

Package ‘inti’

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Type Package

Version 0.6.3

Title Tools and Statistical Procedures in Plant Science

Description The 'inti' package is part of the 'inkaverse' project for developing different procedures and tools used in plant science and experimental designs. The main aim of the package is to support researchers during the planning of experiments and data collection (`tarpu()`), data analysis and graphics (`yupana()`), and technical writing.

Learn more about the 'inkaverse' project at [<https://inkaverse.com/>](https://inkaverse.com/).

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URL <https://inkaverse.com/>, <https://github.com/flavjack/inti>

BugReports <https://github.com/flavjack/inti/issues/>

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DT

Suggests gsheets, knitr, rmarkdown, bookdown

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R topics documented:

colortext	2
design_noreps	3
design_repblock	4
figure2qmd	6
figure2rmd	7
footnotes	7
gdoc2qmd	8
H2cal	8
include_pdf	11
include_table	11
jc_tombola	12
mean_comparison	13
met	14
metamorphosis	15
outliers_remove	16
plot_diag	17
plot_raw	18
plot_smr	20
potato	22
split_folder	23
table2qmd	24
table2rmd	24
tarpuuy	25
tarpuuy_design	25
tarpuuy_plex	27
tarpuuy_plotdesign	29
tarpuuy_traits	30
web_table	32
yupana	33
yupana_analysis	34
yupana_export	35
yupana_import	37
yupana_mvr	38
yupana_reshape	39
Index	41

colortext

Colourise text for display in the terminal

Description

If R is not currently running in a system that supports terminal colours the text will be returned unchanged.

Usage

```
colortext(text, fg = "red", bg = NULL)
```

Arguments

text	character vector
fg	foreground colour, defaults to white
bg	background colour, defaults to transparent

Details

Allowed colours are: black, blue, brown, cyan, dark gray, green, light blue, light cyan, light gray, light green, light purple, light red, purple, red, white, yellow

Author(s)

testthat package

Examples

```
print(colortext("Red", "red"))
cat(colortext("Red", "red"), "\n")
cat(colortext("White on red", "white", "red"), "\n")
```

design_noreps

Experimental design without replications

Description

Function to deploy field-book experiment without replications

Usage

```
design_noreps(  
  factors,  
  type = "sorted",  
  zigzag = FALSE,  
  nrows = NA,  
  serie = 100,  
  seed = NULL,  
  fbname = "inkaverse"  
)
```

Arguments

factors	Lists with names and factor vector [list].
type	Randomization in the list [string: sorted, unsorted]
zigzag	Experiment layout in zigzag [logic: FALSE].
nrows	Experimental design dimension by rows [numeric: value]
serie	Number to start the plot id [numeric: 1000].
seed	Replicability from randomization [numeric: NULL].
fbname	Bar code prefix for data collection [string: "inkaverse"].

Value

A list with the field-book design and parameters

Examples

```
## Not run:

library(inti)

factores <- list("geno" = c(1:99))

fb <- design_noreps(factors = factores
                   , type = "sorted"
                   , zigzag = F
                   , nrows = 10
                   )

dsg <- fb$fieldbook

fb %>%
  tarpuy_plotdesign(fill = "plots")

fb$parameters

## End(Not run)
```

design_repblock

Experimental design in CRD and RCBD

Description

Function to deploy field-book experiment for CRD and RCBD

Usage

```
design_repblock(
  nfactors = 1,
  factors,
  type = "crd",
  rep = 3,
  zigzag = FALSE,
  nrows = NA,
  serie = 100,
  seed = NULL,
  fbname = "inkaverse"
)
```

Arguments

<code>nfactors</code>	Number of factor in the experiment [numeric: 1].
<code>factors</code>	Lists with names and factor vector [list].
<code>type</code>	Type of experimental arrange [string: "crd" "rcbd" "lsd"]
<code>rep</code>	Number of replications in the experiment [numeric: 3].
<code>zigzag</code>	Experiment layout in zigzag [logic: F].
<code>nrows</code>	Experimental design dimension by rows [numeric: value]
<code>serie</code>	Number to start the plot id [numeric: 100].
<code>seed</code>	Replicability from randomization [numeric: NULL].
<code>fbname</code>	Bar code prefix for data collection [string: "inkaverse"].

Value

A list with the field-book design and parameters

Examples

```
## Not run:

library(inti)

factores <- list("geno" = c("A", "B", "C", "D", "D", 1, NA, NA, NULL, "NA")
  , "salt stress" = c(0, 50, 200, 200, "T0", NA, NULL, "NULL")
  , time = c(30, 60, 90)
)

fb <- design_repblock(nfactors = 2
  , factors = factores
  , type = "rcbd"
  , rep = 5
  , zigzag = T
  , seed = 0
  , nrows = 20
```

```

    )

dsg <- fb$fieldbook

fb %>%
  tarpuy_plotdesign(fill = "plots")

fb$parameters

## End(Not run)

```

figure2qmd

Figure to Quarto format

Description

Use Articul8 Add-ons from Google docs to build Rarticles

Usage

```
figure2qmd(text, path = ".", opts = NA)
```

Arguments

text	Markdown text with figure information [string]
path	Image path for figures [path: "." (base directory)]
opts	chunk options in brackets [string: NA]

Details

Quarto option can be included in the title using "{ {}" separated by commas

Value

string mutated

figure2rmd	<i>Figure to Rmarkdown format</i>
------------	-----------------------------------

Description

Use Articul8 Add-ons from Google docs to build Ricles

Usage

```
figure2rmd(text, path = ".", opts = NA)
```

Arguments

text	String with the table information
path	Path of the image for the figure
opts	chunk options in brackets.

