

Package ‘biometryassist’

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Type Package

Title Functions to Assist Design and Analysis of Agronomic Experiments

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Description Provides functions to aid in the design and analysis of agronomic and agricultural experiments through easy access to documentation and helper functions, especially for users who are learning these concepts.

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URL <https://biometryhub.github.io/biometryassist/>

BugReports <https://github.com/biometryhub/biometryassist/issues>

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design	<i>Produces an experimental design with graph of design layout and skeletal ANOVA table</i>
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Description

Produces an experimental design with graph of design layout and skeletal ANOVA table

Usage

```
design(
  type,
  treatments,
  reps,
  nrows,
  ncols,
  brows = NA,
  bcols = NA,
  byrow = TRUE,
  sub_treatments = NULL,
  fac.names = NULL,
  fac.sep = c("", " "),
  plot = TRUE,
  rotation = 0,
  size = 4,
  margin = FALSE,
  save = FALSE,
  savename = paste0(type, "_design"),
  plottype = "pdf",
  seed = TRUE,
  quiet = FALSE,
  ...
)
```

Arguments

<code>type</code>	The type of design. Supported design types are <code>crd</code> , <code>rcbd</code> , <code>lsd</code> , <code>crossed:<type></code> where <code><type></code> is one of the previous types and <code>split</code> . See Details for more information.
<code>treatments</code>	A vector containing the treatment names or labels.
<code>reps</code>	The number of replicates. Not required for Latin Squared Designs.
<code>nrows</code>	The number of rows in the design.
<code>ncols</code>	The number of columns in the design.
<code>brows</code>	For RCBD and Split Plot designs. The number of rows in a block.
<code>bcols</code>	For RCBD and Split Plot designs. The number of columns in a block.
<code>byrow</code>	For split-plot only. Logical (default TRUE). Provides a way to arrange plots within whole-plots when there are multiple possible arrangements.
<code>sub_treatments</code>	A vector of treatments for subplots in a split plot design.
<code>fac.names</code>	Allows renaming of the A level of factorial designs (i.e. those using <code>agricolae::design.ab()</code>) by passing (optionally named) vectors of new labels to be applied to the factors within a list. See examples and details for more information.
<code>fac.sep</code>	The separator used by <code>fac.names</code> . Used to combine factorial design levels. If a vector of 2 levels is supplied, the first separates factor levels and label, and the second separates the different factors.
<code>plot</code>	Logical (default TRUE). If TRUE, display a plot of the generated design. A plot can always be produced later using <code>autoplot()</code> .
<code>rotation</code>	Rotate the text output as Treatments within the plot. Allows for easier reading of long treatment labels. Takes positive and negative values being number of degrees of rotation from horizontal.
<code>size</code>	Increase or decrease the text size within the plot for treatment labels. Numeric with default value of 4.
<code>margin</code>	Logical (default FALSE). Expand the plot to the edges of the plotting area i.e. remove white space between plot and axes.
<code>save</code>	One of FALSE (default)/"none", TRUE/"both", "plot" or "workbook". Specifies which output to save.
<code>savename</code>	A filename for the design to be saved to. Default is the type of the design combined with "_design".
<code>plottype</code>	The type of file to save the plot as. Usually one of "pdf", "png", or "jpg". See <code>ggplot2::ggsave()</code> for all possible options.
<code>seed</code>	Logical (default TRUE). If TRUE, return the seed used to generate the design. If a numeric value, use that value as the seed for the design.
<code>quiet</code>	Logical (default FALSE). Hide the output.
<code>...</code>	Additional parameters passed to <code>ggplot2::ggsave()</code> for saving the plot.


```

# Factorial Design (Crossed, Randomised Complete Block Design), changing separation between factors
des.out <- design(type = "crossed:rcbd", treatments = c(3, 2),
                 reps = 3, nrows = 6, ncols = 3,
                 brows = 6, bcols = 1,
                 seed = 42, fac.sep = c(":", "_"))

# Factorial Design (Nested, Latin Square)
des.out <- design(type = "lsd", treatments = c("A1", "A2", "A3", "A4", "B1", "B2", "B3"),
                 nrows = 7, ncols = 7, seed = 42)

# Split plot design
des.out <- design(type = "split", treatments = c("A", "B"), sub_treatments = 1:4,
                 reps = 4, nrows = 8, ncols = 4, brows = 4, bcols = 2, seed = 42)

# Alternative arrangement of the same design as above
des.out <- design(type = "split", treatments = c("A", "B"), sub_treatments = 1:4,
                 reps = 4, nrows = 8, ncols = 4, brows = 4, bcols = 2,
                 byrow = FALSE, seed = 42)

