)

## *designRowColumn*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## *doQTL\_BIM*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## *doQTL\_CIM*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## *doQTL\_IM*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## *doQTL\_MQM*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## *doQTLanalysis*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## *isContrast* Is Contrast?

**Description**

Determine if the linear function is a contrast or not.

**Usage**

isContrast( contrast)

**Arguments**

contrast

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## *isOrthogonal* Is Orthogonal?

**Description**

Determine if the contrast are all pairwise orthogonal contrast .

**Usage**

isOrthogonal( contrast)

**Arguments**

contrast

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## GEOneStage.test *GxE One Stage Analysis*

**Description**

This function performs multi-environment analysis.

**Usage**

GEOneStage.test(exptl.design = c("RCB", "AugRCB", "AugLS", "Alpha", "RowCol", "LatinAlpha", "LatinRowCol"), data, respvar, geno, row, column = NULL, rep = NULL, env, is.genoRandom = FALSE)

**Arguments**

exptl.design a character string indicating the experimental design to be used and must be one of the following: "RCB" (Randomized Complete Block Design, default), "AugRCB" (Augmented Randomized Complete Block Design), "AugLS" (Augmented Latin Square Design), "Alpha" (Alpha Lattice Design), "RowCol" (Row-Column Design), "LatinAlpha" (Latinized Alpha Lattice Design), or "LatinRowCol" (Latinized Row-Column Design)

data a non-null character string which indicates the name of the data frame containing the variables specified in respvar, geno, row, column, rep and env

respvar a non-empty character vector which indicates the response variable(s) to be used in the analysis

geno a non-empty character vector which indicates the genotype to be used in the analysis

row a non-empty a character vector which indicate the blocking factor for RCB and AugRCB or the row blocking factor for AugLS, RowCol, LatinAlpha and LatinRowCol

column NULL or a character vector which indicate the column blocking factor

rep NULL or a character vector which indicate the replicate

env a non-null character vector which indicate the by variable

is.genoRandom logical with FALSE as default value indicating whether the genotype/treatment will be considered as random or not

**Details**

**Value**

A list containing the following components:

output a list containing the following components:

respvar response variable

nlevelsGeno number of levels of the genotype

nlevelsEnv number of levels of the environment variable

recodedLevels logical whether the levels of the genotype has been recoded

obsread number of observations read

obsused number of observations used in the analysis

responseRate response rate

formula1 formula used in the analysis

model a lmerMod class object

varcomp.table variance covariance table

formula2 formula used for testing the significance of the genotype

testsig.Geno a anova and data frame class object used for testing the significance of the genotypic effect

formula3 formula used for testing the significance of the environment

testing.Env a anova and data frame class object used for testing the significance of the environment effect

formula4 formula used for testing whether there is an interaction between the genotype and the environment

testsig.GenoEnv a anova and data frame class object used for testing whether there is a GxE interaction

means.GenoEnvCode a data frame

residuals a named vector of residuals

fitted values a named vector of predicted values

data data used in the analysis

harmonicMeans harmonic means

MSE mean square error

meansGenoEnv.all a data frame which contains the means of genotype per environment for all response variable performed in the analysis

meansGenoEnvWarning a character vector which indicates whether the component meansGenoEnv.all is empty or not

means.Geno.all a data frame which contains the means and standard error of genotype for all levels of environment for all response variable performed in the analysis

meansGenoWarning a character vector which indicates whether the component means.Geno.all is empty or not

**Author(s)**

Violeta I. Bartolome, Alaine A. Gulles, Rose Imee Zhella A. Morantte, Nellwyn L. Sales

**Reference(s)**

**See Also**

**Examples**

## GEOneStage\_resid *GxE One Stage Residuals*

**Description**

This function consolidates the residuals generated by running GEOneStage.test

**Usage**

GEOneStage\_resid(geOneResult, respvar, is.genoRandom = FALSE)

**Arguments**

geOneResult

respvar

is.genoRandom = FALSE

**Details**

**Value**

A list containing the following components:

residuals a data frame

ge1residWarning a character string indicating whether the component residuals is empty or not

**Author(s)**

Alaine A. Gulles, Rose Imee Zhella A. Morantte, Nellwyn L. Sales

**Reference(s)**

**See Also**

**Examples**

## GETwoStage.dataRecode *Recoding dataset for GxE Two Stage Analysis*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## GETwoStage.test *GxE Two Stage Analysis*

**Description**

This function performs multi-environment two-stage test.

