

Package ‘inti’

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Type Package

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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 (`tarpuv()`), 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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Imports lme4, agricolae, FactoMineR, emmeans, purrr, stringr, stringi,
DT

Suggests gsheets, knitr, rmarkdown

VignetteBuilder knitr

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R topics documented:

colortext	2
footnotes	3
H2cal	4
include_figure	6
include_table	7
jc_tombola	8
mean_comparison	9
met	10
metamorphosis	11
outliers_remove	11
plot_diag	12
plot_raw	13
plot_smr	14
potato	17
tarpu	18
tarpu_design	18
tarpu_plex	20
tarpu_plotdesign	22
tarpu_varlist	23
web_table	23
yupana	24
yupana_analysis	25
yupana_export_smr	26
yupana_import_smr	28
yupana_mvr	29
yupana_reshape	30
Index	32

colortext	<i>Colourise text for display in the terminal.</i>
-----------	--

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")
```

footnotes

Footnotes in tables

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

H2cal

Heritability in plant breeding

Description

Heritability in plant breeding on a genotype difference basis

Usage

```
H2cal(
  data,
  trait,
  gen.name,
  rep.n,
  loc.n = 1,
  year.n = 1,
  loc.name = NULL,
  year.name = NULL,
  ran.model,
  fix.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>loc.n</code>	Number of locations (default = 1). See details.
<code>year.n</code>	Number of years (default = 1). See details.
<code>loc.name</code>	Name of the location (default = NULL). See details.
<code>year.name</code>	Name of the years (default = NULL). See details.
<code>ran.model</code>	The random effects in the model. See examples.
<code>fix.model</code>	The fixed effects in the model. 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).

plot_diag	Show diagnostic plots (default = FALSE).
outliers.rm	Remove outliers (default = FALSE). See references.
trial	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 th fixed and random model.

1. The variance components.
2. Heritability under three approaches: Standard, Cullis and Piepho.
3. Best Linear Unbiased Predictors (BLUPs).
4. Best Linear Unbiased Estimators (BLUEs).
5. Outliers remove.

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

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

The blues calculation is based in the pairwise comparison and its could takes time according the number of the genotypes.

You can specify as `blues = FALSE` for calculate the variance components and blups faster.

For more information review the references.

Value

list

Author(s)

Maria Belen Kistner

Flavio Lozano Isla

References

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).

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)

dt <- potato

hr <- H2cal(data = dt
            , trait = "tubdw"
            , gen.name = "geno"
            , rep.n = 5
            , ran.model = "1 + (1|bloque) + (1|geno)"
            , fix.model = "0 + (1|bloque) + geno"
            , emmeans = TRUE
            , plot_diag = TRUE
            , outliers.rm = TRUE
            )

hr$tabsmr
hr$blues
hr$blups
```

include_figure

Figure with caption and notes

Description

Include figures with title and notes using a data base

Usage

```
include_figure(figure, caption = NA, notes = NA, label = NA)
```

Arguments

figure	Path or URL of the figure.
caption	Figure caption (default = NA).
notes	Figure notes (default = NA).
label	Label for the notes (default = NA).

Value

Figure with caption and notes

Examples

```
library(inti)

figure <- "https://inkaverse.com/reference/figures/logo.png"

figure %>% include_figure(caption = "Title test."
  , notes = "Note test.")
```

include_table	<i>Table with footnotes</i>
---------------	-----------------------------

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,
  group,
  gr_lvl,
  status,
  st_lvl,
  frq,
  date,
  seed = NULL
)

```

Arguments

data	Data frame with the members and their information.
members	Columns with the members names.
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 two level the third level will be both. 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/"
              , "15r7ZwcZZHbEg1t1F6gSFvCTFA-CFzVBWwg3mF1RyKPs/"
              , "edit#gid=172957346")
# browseURL(url)
```

```
fb <- gsheets2tbl(url)

mc <- mean_comparison(data = fb
                      , response = "hi"
                      , model_factors = "geno*treat"
                      , comparison = c("geno", "treat")
                      , test_comp = "TUKEY"
                      )

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	<i>Transform fieldbooks based in a dictionary</i>
---------------	---

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.

outliers_remove	<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)
```

Arguments

data	Experimental design data frame with the factors and traits.
trait	Name of the trait.
model	The fixed or random effects in the model.

Details

Function to remove outliers in MET experiments

Value

list. 1. Table with data 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 = "hi"
  , model = "0 + (1|bloque) + geno"
)

rmout$outliers
```

plot_diag

Diagnostic plots

Description

Function to plot the diagnostic of models

Usage

```
plot_diag(model)
```

Arguments

model	Statistical model.
-------	--------------------

Value

plots

`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

<code>data</code>	raw data
<code>type</code>	Type of graphic. "boxplot" or "scatterplot"
<code>x</code>	Axis x variable
<code>y</code>	Axis y variable
<code>group</code>	Group variable
<code>xlab</code>	Title for the axis x
<code>ylab</code>	Title for the axis y
<code>glab</code>	Title for the legend
<code>ylimits</code>	Limits and break of the y axis c(initial, end, brakes)
<code>xlimits</code>	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 = "treat"
           , color = T
           )

## 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)
library(gsheets)

url <- paste0("https://docs.google.com/spreadsheets/d/"
             , "15r7ZwcZZHbEgl1F6gSFvCTFA-CFzVBWwg3mF1RyKPs/"
             , "edit#gid=172957346")
# browseURL(url)

fb <- gsheets2tbl(url)

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"
          , group = "treat"
          , glab = "tratamientos (cm^{-2})"
          , ylimits = c(0, 1, 0.1)
          , color = c("brown", "blue", "black")
          , sig = "sig"
          ) + theme(legend.position = c(0.3, 0.9), legend.direction="horizontal")