```

des_info

Produces graph of design layout, skeletal ANOVA table and data frame with complete design

Description

Produces graph of design layout, skeletal ANOVA table and data frame with complete design

Usage

```

des_info(
  design.obj,
  nrows,
  ncols,
  brows = NA,
  bcols = NA,
  byrow = TRUE,
  fac.names = NULL,
  fac.sep = c("", " "),
  plot = TRUE,
  rotation = 0,
  size = 4,
  margin = FALSE,
  save = FALSE,
  savename = paste0(design.obj$parameters$design, "_design"),
  plottype = "pdf",
  return.seed = TRUE,
  quiet = FALSE,

```

```
    ...
  )
```

Arguments

design.obj	An agricolae design object.
nrows	The number of rows in the design.
ncols	The number of columns in the design.
brows	For RCBD only. The number of rows in a block.
bcols	For RCBD only. The number of columns in a block.
byrow	For split-plot only. Logical (default: TRUE). Provides a way to arrange plots within whole-plots when there are multiple possible arrangements.
fac.names	Allows renaming of the A level of factorial designs (i.e. those using <code>agricolae::design.ab()</code>) by passing (optionally named) vectors of new labels to be applied to the factors within a list. See examples and details for more information.
fac.sep	The separator used by <code>fac.names</code> . Used to combine factorial design levels. If a vector of 2 levels is supplied, the first separates factor levels and label, and the second separates the different factors.
plot	Logical (default TRUE). If TRUE, display a plot of the generated design. A plot can always be produced later using <code>autoplot()</code> .
rotation	Rotate the text output as Treatments within the plot. Allows for easier reading of long treatment labels. Takes positive and negative values being number of degrees of rotation from horizontal.
size	Increase or decrease the text size within the plot for treatment labels. Numeric with default value of 4.
margin	Logical (default FALSE). Expand the plot to the edges of the plotting area i.e. remove white space between plot and axes.
save	One of FALSE (default)/"none", TRUE/"both", "plot" or "workbook". Specifies which output to save.
savename	A filename for the design to be saved to. Default is the type of the design combined with "_design".
plottype	The type of file to save the plot as. Usually one of "pdf", "png", or "jpg". See <code>ggplot2::ggsave()</code> for all possible options.
return.seed	Logical (default TRUE). Output the seed used in the design?
quiet	Logical (default FALSE). Return the objects without printing output.
...	Additional parameters passed to <code>ggplot2::ggsave()</code> for saving the plot.

Details

If `save = TRUE` (or "both"), both the plot and the workbook will be saved to the current working directory, with filename given by `savename`. If one of either "plot" or "workbook" is specified, only that output is saved. If `save = FALSE` (the default, or equivalently "none"), nothing will be output.

fac.names can be supplied to provide more intuitive names for factors and their levels in factorial designs. They should be specified in a list format, for example `fac.names = list(A_names = c("a", "b", "c"), B_names = c("x", "y", "z"))`. This will result a design output with a column named A_names with levels a, b, c and another named B_names with levels x, y, z. Only the first two elements of the list will be used.

If `fac.sep` is a single element (e.g. `" "`), *this is used to separate all factor labels (e.g. A_1_B_1)*. If it is two elements (e.g. `c(" ", " ")`), the first element separates the factor names and their levels, and the second level separates the two factors (e.g. A1_B1).

... allows extra arguments to be passed to `ggsave` for output of the plot. The details of possible arguments can be found in [ggplot2::ggsave\(\)](#).

Value

A list containing a data frame with the complete design, a `ggplot` object with plot layout, the seed (if `return.seed = TRUE`), and the `satab` object, allowing repeat output of the `satab` table via `cat(output$satab)`.