Value

Mutated string

footnotes	<i>Footnotes in tables</i>
-----------	----------------------------

Description

Include tables footnotes and symbols for kables in pandoc format

Usage

```
footnotes(table, notes = NULL, label = "Note:", notation = "alphabet")
```

Arguments

table	Kable output in pandoc format.
notes	Footnotes for the table.
label	Label for start the footnote.
notation	Notation for the footnotes (default = "alphabet"). See details.

Details

You should use the pandoc format `kable(format = "pipe")`. You can add the footnote symbol using `{hyphen}` in your table. notation could be use: "alphabet", "number", "symbol", "none".

Value

Table with footnotes for word and html documents

 gdoc2qmd

Google docs to Rmarkdown

Description

Use Articul8 Add-ons from Google docs to build Rarticles

Usage

```
gdoc2qmd(file, export = NA, format = "qmd", type = "asis")
```

Arguments

file	Zip file path from Articul8 exported in md format [path]
export	Path to export the files [path: NA (file directory)]
format	Output format [string: "qmd" "rmd"]
type	output file type [string: "asis" "list", "listfull", "full"]

Details

Document rendering until certain point: "#| end" Include for next page: "#| newpage" You can include the cover page params using "#|" in a Google docs table

Value

path

 H2cal

Broad-sense heritability in plant breeding

Description

Heritability in plant breeding on a genotype difference basis

Usage

```
H2cal(
  data,
  trait,
  gen.name,
  rep.n,
  env.n = 1,
  year.n = 1,
  env.name = NULL,
  year.name = NULL,
```

```

    fixed.model,
    random.model,
    summary = FALSE,
    emmeans = FALSE,
    weights = NULL,
    plot_diag = FALSE,
    outliers.rm = FALSE,
    trial = NULL
  )

```

Arguments

<code>data</code>	Experimental design data frame with the factors and traits.
<code>trait</code>	Name of the trait.
<code>gen.name</code>	Name of the genotypes.
<code>rep.n</code>	Number of replications in the experiment.
<code>env.n</code>	Number of environments (default = 1). See details.
<code>year.n</code>	Number of years (default = 1). See details.
<code>env.name</code>	Name of the environments (default = NULL). See details.
<code>year.name</code>	Name of the years (default = NULL). See details.
<code>fixed.model</code>	The fixed effects in the model (BLUEs). See examples.
<code>random.model</code>	The random effects in the model (BLUPs). See examples.
<code>summary</code>	Print summary from random model (default = FALSE).
<code>emmeans</code>	Use emmeans for calculate the BLUEs (default = FALSE).
<code>weights</code>	an optional vector of ‘prior weights’ to be used in the fitting process (default = NULL).
<code>plot_diag</code>	Show diagnostic plots for fixed and random effects (default = FALSE). Options: "base", "ggplot". .
<code>outliers.rm</code>	Remove outliers (default = FALSE). See references.
<code>trial</code>	Column with the name of the trial in the results (default = NULL).

Details

The function allows to made the calculation for individual or multi-environmental trials (MET) using fixed and random model.

1. The variance components based in the random model and the population summary information based in the fixed model (BLUEs).
2. Heritability under three approaches: Standard (ANOVA), Cullis (BLUPs) and Piepho (BLUEs).
3. Best Linear Unbiased Estimators (BLUEs), fixed effect.
4. Best Linear Unbiased Predictors (BLUPs), random effect.
5. Table with the outliers removed for each model.

For individual experiments is necessary provide the `trait`, `gen.name`, `rep.n`.

For MET experiments you should `env.n` and `env.name` and/or `year.n` and `year.name` according your experiment.

The BLUEs calculation based in the pairwise comparison could be time consuming with the increase of the number of the genotypes. You can specify `emmeans = FALSE` and the calculate of the BLUEs will be faster.

If `emmeans = FALSE` you should change 1 by 0 in the fixed model for exclude the intersect in the analysis and get all the genotypes BLUEs.

For more information review the references.

Value

list

Author(s)

Maria Belen Kistner

Flavio Lozano Isla

References

Bernal Vasquez, Angela Maria, et al. "Outlier Detection Methods for Generalized Lattices: A Case Study on the Transition from ANOVA to REML." *Theoretical and Applied Genetics*, vol. 129, no. 4, Apr. 2016.

Buntaran, H., Piepho, H., Schmidt, P., Ryden, J., Halling, M., and Forkman, J. (2020). Cross validation of stagewise mixed model analysis of Swedish variety trials with winter wheat and spring barley. *Crop Science*, 60(5).