## 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 experimentl 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)

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

```
tarpuv_design(
  data,
  n_factors = 1,
  type = "crd",
  rep = 2,
  serie = 2,
  seed = 0,
  qr = "fb"
)
```

Arguments

data	Experimental design data frame with the factors and level. See examples.
n_factors	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).
serie	Digits in the plot id (default = 2).
seed	Replicability of draw results (default = 0) always random. See details.
qr	Bar code 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. n_factors = 1: crd, rcbd, lsd, lattice. n_factors = 2 (factorial): split_crd, split_rcbd n_factors >= 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/"
             , "1wXzDc60F0FgDgjGiZX8qYB8hzvgspoPf-qUS5AsScus/edit#gid=1296863855")
# browseURL(url)

fb <- gsheets2tbl(url)

tarpuv_design(data = fb)
```

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

tarpuy_plex	<i>Fieldbook plan information</i>
-------------	-----------------------------------

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,  
  album = NULL,  
  github = NULL,  
  nfactor = 2,  
  design = "rcbd",  
  rep = 3,  
  serie = 2,  
  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.
album	link with the photos of the project.
github	link with the github repository.
nfactor	Number of factors for the design.
design	Type of design.
rep	Number of replication.
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,  
  dim = NULL,  
  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.
dim	Dimension for reshape the design arrangement.
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

tarpuv_varlist	<i>Fieldbook variable list</i>
----------------	--------------------------------

Description

Function to include the variables to evaluate in the fieldbook design.

Usage

```
tarpuv_varlist(fieldbook, varlist = NULL)
```

Arguments

fieldbook	Data frame with the fieldbook.
varlist	Data frame with the variables information. See examples.

Details

The function allows to include the arguments in the sheet that have the information of the variables. You should include 3 columns in the sheet: {abbreviation}, {evaluation} and {sampling}. See examples. The information will be extracted automatically and deploy the list of variable for the fieldbook design. If you will be evaluate the experimental unit one time you should set 1.

Value

data frame

web_table	<i>HTML tables for markdown documents</i>
-----------	---

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
)
```

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 "60vh"

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	<i>Fieldbook analysis report</i>
-----------------	----------------------------------

Description

Function to create a complete report of the fieldbook

Usage

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

Arguments

data	Field book data.
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)
library(gsheets)

url <- paste0("https://docs.google.com/spreadsheets/d/"
             , "15r7ZwcZZHbEglt1F6gSFvCTFA-CFzVBWwg3mF1RyKPs/edit#gid=946957922")
# browseURL(url)

fb <- gsheets2tbl(url)

yrs <- yupana_analysis(data = fb
                      , response = "spad_83"
                      , model_factors = "geno + treat"
                      , comparison = c("geno", "treat")
                      )

yrs$meancomp

## End(Not run)
```

yupana_export_smr *Graph options to export*

Description

Function to export the graph options and model parameters

Usage

```
yupana_export_smr(
  data,
  response,
  comparison,
  model,
  test_comp = NA,
  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),
sig_level = NA
)

```

Arguments

data	Fieldbook data.
response	Model used for the experimental design.
comparison	Factor to compare
model	Model used in the analysis
test_comp	Type of test comparison
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
sig_level	Level of significance for the test

Value

data frame

Examples

```
## Not run:

library(inti)
library(gsheets)

url <- paste0("https://docs.google.com/spreadsheets/d/"
             , "15r7ZwcZZHbEg1t1F6gSFvCTFA-CFzVBWwg3mF1RyKPs/"
             , "edit#gid=172957346")
# browseURL(url)

fb <- gsheets2tbl(url)

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

mc$comparison

## End(Not run)
```

yupana_import_smr

Import information from data summary

Description

Graph summary data

Usage

```
yupana_import_smr(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=1948849836")
# browseURL(url)

data <- gsheets2tbl(url)

info <- yupana_import_smr(data)

info

plot_smr(data = info$data
         , type = info$type
         , x = info$x
         , y = info$y
         , group = info$group
         , ylimits = info$ylimits
         , color = info$color
         )

## 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.
summary_by	Variables for group the analysis.
groups	Groups for color in PCA.
variables	Variables to be use in the analysis.

Details

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

Value

result and plots

Examples

```
## Not run:

library(inti)
library(gsheets)

url <- paste0("https://docs.google.com/spreadsheets/d/"
             , "17vZ6ZqF1Ei2XsYyCcZD3WRa01BQUQDrzMqs-3F0TZ2Y/"
             , "edit#gid=120747730")
# browseURL(url)

fb <- gsheets2tbl(url)

mv <- fieldbook_mvr(data = fb
                   , last_factor = "block"
                   , summary_by = c("treat")
                   , groups = "treat"
                   )

## 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.
sep	Character that separates the last value.
new_colname	The new name for the column created.
from_var	The first variable in case you want to exclude several variables.
to_var	The last variable in case you want to exclude several variables.
exc_factors	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, [10](#)
potato, [17](#)

colortext, [2](#)

footnotes, [3](#)

H2cal, [4](#)

include_figure, [6](#)

include_table, [7](#)

jc_tombola, [8](#)

mean_comparison, [9](#)

met, [10](#)

metamorphosis, [11](#)

outliers_remove, [11](#)

plot_diag, [12](#)

plot_raw, [13](#)

plot_smr, [14](#)

potato, [17](#)

tarpuuy, [18](#)

tarpuuy_design, [18](#)

tarpuuy_plex, [20](#)

tarpuuy_plotdesign, [22](#)

tarpuuy_varlist, [23](#)

web_table, [23](#)

yupana, [24](#)

yupana_analysis, [25](#)

yupana_export_smr, [26](#)

yupana_import_smr, [28](#)

yupana_mvr, [29](#)

yupana_reshape, [30](#)