Examples

```
library(agricolae)

# Completely Randomised Design
trt <- c(1, 5, 10, 20)
rep <- 5
outdesign <- design.crd(trt = trt, r = rep, seed = 42)
des.out <- des_info(design.obj = outdesign, nrows = 4, ncols = 5)

# Randomised Complete Block Design
trt <- LETTERS[1:11]
rep <- 4
outdesign <- design.rcbd(trt = trt, r = rep, seed = 42)
des.out <- des_info(
  design.obj = outdesign, nrows = 11,
  ncols = 4, brows = 11, bcols = 1
)

# Latin Square Design
trt <- c("S1", "S2", "S3", "S4")
outdesign <- design.lsd(trt)
des.out <- des_info(design.obj = outdesign, nrows = 4, ncols = 4)

# Factorial Design (Crossed, Completely Randomised)
trt <- c(3, 2) # Factorial 3 x 2
rep <- 3
outdesign <- design.ab(trt, r = rep, design = "crd")
des.out <- des_info(design.obj = outdesign, nrows = 6, ncols = 3)

# Factorial Design (Crossed, Completely Randomised), renaming factors
trt <- c(3, 2) # Factorial 3 x 2
rep <- 3
outdesign <- design.ab(trt, r = rep, design = "crd")
```

```

des.out <- des_info(design.obj = outdesign, nrows = 6, ncols = 3,
                  fac.names = list(N = c(50, 100, 150),
                                   Water = c("Irrigated", "Rain-fed")))

# Factorial Design (Nested, Latin Square)
trt <- c("A1", "A2", "A3", "A4", "B1", "B2", "B3")
outdesign <- design.lsd(trt)
des.out <- des_info(design.obj = outdesign, nrows = 7, ncols = 7)

# Split plot design
trt1 <- c("A", "B")
trt2 <- 1:4
rep <- 4
outdesign <- design.split(trt1, trt2, r = rep)
des.out <- des_info(design.obj = outdesign, nrows = 8, ncols = 4, brows = 4, bcols = 2)

```

install_asreml

Install or Update the ASReML-R package

Description

Helper functions for installing or updating the ASReML-R package, intended to reduce the difficulty of finding the correct version for your operating system and R version.

Usage

```

install_asreml(
  library = .libPaths()[1],
  quiet = FALSE,
  force = FALSE,
  keep_file = FALSE
)

update_asreml(...)

```

Arguments

library	Library location to install ASReML-R. Uses first option in <code>.libPaths()</code> by default.
quiet	Logical (default FALSE). Should package be installed quietly?
force	Logical (default FALSE). Force ASReML-R to install. Useful for upgrading if it is already installed.
keep_file	Should the downloaded asreml package file be kept? Default is FALSE. TRUE downloads to current directory. A file path can also be provided to save to another directory. See Details for more information.
...	other arguments passed to <code>install_asreml()</code>

Details

The ASReml-R package file is downloaded from a shortlink, and if `keep_file` is TRUE, the package archive file will be saved in the current directory. If a valid path is provided in `keep_file`, the file will be saved to that path, but directory is assumed to exist and will not be created. If `keep_file` does not specify an existing, valid path, an error will be shown.

Value

Silently returns TRUE if `asreml` installed successfully or already present, FALSE otherwise. Optionally prints a confirmation message on success.

Examples

```
## Not run:
# Example 1: download and install asreml
install_asreml()

# Example 2: install asreml and save file for later
install_asreml(keep_file = TRUE)

## End(Not run)
```

logl_test

Log-likelihood test for comparing terms in ASReml-R models

Description

Log-likelihood test for comparing terms in ASReml-R models

Usage

```
logl_test(
  model.obj,
  rand.terms = NULL,
  resid.terms = NULL,
  decimals = 3,
  numeric = FALSE,
  quiet = FALSE
)
```

Arguments

<code>model.obj</code>	An ASReml-R model object
<code>rand.terms</code>	Random terms from the model. Default is NULL.
<code>resid.terms</code>	Residual terms from the model. Default is NULL.
<code>decimals</code>	Controls rounding of decimal places in output. Default is 3 decimal places.

numeric	Return p-values as numeric? Default is that they are characters, where very small values shown as less than a small number. See details for more.
quiet	Logical (default: FALSE). Hide warnings and messages?

Details

Typically p-values cannot be 0, and are usually just below some threshold of accuracy in calculation of probability.

Value

A dataframe containing the results of the test.