Schmidt, P., J. Hartung, J. Bennewitz, and H.P. Piepho. 2019. Heritability in Plant Breeding on a Genotype Difference Basis. *Genetics* 212(4).

Schmidt, P., J. Hartung, J. Rath, and H.P. Piepho. 2019. Estimating Broad Sense Heritability with Unbalanced Data from Agricultural Cultivar Trials. *Crop Science* 59(2).

Tanaka, E., and Hui, F. K. C. (2019). *Symbolic Formulae for Linear Mixed Models*. In H. Nguyen (Ed.), *Statistics and Data Science*. Springer.

Zystro, J., Colley, M., and Dawson, J. (2018). *Alternative Experimental Designs for Plant Breeding*. In *Plant Breeding Reviews*. John Wiley and Sons, Ltd.

Examples

```
library(inti)

dt <- potato

hr <- H2cal(data = dt
            , trait = "stemdw"
            , gen.name = "geno"
            , rep.n = 5
            , fixed.model = "0 + (1|bloque) + geno"
```

```

      , random.model = "1 + (1|bloque) + (1|geno)"
      , emmeans = TRUE
      , plot_diag = FALSE
      , outliers.rm = TRUE
    )

hr$tabsmr
hr$blues
hr$blups
hr$outliers

```

include_pdf

Include PDF in markdown documents

Description

Insert PDF files in markdown documents

Usage

```
include_pdf(file, width = "100%", height = "600")
```

Arguments

file	file path from pdf file.
width	width preview file.
height	height preview file.

Value

html code for markdown

include_table

Table with footnotes

Description

Include tables with title and footnotes for word and html documents

Usage

```
include_table(table, caption = NA, notes = NA, label = NA, notation = "none")
```

Arguments

table	Data frame.
caption	Table caption (default = NULL). See details.
notes	Footnotes for the table (default = NA). See details.
label	Label for start the footnote (default = NA).
notation	Notation for the symbols and footnotes (default = "none") Others: "alphabet", "number", "symbol".

Value

Table with caption and footnotes

Examples

```
library(inti)

table <- data.frame(
  x = rep_len(1, 5)
  , y = rep_len(3, 5)
  , z = rep_len("c", 5)
)

table %>% inti::include_table(
  caption = "Title caption b) line 0
  a) line 1
  b) line 2"
  , notes = "Footnote"
  , label = "Where:"
)
```

 jc_tombola

Journal Club Tombola

Description

Function for arrange journal club schedule

Usage

```
jc_tombola(
  data,
  members,
  papers = 1,
  group = NA,
  gr_lvl = NA,
```

```

    status = NA,
    st_lvl = "active",
    frq = 7,
    date = NA,
    seed = NA
  )

```

Arguments

data	Data frame with members and their information.
members	Columns with the members names.
papers	Number of paper by meeting
group	Column for arrange the group.
gr_lvl	Levels in the groups for the arrange. See details.
status	Column with the status of the members.
st_lvl	Level to confirm the assistance in the JC. See details.
frq	Number of the day for each session.
date	Date when start the first session of JC.
seed	Number for replicate the results (default = date).

Details

The function could consider n levels for `gr_lvl`. In the case of more levels using "both" or "all" will be the combination. The suggested levels for `st_lvl` are: active or spectator. Only the "active" members will enter in the schedule.

Value

data frame with the schedule for the JC

mean_comparison	<i>Mean comparison test</i>
-----------------	-----------------------------

Description

Function to compare treatment from lm or aov using data frames

Usage

```

mean_comparison(
  data,
  response,
  model_factors,
  comparison,
  test_comp = "SNK",
  sig_level = 0.05
)

```

Arguments

data	Fieldbook data.
response	Model used for the experimental design.
model_factors	Factor in the model.
comparison	Significance level for the analysis (default = 0.05).
test_comp	Comparison test (default = "SNK"). Others: "TUKEY", "DUNCAN".
sig_level	Significance level for the analysis (default = 0.05).

Value

list

Examples

```
## Not run:

library(inti)
library(gsheets)

url <- paste0("https://docs.google.com/spreadsheets/d/"
             , "15r7ZwcZZHbEglt1F6gSFvCTFA-CFzVBWwg3mF1RyKPs/"
             , "edit#gid=172957346")
# browseURL(url)

fb <- gsheets2tbl(url)

mc <- mean_comparison(data = fb
                     , response = "spad_29"
                     , model_factors = "bloque* geno*treat"
                     , comparison = c("geno", "treat")
                     , test_comp = "SNK"
                     )

mc$comparison
mc$stat

## End(Not run)
```

met

Swedish cultivar trial data

Description

The datasets were obtained from official Swedish cultivar tests. Dry matter yield was analyzed. All trials were laid out as alpha-designs with two replicates. Within each replicate, there were five to seven incomplete blocks.