**Usage**

GETwoStage.test(data, respvar, stderr = NULL, sigma2, numrep, geno, env, weight = c("none", "stderr", "stdmean"), is.genoRandom = FALSE)

**Arguments**

data a non-null character string which indicates the name of the data frame containing the variables specified in respvar, geno, row, column, rep and env

respvar a non-empty character vector which indicates the response variable(s) to be used in the analysis

stderr NULL or a character vector which indicates the standard error to be used in the analysis

sigma2 a non-empty character vector which indicates the variance to be used in the analysis

numrep a non-empty character vector which indicates the column name of the number of replicates to be used in the analysis

geno a non-empty character vector which indicates the genotype to be used in the analysis

env a non-null character vector which indicate the by variable

geno a non-empty character string which indicates the weight to be used for the analysis and must be one of the following: "none", "stderr", or "stdmean".

is.genoRandom logical with FALSE as default value indicating whether the genotype/treatment will be considered as random or not

**Details**

**Value**

A list whose length is equivalent to the number of response variable used in the analysis. Each list contains the following components:

respvar a character string indicating the response variable

obsread a numeric value indicating the number of observation that was read in the data set for a particular response variable

obsused a numeric value indicating the number of observation that was used in the analysis for a particular response variable

responseRate a numeric value indicating the response rate

nlevelsGeno number of levels of genotype

nlevelsEnv number of levels of environment

recodedLevels logical indicating whether the levels of the genotype are recoded or not

formula1

model

varcomp.table

sedTable

means.Geno

means.Env

residuals

fitted.values

data

**Author(s)**

Violeta I. Bartolome, Alaine A. Gulles, Rose Imee Zhella A. Morantte, Nellwyn L. Sales

**Reference(s)**

**See Also**

**Examples**

## GETwoStage\_resid *GxE Two Stage Residuals*

**Description**

This function consolidates the residuals generated by running GETwoStage.test

**Usage**

GETwoStage\_resid(ge2sout, respvar, is.genoRandom = FALSE)

**Arguments**

ge2sout result from the function GETwoStage.test

respvar a character vector indicating the response variable used in the analysis

is.genoRandom logical indicating whether the genotype will be treated as random or not

**Details**

**Value**

A list containing the following components:

residuals a data frame

ge2residWarning a character string indicating whether the component residuals is empty or not

**Author(s)**

Alaine A. Gulles, Rose Imee Zhella A. Morantte, Nellwyn L. Sales

**Reference(s)**

**See Also**

**Examples**

## *getVarInfo* Get Variable Information

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## genoNpheno.corr *Genotypic and Phenotypic Correlation*

**Description**

This function outputs genotypic and phenotypic correlation.

**Usage**

**genoNpheno.corr(exptl.design = c("RCB", "AugRCB", "AugLS", "Alpha", "RowCol", "LatinAlpha", "LatinRowCol"), data, respvar, geno, row, column = NULL, rep = NULL, env, excludeLevels = FALSE, excludeList = NULL)**

**Arguments**

exptl.design a character string indicating the experimental design to be used and must be one of the following: "RCB" (Randomized Complete Block Design, default), "AugRCB" (Augmented Randomized Complete Block Design), "AugLS" (Augmented Latin Square Design), "Alpha" (Alpha Lattice Design), "RowCol" (Row-Column Design), "LatinAlpha" (Latinized Alpha Lattice Design), or "LatinRowCol" (Latinized Row-Column Design)

data a non-null character string which indicates the name of the data frame containing the variables specified in respvar, geno, row, column, rep and env

respvar a non-empty character vector which indicates the response variable(s) to be used in the analysis

geno a non-empty character vector which indicates the genotype to be used in the analysis

row a non-empty a character vector which indicate the blocking factor for RCB and AugRCB or the row blocking factor for AugLS, RowCol, LatinAlpha and LatinRowCol

column NULL or a character vector which indicate the column blocking factor

rep NULL or a character vector which indicate the replicate

env NULL or a character vector which indicate the by variable

excludeCheck logical with FALSE as default value indicating whether checks will be excluded

excludelist NULL or a character vector which indicate the levels of genotype that will be considered as checks