Examples

```
## Not run:
library(asreml)
dat <- asreml::oats
dat <- dat[order(dat$Row, dat$Column),]

#Fit ASReml Model
model.asr <- asreml(yield ~ Nitrogen + Variety + Nitrogen:Variety,
                    random = ~ Blocks + Blocks:Wplots,
                    residual = ~ ar1(Row):ar1(Column),
                    data = dat)

oats.logl <- logl_test(
  model.obj = model.asr, rand.terms = c("Blocks", "Blocks:Wplots"),
  resid.terms = c("ar1(Row)", "ar1(Column)")
)
oats.logl

## End(Not run)
```

multiple_comparisons *Multiple Comparison Tests*

Description

A function for comparing and ranking predicted means with Tukey's Honest Significant Difference (HSD) Test.

Usage

```
multiple_comparisons(
  model.obj,
  classify,
  sig = 0.05,
  int.type = "ci",
```

```

    trans = NA,
    offset = NA,
    decimals = 2,
    descending = FALSE,
    plot = FALSE,
    label_height = 0.1,
    rotation = 0,
    save = FALSE,
    savename = "predicted_values",
    order,
    pred.obj,
    pred,
    ...
  )

```

Arguments

model.obj	An ASReml-R or aov model object. Will likely also work with <code>lme</code> (<code>nlme::lme()</code>), <code>lmerMod</code> (<code>lme4::lmer()</code>) models as well.
classify	Name of predictor variable as string.
sig	The significance level, numeric between 0 and 1. Default is 0.05.
int.type	The type of confidence interval to calculate. One of <code>ci</code> , <code>1se</code> or <code>2se</code> . Default is <code>ci</code> .
trans	Transformation that was applied to the response variable. One of <code>log</code> , <code>sqrt</code> , <code>logit</code> or <code>inverse</code> . Default is <code>NA</code> .
offset	Numeric offset applied to response variable prior to transformation. Default is <code>NA</code> . Use 0 if no offset was applied to the transformed data. See Details for more information.
decimals	Controls rounding of decimal places in output. Default is 2 decimal places.
descending	Logical (default <code>FALSE</code>). Order of the output sorted by the predicted value. If <code>TRUE</code> , largest will be first, through to smallest last.
plot	Automatically produce a plot of the output of the multiple comparison test? Default is <code>FALSE</code> . This is maintained for backwards compatibility, but the preferred method now is to use <code>autoplot(<multiple_comparisons output>)</code> . See <code>autoplot.mct()</code> for more details.
label_height	Height of the text labels above the upper error bar on the plot. Default is 0.1 (10%) of the difference between upper and lower error bars above the top error bar.
rotation	Rotate the text output as Treatments within the plot. Allows for easier reading of long treatment labels. Number between 0 and 360 (inclusive) - default 0
save	Logical (default <code>FALSE</code>). Save the predicted values to a csv file?
savename	A file name for the predicted values to be saved to. Default is <code>predicted_values</code> .
order	Deprecated. Use <code>descending</code> instead.
pred.obj	Deprecated. Predicted values are calculated within the function from version 1.0.1 onwards.

pred Deprecated. Use `classify` instead.
 ... Other arguments passed through to `predict.asreml()`.

Details

Some transformations require that data has a small offset applied, otherwise it will cause errors (for example taking a log of 0, or square root of negative values). In order to correctly reverse this offset, if the `trans` argument is supplied, an offset value must also be supplied. If there was no offset required for a transformation, then use a value of 0 for the `offset` argument.

Value

A list containing a data frame with predicted means, standard errors, confidence interval upper and lower bounds, and significant group allocations (named `predicted_values`), as well as a plot visually displaying the predicted values (named `predicted_plot`). If some of the predicted values are aliased, a warning is printed, and the aliased treatment levels are returned in the output (named `aliased`).

