

# Package ‘agricolaeplotr’

January 22, 2025

**Type** Package

**Title** Visualization of Design of Experiments from the 'agricolae' Package

**Version** 0.6.0

**Maintainer** Jens Harbers <jensharbers@gmail.com>

## Description

Visualization of Design of Experiments from the 'agricolae' package with 'ggplot2' framework  
The user provides an experiment design from the 'agricolae' package, calls the corresponding function and will receive a visualization with 'ggplot2' based functions that are specific for each design. As there are many different designs, each design is tested on its type.  
The output can be modified with standard 'ggplot2' commands or with other packages with 'ggplot2' function extensions.

**License** GPL (>= 3)

**Encoding** UTF-8

**Imports** ggplot2, agricolae, raster, sp (>= 2.0.0), methods, FieldHub, utils, tibble, sf, dplyr, tidyr, stringr, stplanr, ggspatial

**RoxygenNote** 7.2.3

**Language** en-US

**Suggests** testthat (>= 3.0.0), knitr, rmarkdown, leaflet

**Config/testthat/edition** 3

**BugReports** <https://github.com/jensharbers/agricolaeplotr/issues>

**URL** <https://github.com/jensharbers/agricolaeplotr>

**Depends** R (>= 4.0)

**VignetteBuilder** knitr

**Note** 'None'

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2025-01-22 13:20:02 UTC

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---

`citations`*Citation*

---

**Description**

Generates citations of all loaded packages

**Usage**

```
citations(includeURL = TRUE, bibtex = TRUE)
```

**Arguments**

`includeURL`      boolean, Should the URL be returned?  
`bibtex`            boolean, Should the citations be returned as bibtex?

**Value**

printed output to console

**Examples**

```
library(ggplot2)  
library(agricolaeplotr)  
library(agricolae)  
library(raster)  
citations()
```

---

`DOE_obj`*Measures of a Field Design*

---

**Description**

Returns a list with several useful information about the experiment

**Usage**

```
DOE_obj(p)
```

**Arguments**

`p`                    ggplot object containing the data of the plot

**Value**

a list with several useful information about the experiment and the field

**Examples**

```
library(agricolae)
library(agricolaeplotr)
trt = c(2,3,4,5,6)
outdesign1 <- design.crd(trt,r=5,serie=2,2543,'Mersenne-Twister')
p <- plot_design_crd(outdesign1,
                     ncols = 7,
                     nrows = 4,
                     width = 10,
                     height = 10,
                     reverse_y = TRUE)
stats <- DOE_obj(p)
stats
```

---

full\_control\_positions

*full\_control\_positions*

---

**Description**

This function provides full control about the plotting. The user also may shift the coordinates as liked.

**Usage**

```
full_control_positions(
  design,
  x = "col",
  y = "row",
  factor_name = "trt",
  labels = "plots",
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_y = FALSE,
  reverse_x = FALSE,
  way_x = 0,
  way_y = 0,
  shift_columns = 0,
  shift_rows = 0,
  shift_x = 0,
  shift_y = 0,
  dist_x = 1,
  dist_y = 1,
  n_shift_columns = 0,
  n_shift_rows = 0,
  start_origin = FALSE
)
```

**Arguments**

design	data.frame containing the row and columns of an experiment
x	Describes the x coordinates of a experiment design
y	Describes the y coordinates of a experiment design
factor_name	string Which factor should be used for plotting, needs to be a column in outdesign\$book
labels	string Describes the column from that the plots are taken to display them
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width
space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE
way_x	numeric vector indicates the shift of the nth-plot in x-axis.
way_y	numeric vector indicates the shift of the nth-plot in y-axis.
shift_columns	numeric indicates the shift of the given plots of a specific row by n units in x-axis.
shift_rows	numeric indicates the shift of the given plots of a specific column by n units in y-axis.
shift_x	numeric indicates the shift in units in x-axis.
shift_y	numeric indicates the shift in units for the y-axis.
dist_x	numeric indicates the shift in plots in x-axis.
dist_y	numeric indicates the shift in plots for the y-axis.
n_shift_columns	numeric vector indicating the number of plots of shift_columns. negative number indicate shift to left, otherwise right
n_shift_rows	numeric vector indicating the number of plots of shift_rows. negative number indicate shift to left, otherwise right
start_origin	boolean. Should the design start at the origin (0 0)?