Usage

```
met
```

Format

A data frame with 1069 rows and 8 variables:

zone Sweden is divided into three different agricultural zones: South, Middle, and North

location Locations: 18 location in the Zones

rep Replications (4): number of replication in the experiment

alpha Incomplete blocks (8) in the alpha-designs

cultivar Cultivars (30): genotypes evaluated

yield Yield in kg/ha

year Year (1): 2016

env enviroment (18): combination zone + location + year

Source

[doi:10.1002/csc2.20177](https://doi.org/10.1002/csc2.20177)

metamorphosis

Transform fieldbooks based in a dictionary

Description

Transform entire fieldbook according to data a dictionary

Usage

```
metamorphosis(fieldbook, dictionary, from, to, index, colnames)
```

Arguments

fieldbook	Data frame with the original information.
dictionary	Data frame with new names and categories. See details.
from	Column of the dictionary with the original names.
to	Column of the dictionary with the new names.
index	Column of the dictionary with the type and level of the variables.
colnames	Character vector with the name of the columns.

Details

The function require at least three columns.

1. Original names (from).
2. New names (to).
3. Variable type (index).

Value

List with two objects. 1. New data frame. 2. Dictionary.

<code>outliers_remove</code>	<i>Remove outliers</i>
------------------------------	------------------------

Description

Use the method M4 in Bernal Vasquez (2016). Bonferroni Holm test to judge residuals standardized by the re scaled MAD (BH MADR).

Usage

```
outliers_remove(data, trait, model, drop_na = TRUE)
```

Arguments

<code>data</code>	Experimental design data frame with the factors and traits.
<code>trait</code>	Name of the trait.
<code>model</code>	The fixed or random effects in the model.
<code>drop_na</code>	drop NA values from the data.frame

Details

Function to remove outliers in MET experiments

Value

list. 1. Table with date without outliers. 2. The outliers in the dataset.

References

Bernal Vasquez, Angela Maria, et al. "Outlier Detection Methods for Generalized Lattices: A Case Study on the Transition from ANOVA to REML." *Theoretical and Applied Genetics*, vol. 129, no. 4, Apr. 2016.

Examples

```
library(inti)

rmout <- outliers_remove(
  data = potato
  , trait = "stemdw"
  , model = "0 + treat*geno + (1|bloque) + geno"
  , drop_na = FALSE
)

rmout
```

plot_diag

Diagnostic plots

Description

Function to plot the diagnostic of models

Usage

```
plot_diag(model, title = NA)
```

Arguments

model	Statistical model
title	Plot title

Value

plots

Examples

```
## Not run:

dt <- potato

lm <- aov(stemdw ~ bloque + geno*treat, dt)

#lm <- lme4::lmer(stemdw ~ bloque + (1|geno:treat), dt)

plot(lm, which = 1)
plot_diag(lm)[3]

plot(lm, which = 2)
```

```
plot_diag(lm)[2]

plot(lm, which = 3)
plot_diag(lm)[4]

plot(lm, which = 4)
plot_diag(lm)[1]

## End(Not run)
```

plot_raw

Plot raw data

Description

Function use the raw data for made a boxplot graphic

Usage

```
plot_raw(
  data,
  type = "boxplot",
  x,
  y,
  group = NULL,
  xlab = NULL,
  ylab = NULL,
  glab = NULL,
  ylimits = NULL,
  xlimits = NULL,
  xrotation = NULL,
  legend = "top",
  xtext = NULL,
  gtext = NULL,
  color = TRUE,
  linetype = 1,
  opt = NULL
)
```

Arguments

data	raw data
type	Type of graphic. "boxplot" or "scatterplot"
x	Axis x variable
y	Axis y variable

group	Group variable
xlab	Title for the axis x
ylab	Title for the axis y
glab	Title for the legend
ylimits	Limits and break of the y axis c(initial, end, brakes)
xlimits	For scatter plot. Limits and break of the x axis c(initial, end, brakes)
xrotation	Rotation in x axis c(angle, h, v)
legend	the position of legends ("none", "left", "right", "bottom", "top", or two-element numeric vector)
xtext	Text labels in x axis using a vector
gtext	Text labels in groups using a vector
color	Colored figure (TRUE), black & white (FALSE) or color vector
linetype	Line type for regression. Default = 0
opt	Add new layers to the plot

Details

You could add additional layer to the plot using "+" with ggplot2 options

Value

plot

Examples

```
## Not run:
```

```
library(inti)
```

```
fb <- potato
```

```
fb %>%
```

```
  plot_raw(type = "box"
            , x = "geno"
            , y = "twue"
            , group = NULL
            , ylab = NULL
            , xlab = NULL
            , glab = ""
            )
```

```
fb %>%
```

```
  plot_raw(type = "sca"
            , x = "geno"
            , y = "twue"
            , group = "treat")
```

```

        , color = c("red", "blue")
      )

## End(Not run)

```

plot_smr

Plot summary data

Description

Graph summary data into bar o line plot

Usage

```

plot_smr(
  data,
  type = NULL,
  x = NULL,
  y = NULL,
  group = NULL,
  xlab = NULL,
  ylab = NULL,
  glab = NULL,
  ylimits = NULL,
  xrotation = c(0, 0.5, 0.5),
  xtext = NULL,
  gtext = NULL,
  legend = "top",
  sig = NULL,
  sigsize = 3,
  error = NULL,
  color = TRUE,
  opt = NULL
)

