

# Package ‘inti’

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**Type** Package

**Version** 0.4.4

**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/).

**Date** 2021-10-01

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

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

**Depends** shiny, ggplot2, dplyr, tidyr, tibble, R (>= 2.10)

**Imports** lme4, agricolae, FactoMineR, emmeans, purrr, stringr, stringi, DT

**Suggests** gsheet, knitr, rmarkdown

**VignetteBuilder** knitr

**License** GPL-3 | file LICENSE

**LazyData** true

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---

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).

<code>plot_diag</code>	Show diagnostic plots (default = FALSE).
<code>outliers.rm</code>	Remove outliers (default = FALSE). See references.
<code>trial</code>	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,
  papers = 1,
  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.
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 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** environment (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 or 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(gsheet)

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

fb <- gsheet2tbl(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      *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)
library(gsheets)

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

fb <- gsheets2tbl(url)

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

yrs$meancomp

yrs$anova %>% summary()

## 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(gsheet)

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

fb <- gsheets2tbl(url)

mv <- yupana_mvr(data = fb
                , last_factor = "bloque"
                , summary_by = c("geno", "treat")
                , groups = NULL
                )

FactoMineR::plot.PCA(mv$pca, choix = "ind", habillage = mv$param$groups)

## 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

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