**Value**

ggplot graphic that can be modified, if wished

**Examples**

```

library(agricolaeplotr)
library(agricolae)
library(ggplot2)
varieties<-c('perricholi','yungay','maria bonita','tomasa')
outdesign <-design.youden(varieties,r=2,serie=2,seed=23)
design <- outdesign$book
design
p <- full_control_positions(design,"col","row","varieties","plots",
                           width=3,height=4.5,
                           space_width=0.5,space_height=0.5,
                           shift_x=(-0.5*3) + (-0.5*3*0.5),shift_y=-0.5*4.5 + (-0.5*4.5*0.5))
p
p <- full_control_positions(design,"col","row","varieties","plots",
                           width=3,height=4.5,
                           space_width=0.13,space_height=0.445,
                           shift_x=(-0.5*3) + (-0.5*3*(1-0.13)),shift_y=-0.5*4.5 + (-0.5*4.5*(1-0.445)))
p
varieties<-LETTERS[1:12]
outdesign <-design.youden(varieties,r=12,serie=2,seed=23)
design <- outdesign$book
p <- full_control_positions(design,"col","row","varieties","plots",
                           width=3,height=4.5,
                           space_width=1,space_height=1,
                           shift_x=-0.5*3,shift_y=-0.5*4.5)
p
p <- full_control_positions(design,"col","row","varieties","plots",
                           width=3,height=4.5,
                           space_width=0.93,space_height=0.945,
                           start_origin = TRUE)
p
p <- full_control_positions(design,"col","row","varieties","plots",
                           width=3,height=4.5,
                           space_width=0.93,space_height=0.945,way_x = c(2,6,8,10,12),way_y=c(3,8),dist_x=2,dist_y=4,
                           start_origin = TRUE, reverse_y = FALSE, reverse_x = FALSE);p
p <- full_control_positions(design,"col","row","varieties","plots",
                           width=3,height=4.5,
                           space_width=0.93,space_height=0.945,
                           way_x = c(2,4,6,8,10,12),way_y=c(3,8),
                           start_origin = FALSE, reverse_y = FALSE,
                           reverse_x = FALSE);p
p <- full_control_positions(design,"col","row","varieties","plots",
                           width=3,height=4.5,shift_columns=c(4,8),
                           shift_rows=c(3,5,9),
                           n_shift_columns=c(1,5),
                           n_shift_rows=c(1,-2,6),
                           space_width=0.93,space_height=0.945,
                           way_x = c(2,4,6,8,10,12),way_y=c(3,8),

```

```
start_origin = TRUE, reverse_y = FALSE,  
reverse_x = FALSE);p
```

---

```
make_polygons      make_polygons
```

---

## Description

This function coerces all rectangles from a 'ggplot' object to 'SpatialPolygonDataFrame'.

## Usage

```
make_polygons(  
  ggplot_object,  
  north = 3454206.89,  
  east = 5939183.21,  
  projection_input = "+init=epsg:31467",  
  projection_output = "+init=epsg:4326"  
)
```

## Arguments

ggplot_object	saved ggplot object, containing the coordinates of the rectangles of a 'ggplot' object of the first two layers
north	float added to the rows to have a northing ordinate
east	float added to the rows to have a easting ordinate
projection_input	string defines in which EPSG projection the ggplot object should be converted to a raster object? a projection with a metric unit is highly recommended
projection_output	string defines in which EPSG projection the SpatialPolygonDataFrame should be exported.