References

Jørgensen, E. & Pedersen, A. R. How to Obtain Those Nasty Standard Errors From Transformed Data - and Why They Should Not Be Used. <https://citeseerx.ist.psu.edu/viewdoc/download?doi=10.1.1.47.9023&rep=rep1&type=pdf>

Examples

```
# Fit aov model
model <- aov(Petal.Length ~ Species, data = iris)

# Display the ANOVA table for the model
anova(model)

# Determine ranking and groups according to Tukey's Test
pred.out <- multiple_comparisons(model, classify = "Species")

# Display the predicted values table
pred.out

# Show the predicted values plot
autoplot(pred.out, label_height = 0.5)

## Not run:
# ASReML-R Example
library(asreml)

#Fit ASReML Model
model.asr <- asreml(yield ~ Nitrogen + Variety + Nitrogen:Variety,
                   random = ~ Blocks + Blocks:Wplots,
                   residual = ~ units,
```

```
data = asreml::oats)

wald(model.asr) #Nitrogen main effect significant

#Determine ranking and groups according to Tukey's Test
pred.out <- multiple_comparisons(model.obj = model.asr, classify = "Nitrogen",
                                descending = TRUE, decimals = 5)

pred.out
## End(Not run)
```

print.mct

Print method for multiple_comparisons

Description

Print method for multiple_comparisons

Usage

```
## S3 method for class 'mct'
print(x, ...)
```

Arguments

x An mct object to print to the console.
... Arguments passed to methods.

Value

The original object invisibly.

See Also

[multiple_comparisons\(\)](#)

Examples

```
dat.aov <- aov(Petal.Width ~ Species, data = iris)
output <- multiple_comparisons(dat.aov, classify = "Species")
print(output)
```

`resplot`*Residual plots of linear models.*

Description

Produces plots of residuals for assumption checking of linear (mixed) models.

Usage

```
resplot(  
  model.obj,  
  shapiro = TRUE,  
  call = FALSE,  
  label.size = 10,  
  axes.size = 10,  
  call.size = 9,  
  mod.obj  
)
```

Arguments

<code>model.obj</code>	An aov, lm, lme (<code>nlme::lme()</code>), lmerMod (<code>lme4::lmer()</code>), asreml or mmer (sommer) model object.
<code>shapiro</code>	(Logical) Display the Shapiro-Wilks test of normality on the plot?
<code>call</code>	(Logical) Display the model call on the plot?
<code>label.size</code>	A numeric value for the size of the label (A,B,C) font point size.
<code>axes.size</code>	A numeric value for the size of the axes label font size in points.
<code>call.size</code>	A numeric value for the size of the model displayed on the plot.
<code>mod.obj</code>	Deprecated to be consistent with other functions. Please use <code>model.obj</code> instead.

Value

A list containing ggplot2 objects which are diagnostic plots.

Examples

```
dat.aov <- aov(Petal.Length ~ Petal.Width, data = iris)  
resplot(dat.aov)  
resplot(dat.aov, call = TRUE)
```

variogram	<i>Variogram plots for spatial models.</i>
-----------	--

Description

Produces variogram plots for checking spatial trends.

Usage

```
variogram(  
  model.obj,  
  row = NA,  
  column = NA,  
  horizontal = TRUE,  
  palette = "default"  
)
```

Arguments

model.obj	An asreml model object.
row	A row variable.
column	A column variable.
horizontal	Logical (default TRUE). The direction the plots are arranged. The default TRUE places the plots above and below, while FALSE will place them side by side.
palette	A string specifying the colour scheme to use for plotting. The default value ("default") is equivalent to "rainbow". Colour blind friendly palettes can also be provided via options "colour blind" (or "color blind", both equivalent to "viridis"), "magma", "inferno", "plasma" or "cividis". The "Spectral" palette from <code>scales::brewer_pal()</code> is also possible.

Value

A ggplot2 object.

References

- S. P. Kaluzny, S. C. Vega, T. P. Cardoso, A. A. Shelly, "S+SpatialStats: User's Manual for Windows® and UNIX®" *Springer New York*, 2013, p. 68, <https://books.google.com.au/books?id=iADkBwAAQBAJ>.
- A. R. Gilmour, B. R. Cullis, A. P. Verbyla, "Accounting for Natural and Extraneous Variation in the Analysis of Field Experiments." *Journal of Agricultural, Biological, and Environmental Statistics* 2, no. 3, 1997, pp. 269–93, <https://doi.org/10.2307/1400446>.

Examples

```
## Not run:
library(asreml)
oats <- asreml::oats
oats <- oats[order(oats$Row, oats$Column),]
model.asr <- asreml(yield ~ Nitrogen + Variety + Nitrogen:Variety,
                    random = ~ Blocks + Blocks:Wplots,
                    residual = ~ ar1(Row):ar1(Column),
                    data = oats)
variogram(model.asr)

## End(Not run)
```


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