**Details**

**Value**

A list containing the following components:

EnvLevels

GenoCorr a matrix indicating the genotypic correlation between variables

PhenoCorr a matrix indicating the phenotypic correlation between variables

NumObs

**Author(s)**

Alaine A. Gulles, Rose Imee Zhella A. Morantte, Nellwyn L. Sales

**Reference(s)**

**See Also**

**Examples**

## graphLine *Response Plot*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## graph\_sea\_boxhist *Create box plot or histogram*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## graph\_sea\_diagplots *Create box plot or histogram*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## Heatmap *Test for Homogeneity of Variances*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## is.wholenumber *Wholenumber*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## *manageQTLmissing*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## modelComparisonTable *Model Comparison*

**Description**

This functions constructs model comparison table when model1 and model2 are fitted using REML = TRUE and the terms to be tested is random

**Usage**

modelComparisonTable(model1, model2)

**Arguments**

model1 resulting R object when lmer function is called using REML = TRUE (full model)

model2 resulting R object when lmer function is called using REML = TRUE (full model)

**Details**

**Value**

A data frame

**Author(s)**

Nellwyn L. Sales

**Reference(s)**

**See Also**

**Examples**

## printDataFrame *Printing Data Frames*

**Description**

Print a data frame.

**Usage**

printDataFrame(data)

**Arguments**

data object of class data.frame

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

print

data.frame

**Examples**

## printLayout *Print Layout*

**Description**

Print randomization layout.

**Usage**

printLayout(trmt, plotNum, RowLabel = NULL, ColLabel = NULL, title = NULL)

**Arguments**

trmt an R object

plotNum an R object

RowLabel NULL or an R object

ColLabel NULL or an R object

title NULL or a character string which indicate the label for each layout to be printed

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

RCBD1 <- designRCBD(generate = list(A = 4), r = 2, trial = 1, numFieldRow = 4, rowPerBlk = 4, serpentine = TRUE, display = TRUE, file = "RCBDOneFactor.csv")

printLayout(trmt = RCBD1$layout[[1]], plotNum = RCBD1$plotNum, RowLabel = rownames(RCBD1$layout[[1]]), ColLabel = colnames(RCBD1$layout[[1]]))

## *QTL\_dataprep*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## *qtl\_cimwur*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## SortCases *Sort the observation of a dataset*

**Description**

This function rearranges the observation of the data frame based on the value of one or more sorting variables.

**Usage**

SortCases(data, var, grp, sortBy = “ascending”)

**Arguments**

data a data frame or name of the data frame

var a non-empty character vector which indicates the variable(s) which will be the basis for sorting the data frame

sortBy a character string or vector which indicates the order by which the variable will be sorted. Possible value are “ascending” and/or “descending”

**Details**

If var contains more than one item, observations are sorted for each variable within categories of the preceding variable of the argument var. Further, each variable can be rearrange in ascending or descending order, with ascending order as the default option.

The default value for sortBy is ascending. The arguments var and sortBy must be of the same length. Incase var contains more than one item and sortBy has only one item, the variables will be rearrange according to sortBy. If sortBy contains more items than var, the programs creates a new vector of sortBy with the same length as var. If var contains more items than sortBy, the programs creates a new vector of sortBy with the same length as var

**Value**

A data frame.

**Author(s)**

Alaine A. Gulles

**Reference(s)**

**See Also**

**Examples**

## ssa.pairwise *Pairwise Mean Comparisons after Single Site Analysis*

**Description**

This function performs pairwise mean comparison for single site analysis.