```

Arguments

data	Output from summary data
type	Type of graphic. "bar" or "line"
x	Axis x variable
y	Axis y variable
group	Group variable
xlab	Title for the axis x
ylab	Title for the axis y

glab	Title for the legend
ylimits	limits of the y axis c(initial, end, brakes)
xrotation	Rotation in x axis c(angle, h, v)
xtext	Text labels in x axis using a vector
gtext	Text labels in group using a vector
legend	the position of legends ("none", "left", "right", "bottom", "top", or two-element numeric vector)
sig	Column with the significance
sigsize	Font size in significance letters
error	Show the error bar ("ste" or "std")
color	colored figure (TRUE), black & white (FALSE) or color vector
opt	Add news layer to the plot

Details

If the table is a out put of mean_comparison(graph_opts = TRUE) function. Its contain all the parameter for the plot.

You could add additional layer to the plot using "+" with ggplot2 options

Value

plot

Examples

```
## Not run:

library(inti)

fb <- potato#'

yrs <- yupana_analysis(data = fb
                       , response = "hi"
                       , model_factors = "geno*treat"
                       , comparison = c("geno", "treat")
                       )

yrs$meancomp %>%
  plot_smr(type = "line"
           , x = "geno"
           , y = "hi"
           , xlab = ""
           , group = "treat"
           , glab = "Tratamientos"
           , ylimits = c(0, 1, 0.2)
           , color = c("red", "black")
           , gtext = c("Irrigado", "Sequia")
```

```
)
## End(Not run)
```

potato

Water use efficiency in 15 potato genotypes

Description

Experiment to evaluate the physiological response from 15 potato genotypes under water deficit condition. The experiment had a randomized complete block design with five replications. The stress started at 30 day after planting.

Usage

```
potato
```

Format

A data frame with 150 rows and 17 variables:

treat Water deficit treatments: sequia, irrigado

geno 15 potato genotypes

bloque blocks for the experimental design

spad_29 Relative chlorophyll content (SPAD) at 29 day after planting

spad_83 Relative chlorophyll content (SPAD) at 84 day after planting

rwc_84 Relative water content (percentage) at 84 day after planting

op_84 Osmotic potential (Mpa) at 84 day after planting

leafdw leaf dry weight (g)

stemdw stem dry weight (g)

rootdw root dry weight (g)

tubdw tuber dry weight (g)

biomdw total biomass dry weight (g)

hi harvest index

ttrans total transpiration (l)

wue water use efficiency (g/l)

twue tuber water use efficiency (g/l)

lfa leaf area (cm²)

`split_folder`*Split folder*

Description

Function to split folder by size or number of elements

Usage

```
split_folder(  
  folder,  
  export,  
  units = "megas",  
  size = 500,  
  zip = TRUE,  
  remove = FALSE  
)
```

Arguments

<code>folder</code>	Path of folder to split (path).
<code>export</code>	Path to export the split folders (path).
<code>units</code>	Units to split folder (string: "megas", "number").
<code>size</code>	Folder size by the units selected (numeric).
<code>zip</code>	Zip split folders (logical).
<code>remove</code>	Remove the split folder after zip (logical).

Value

zip files

Examples

```
## Not run:  
  
split_folder("pictures/QUINOA 2018-2019 SC SEEDS EDWIN - CAMACANI/"  
  , "pictures/split_num", remove = T, size = 400, units = "number")  
  
## End(Not run)
```

Table to Quarto format

Description

Use Articul8 Add-ons from Google docs to build Rarticles

Usage

```
table2qmd(text, type = "asis")
```

Arguments

text	Markdown text with table information (string)
type	output file type [strig: "asis" "list", "listfull", "full"]

Value

string mutated

table2rmd

Table to Rmarkdown format

Description

Use Articul8 Add-ons from Google docs to build Rarticles

Usage

```
table2rmd(text, opts = NA)
```

Arguments

text	String with the table information
opts	chunk options in brackets.

Value

Mutated string

tarpuy

Interactive fieldbook designs

Description

Invoke RStudio addin to create fieldbook designs

Usage

```
tarpuy(dependencies = FALSE)
```

Arguments

`dependencies` Install package dependencies for run the app

Details

Tarpuy allow to create experimental designs under an interactive app.

Value

Shiny app

Examples

```
if(interactive()){  
  inti::tarpuy()  
}
```

tarpuy_design

Fieldbook experimental designs

Description

Function to deploy experimental designs

Usage

```
tarpuy_design(
  data,
  nfactors = 1,
  type = "crd",
  rep = 2,
  zigzag = FALSE,
  nrows = NA,
  serie = 100,
  seed = NULL,
  fbname = NA
)
```

Arguments

data	Experimental design data frame with the factors and level. See examples.
nfactors	Number of factor in the experiment(default = 1). See details.
type	Type of experimental arrange (default = "crd"). See details.
rep	Number of replications in the experiment (default = 3).
zigzag	Experiment layout in zigzag [logic: FALSE].
nrows	Experimental design dimension by rows [numeric: value]
serie	Number to start the plot id [numeric: 100].
seed	Replicability of draw results (default = 0) always random. See details.
fbname	Barcode prefix for data collection.

Details

The function allows to include the arguments in the sheet that have the information of the design. You should include 2 columns in the sheet: {arguments} and {values}. See examples. The information will be extracted automatically and deploy the design. nfactors = 1: crd, rcbd, lsd, lattice. nfactors = 2 (factorial): split-crd, split-rcbd split-lsd nfactors >= 2 (factorial): crd, rcbd, lsd.

Value

A list with the fieldbook design

Examples

```
## Not run:

library(inti)
library(gsheets)

url <- paste0("https://docs.google.com/spreadsheets/d/"
  , "1_BVzChX_-1zXhB7HAm6FeSrww9iKfZ39_S18NFC6k7U/edit#gid=1868565342")
```

```
# browseURL(url)

fb <- gsheets2tbl(url)

dsg <- fb %>% tarpuy_design()

dsg %>%
  tarpuy_plotdesign()

## End(Not run)
```

tarpuy_plex

Fieldbook plan information

Description

Information for build a plan for an experiment (PLEX)

Usage

```
tarpuy_plex(
  data = NULL,
  idea = NULL,
  goal = NULL,
  hypothesis = NULL,
  rationale = NULL,
  objectives = NULL,
  plan = NULL,
  institutions = NULL,
  researchers = NULL,
  manager = NULL,
  location = NULL,
  altitude = NULL,
  georeferencing = NULL,
  environment = NULL,
  start = NA,
  end = NA,
  about = NULL,
  fieldbook = NULL,
  gdocs = NULL,
  github = NULL,
  album = NULL,
  nfactor = 2,
  design = "rcbd",
  rep = 3,
  zigzag = FALSE,
  nrows = NA,
```

```

    serie = 100,
    seed = 0
)

```

Arguments

data	Data with the fieldbook information.
idea	How the idea was born.
goal	The main goal of the project.
hypothesis	What are the expected results.
rationale	Based in which evidence is planned the experiment.
objectives	The objectives of the project.
plan	General description of the project (M & M).
institutions	Institutions involved in the project.
researchers	Persons involved in the project.
manager	Persons responsible of the collection of the data.
location	Location of the project.
altitude	Altitude of the experiment (m.a.s.l).
georeferencing	Georeferencing information.
environment	Environment of the experiment (greenhouse, lab, etc).
start	The date of the start of the experiments.
end	The date of the end of the experiments.
about	Short description of the project.
fieldbook	Name or ID for the fieldbook/project.
gdocs	link for Google Docs
github	link with the github repository.
album	link with the photos of the project.
nfactor	Number of factors for the design.
design	Type of design.
rep	Number of replication.
zigzag	Experiment layout in zigzag [logic: F]
nrows	Experimental design dimension by rows [numeric: value]
serie	Number of digits in the plots.
seed	Seed for the randomization.

Details

Provide the information available.

Value

data frame or list of arguments:

1. info
2. variables
3. design
4. logbook
5. timetable
6. budget

tarpuy_plotdesign *Fieldbook plot experimental designs*

Description

Plot fieldbook sketch designs based in experimental design

Usage

```
tarpuy_plotdesign(  
  data,  
  factor = NA,  
  fill = "plots",  
  xlab = NULL,  
  ylab = NULL,  
  glab = NULL  
)
```

Arguments

data	Experimental design data frame with the factors and level. See examples.
factor	Vector with the name of the columns with the factors.
fill	Value for fill the experimental units (default = "plots").
xlab	Title for x axis.
ylab	Title for y axis.
glab	Title for group axis.

Details

The function allows to plot the experimental design according the field experiment design.

Value

plot

Examples

```
## Not run:

library(inti)
library(gsheet)

url <- paste0("https://docs.google.com/spreadsheets/d/"
              , "1_BVzChX_-lzXhB7HAm6FeSrwq9iKfZ39_S18NFC6k7U/edit#gid=1834109539")
# browseURL(url)

fb <- gsheets2tbl(url)

dsg <- fb %>% tarpuy_design()

dsg

dsg %>% str()

dsg %>%
  tarpuy_plotdesign()

## End(Not run)
```

tarpuy_traits

Field book traits

Description

Function to export field book and traits for be used in field book app.

Usage

```
tarpuy_traits(fieldbook = NULL, last_factor = NULL, traits = NULL)
```

Arguments

fieldbook	Experiment field book [dataframe].
last_factor	Last factor in the field book [string: colnames]
traits	Traits information [dataframe or list].