**Usage**

ssa.pairwise(model, type = "Tukey", alpha = 0.05, control.level = NULL)

**Arguments**

model resulting R object from the ssa.test function

type a character string indicating the type of pairwise mean comparison to be performed and must be one of the following: "Tukey" (default value) or "Dunnett"

alpha = 0.05 a single numeric value with 0.5 as the default value indicating the level of significance to be used when one perform the pairwise mean comparison

control.level NULL or a character vector indicating the levels of genotype or treatment to be considered as controls

**Details**

If control.level = NULL and the levels of the treatment is at most 15, will perform all pairwise mean comparison using the Tukey method.

**Value**

A list containing the following components:

result a data frame containing the pairs of treatment that are significantly different at specified level of significance

controlTestWarning a character vector indicating the warning messages encountered when the analysis is performed, if any

**Author(s)**

Alaine A. Gulles, Rose Imee Zhella A. Morantte, Nellwyn L. Sales

**Reference(s)**

**See Also**

**Examples**

## ssa.resid *Residuals for Single SiteAnalysis*

**Description**

This function is for consolidating residuals from single site analysis.

**Usage**

ssa.resid(data, ssaResult, respvar, env, is.genoRandom = FALSE)

**Arguments**

data a non-null character string which indicates the name of the data frame to be used for the analysis

ssaResult resulting R object from the ssa.test function

respvar a non-empty character vector which indicates the response variable(s) to be used in the analysis

env a character vector which indicate the by variable

is.genoRandom logical with FALSE as default value indicating whether the genotype/treatment will be considered as random or not

**Details**

**Value**

A list containing the following components:

residuals a data frame

residWarning a character vector indicating the warning messages encountered when the analysis is performed, if any

**Author(s)**

Alaine A. Gulles, Rose Imee Zhella A. Morantte, Nellwyn L. Sales

**Reference(s)**

**See Also**

**Examples**

## ssa.test *Single Site Analysis*

**Description**

This function performs single-environment analysis

**Usage**

ssa.test(exptl.design = c("RCB", "AugRCB", "AugLS", "Alpha", "RowCol", "LatinAlpha", "LatinRowCol"), data, respvar, geno, row, column = NULL, rep = NULL, env = NULL, is.random = FALSE, excludeCheck=FALSE, checkList = NULL)

**Arguments**

exptl.design a character string indicating the experimental design to be used and must be one of the following: "RCB" (Randomized Complete Block Design, default), "AugRCB" (Augmented Randomized Complete Block Design), "AugLS" (Augmented Latin Square Design), "Alpha" (Alpha Lattice Design), "RowCol" (Row-Column Design), "LatinAlpha" (Latinized Alpha Lattice Design), or "LatinRowCol" (Latinized Row-Column Design)

data a non-null character string which indicates the name of the data frame containing the variables specified in respvar, geno, row, column, rep and env

respvar a non-empty character vector which indicates the response variable(s) to be used in the analysis

geno a non-empty character vector which indicates the genotype to be used in the analysis

row a non-empty a character vector which indicate the blocking factor for RCB and AugRCB or the row blocking factor for AugLS, RowCol, LatinAlpha and LatinRowCol

column NULL or a character vector which indicate the column blocking factor

rep NULL or a character vector which indicate the replicate

env NULL or a character vector which indicate the by variable

is.random logical with FALSE as default value indicating whether the genotype/treatment will be considered as random or not

excludeCheck logical with FALSE as default value indicating whether checks will be excluded

checklist NULL or a character vector which indicate the levels of genotype that will be considered as checks

**Details**

**Value**

**Author(s)**

Violeta I. Bartolome, Alaine A. Gulles, Rose Imee Zhella A. Morantte, Nellwyn L. Sales

**Reference(s)**

**See Also**

**Examples**

## *testQTLsegregation*

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

## trimStrings

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

**Description**

**Usage**

**Arguments**

**Details**

**Value**

**Author(s)**

**Reference(s)**

**See Also**

**Examples**

**DATA SET**

## Gerua *Gerua*

**Description**

**Formats**

This data frame contains the following columns:

REP a factor with 3 levels (1 to 3) denoting the replicates

TPL a factor with 2 levels (D and N)

CULT a factor with 26 levels

DFF a numeric vector of number of days after flowering

PLHT a numeric vector of plant height

PNCLE a numeric vector of number of panicle

GRNYLD a numeric vector of grain yield

**Details**

**Source**

**Examples**