Details

For the traits parameters you can used shown in the field Book app

Value

list

Examples

```
library(inti)

fieldbook <- inti::potato

traits <- list(
  list(variable = "altura de planta"
        , abbreviation = "altp"
        , format = "numeric"
        , when = "30, 40, 50"
        , samples = 3
        , units = "cm"
        , details = NA
        , minimum = 0
        , maximum = 100
        )
  , list(variable = "severidad"
        , abbreviation = "svr"
        , format = "categorical"
        , when = "30, 40, 50"
        , samples = 1
        , units = "scale"
        , details = NA
        , categories = "1, 3, 5, 7, 9"
        )
  , list(variable = "foto"
        , abbreviation = "foto"
        , format = "photo"
        , when = "hrv, pshrv"
        , samples = 1
        , units = "image"
        , details = NA
        )
  , list(variable = "germinacion"
        , abbreviation = "ger"
        , format = "boolean"
        , when = "30, 40, 50"
        , samples = 1
        , units = "logical"
        , details = NA
        )
)

fbapp <- tarpuy_traits(fieldbook, last_factor = "bloque", traits)

## Not run:

library(inti)
library(gsheets)

url_fb <- paste0("https://docs.google.com/spreadsheets/d/")
```

```

      , "1_BVzChX_-lzXhB7HAm6FeSrwq9iKfZ39_Sl8NFC6k7U/edit#gid=150858522")

fb <- gsheets2tbl(url_fb)

url_ds <- paste0("https://docs.google.com/spreadsheets/d/"
  , "1_BVzChX_-lzXhB7HAm6FeSrwq9iKfZ39_Sl8NFC6k7U/edit#gid=1255730357")

ds <- gsheets2tbl(url_ds)

fb <- ds %>% tarpuy_design()

url_trt <- paste0("https://docs.google.com/spreadsheets/d/"
  , "1_BVzChX_-lzXhB7HAm6FeSrwq9iKfZ39_Sl8NFC6k7U/edit#gid=2106059499")

traits <- gsheets2tbl(url_trt)

fbapp <- tarpuy_traits(fb, last_factor = "cols", traits)

dsg <- fbapp[[1]]

## End(Not run)

```

web_table

HTML tables for markdown documents

Description

Export tables with download, pasta and copy buttons

Usage

```

web_table(
  data,
  caption = NULL,
  digits = 2,
  rnames = FALSE,
  buttons = NULL,
  file_name = "file",
  scrolly = NULL,
  columnwidth = "200px",
  width = "100%"
)

```

Arguments

data	Dataset.
caption	Title for the table.

digits	Digits number in the table exported.
rnames	Row names.
buttons	Buttons: "excel", "copy" or "none". Default c("excel", "copy")
file_name	Excel file name
scrolly	Windows height to show the table. Default "45vh"
columnwidth	Column width. Default '200px'
width	Width in pixels or percentage (Defaults to automatic sizing)

Value

table in markdown format for html documents

Examples

```
## Not run:

library(inti)

met %>%
  web_table(caption = "Web table")

## End(Not run)
```

yupana

Interactive data analysis

Description

Invoke RStudio addin to analyze and graph experimental design data

Usage

```
yupana(dependencies = FALSE)
```

Arguments

dependencies Install package dependencies for run the app

Details

Yupana: data analysis and graphics for experimental designs.

Value

Shiny app

Examples

```
if(interactive()){  
  inti::yupana()  
}
```

yupana_analysis *Fieldbook analysis report*

Description

Function to create a complete report of the fieldbook

Usage

```
yupana_analysis(  
  data,  
  last_factor = NULL,  
  response,  
  model_factors,  
  comparison,  
  test_comp = "SNK",  
  sig_level = 0.05,  
  plot_dist = "boxplot",  
  plot_diag = FALSE,  
  digits = 2  
)
```

Arguments

data	Field book data.
last_factor	The last factor in your fieldbook.
response	Response variable.
model_factors	Model used for the experimental design.
comparison	Factors to compare
test_comp	Comprasion test c("SNK", "TUKEY", "DUNCAN")
sig_level	Significal test (default: p = 0.005)
plot_dist	Plot data distribution (default = "boxplot")
plot_diag	Diagnostic plots for model (default = FALSE).
digits	Digits number in the table exported.

Value

list

Examples

```
## Not run:

library(inti)

fb <- potato

rsl <- yupana_analysis(data = fb
                      , last_factor = "bloque"
                      , response = "spad_83"
                      , model_factors = "geno * treat"
                      , comparison = c("geno", "treat")
                      )

## End(Not run)
```

yupana_export

Graph options to export

Description

Function to export the graph options and model parameters

Usage

```
yupana_export(
  data,
  type = NA,
  xlab = NA,
  ylab = NA,
  glab = NA,
  ylimits = NA,
  xrotation = c(0, 0.5, 0.5),
  xtext = NA,
  gtext = NA,
  legend = "top",
  sig = NA,
  error = NA,
  color = TRUE,
  opt = NA,
  dimension = c(20, 10, 100)
)
```

Arguments

data	Result from yupana_analysis or yupana_import.
type	Plot type
xlab	Title for the axis x
ylab	Title for the axis y
glab	Title for the legend
ylimits	limits of the y axis
xrotation	Rotation in x axis c(angle, h, v)
xtext	Text labels in x axis
gtext	Text labels in group
legend	the position of legends ("none", "left", "right", "bottom", "top", or two-element numeric vector)
sig	Column with the significance
error	Show the error bar ("ste" or "std").
color	colored figure (TRUE), otherwise black & white (FALSE)
opt	Add news layer to the plot
dimension	Dimension of graphs

Value

data frame

Examples

```
## Not run:

library(inti)
library(gsheets)

url <- paste0("https://docs.google.com/spreadsheets/d/"
              , "15r7ZwcZZHbEglt1F6gSFvCTFA-CFzVBWwg3mF1RyKPs/edit#gid=172957346")
# browseURL(url)

fb <- gsheets2tbl(url)

smr <- yupana_analysis(data = fb
                      , last_factor = "bloque"
                      , response = "spad_83"
                      , model_factors = "block + geno*treat"
                      , comparison = c("geno", "treat")
                      )

gtab <- yupana_export(smr, type = "line", ylimits = c(0, 100, 2))

#> import
```

```
url <- paste0("https://docs.google.com/spreadsheets/d/"
             , "15r7ZwcZZHbEglt1F6gSFvCTFA-CFzVBWwg3mF1RyKPs/edit#gid=1202800640")
# browseURL(url)

fb <- gsheets2tbl(url)

info <- yupana_import(fb)

etab <- yupana_export(info)

info2 <- yupana_import(etab)

etab2 <- yupana_export(info2)

## End(Not run)
```

yupana_import	<i>Import information from data summary</i>
---------------	---

Description

Graph summary data

Usage

```
yupana_import(data)
```

Arguments

data Summary information with options

Value

list

Examples

```
## Not run:

library(inti)
library(gsheets)

url <- paste0("https://docs.google.com/spreadsheets/d/"
             , "15r7ZwcZZHbEglt1F6gSFvCTFA-CFzVBWwg3mF1RyKPs/edit#gid=338518609")
# browseURL(url)
```

```
fb <- gsheets2tbl(url)

info <- yupana_import(fb)

## End(Not run)
```

yupana_mvr

Multivariate Analysis

Description

Multivariate analysis for PCA and HCPC

Usage

```
yupana_mvr(
  data,
  last_factor = NULL,
  summary_by = NULL,
  groups = NULL,
  variables = NULL
)
```

Arguments

data	Field book data.
last_factor	The last factor in your fieldbook [string: NULL].
summary_by	Variables for group the analysis.
groups	Groups for color in PCA.
variables	Variables to be use in the analysis [string: NULL].

Details

Compute and plot information for multivariate analysis (PCA, HCPC and correlation).

Value

result and plots

Examples

```
## Not run:

library(inti)

fb <- inti::potato

mv <- yupana_mvr(data = fb
  , last_factor = "geno"
  , summary_by = c("geno", "treat")
  , groups = "treat"
  , variables = c("all")
  #, variables = c("wue", "twue")
  )

mv$plot[1]

mv$data

## End(Not run)
```

yupana_reshape

Fieldbook reshape

Description

Function to reshape fieldbook according a separation character

Usage

```
yupana_reshape(
  data,
  last_factor,
  sep,
  new_colname,
  from_var = NULL,
  to_var = NULL,
  exc_factors = NULL
)
```

Arguments

`data` Field book raw data.

`last_factor` The last factor in your field book.

<code>sep</code>	Character that separates the last value.
<code>new_colname</code>	The new name for the column created.
<code>from_var</code>	The first variable in case you want to exclude several variables.
<code>to_var</code>	The last variable in case you want to exclude several variables.
<code>exc_factors</code>	Factor to exclude during the reshape.

Details

If you variable name is `variable_evaluation_rep`. The reshape function will help to create the column `rep` and the new variable name will be `variable_evaluation`.

Value

data frame

Index

- * **datasets**
 - met, [14](#)
 - potato, [22](#)
- colortext, [2](#)
- design_noreps, [3](#)
- design_repblock, [4](#)
- figure2qmd, [6](#)
- figure2rmd, [7](#)
- footnotes, [7](#)
- gdoc2qmd, [8](#)
- H2cal, [8](#)
- include_pdf, [11](#)
- include_table, [11](#)
- jc_tombola, [12](#)
- mean_comparison, [13](#)
- met, [14](#)
- metamorphosis, [15](#)
- outliers_remove, [16](#)
- plot_diag, [17](#)
- plot_raw, [18](#)
- plot_smr, [20](#)
- potato, [22](#)
- split_folder, [23](#)
- table2qmd, [24](#)
- table2rmd, [24](#)
- tarpuuy, [25](#)
- tarpuuy_design, [25](#)
- tarpuuy_plex, [27](#)
- tarpuuy_plotdesign, [29](#)
- tarpuuy_traits, [30](#)
- web_table, [32](#)
- yupana, [33](#)
- yupana_analysis, [34](#)
- yupana_export, [35](#)
- yupana_import, [37](#)
- yupana_mvr, [38](#)
- yupana_reshape, [39](#)