## Value

a SpatialPolygonDataFrame object

## Examples

```
library(agricolaeplotr)  
library(agricolae)  
trt = c(2,3,4)  
outdesign1 <- design.crd(trt,r=5,serie=2,2543,'Mersenne-Twister')  
plt <- plot_design_crd(outdesign1,ncols = 13,nrows = 3)  
spat_df <- make_polygons(plt)  
spat_df
```

---

 plot\_alpha

*Plot Alpha design Experiments*


---

### Description

Plot a design of an experiment with an alpha design from agricolae design.alpha

### Usage

```
plot_alpha(
  design,
  x = "cols",
  y = "block",
  factor_name = "trt",
  labels = "plots",
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_y = FALSE,
  reverse_x = FALSE
)
```

### Arguments

design	outdesign from agricolae package
x	Describes the x coordinates of a experiment design
y	Describes the y coordinates of a experiment design
factor_name	Which factor should be used for plotting, needs to be a column in outdesign\$book
labels	Describes the column from that the plots are taken to display them
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width
space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE

### Value

ggplot graphic that can be modified, if wished



**Examples**

```

library(agricolaeplotr)
library(agricolae)
trt<-1:30
t <- length(trt)
# size block k
k<-3
# Blocks s
s<-t/k
# replications r
r <- 2
outdesign<- design.alpha(trt,k,r,serie=2)
plot_alpha(outdesign)

```

plot\_bib

*Plot Randomized Balanced Incomplete Block Designs***Description**

Plot a design of an experiment with an Randomized Balanced Incomplete Block Designs (BIB) from design.bib

**Usage**

```

plot_bib(
  design,
  y = "block",
  factor_name = "trt",
  labels = "plots",
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_y = FALSE,
  reverse_x = FALSE
)

```

**Arguments**

design	outdesign from agricolae package
y	Describes the y coordinates of a experiment design
factor_name	Which factor should be used for plotting, needs to be a column in outdesign\$book
labels	Describes the column from that the plots are taken to display them
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment

space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width
space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE

**Value**

ggplot graphic that can be modified, if wished

**Examples**

```
library(agricolaeplotr)
library(agricolae)
trt<-c('A', 'B', 'C', 'D')
k<-3
outdesign<-design.bib(trt,k,serie=2,seed =41,kinds = 'Super-Duper') # seed = 41
plot_bib(outdesign)
#now let us change position of the columns
plot_bib(outdesign,reverse_x = TRUE)
```

---

plot\_cyclic

*Plot Cyclic Design*

---

**Description**

Plot a design of an experiment with an cyclic design from agricolae design.cyclic

**Usage**

```
plot_cyclic(
  design,
  y = "block",
  factor_name = "trt",
  labels = "plots",
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_y = FALSE,
  reverse_x = FALSE
)
```

**Arguments**

design	outdesign from agricolae package
y	Describes the y coordinates of a experiment design
factor_name	Which factor should be used for plotting, needs to be a column in outdesign\$book
labels	Describes the column from that the plots are taken to display them
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width
space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE

**Value**

ggplot graphic that can be modified, if wished

**Examples**

```
library(agricolaeplotr)
library(agricolae)
k <- 2
r <- 6
trt <-c('CIP-101', 'CIP-201', 'CIP-301', 'CIP-401', 'CIP-501', LETTERS[1:2])
outdesign<- design.cyclic(trt,k=k, r=r, serie=3, rowcol=TRUE)
plot_cyclic(outdesign, factor_name = 'trt')
```

---

plot\_dau

*Plot Design of Augmented Blocks (dau)*

---

**Description**

Plot a design of an experiment with an augmented block design from agricolae design.dau

**Usage**

```
plot_dau(
  design,
  y = "block",
  factor_name = "trt",
  labels = "plots",
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_y = FALSE,
  reverse_x = FALSE
)
```

**Arguments**

design	outdesign from agricolae package
y	Describes the y coordinates of a experiment design
factor_name	Which factor should be used for plotting, needs to be a column in outdesign\$book
labels	Describes the column from that the plots are taken to display them
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width
space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE

**Value**

ggplot graphic that can be modified, if wished

**Examples**

```
library(agricolaeplotr)
library(agricolae)
T1<-c('A','B','C','D','E','F')
T2<-letters[19:26]
outdesign <-design.dau(T1,T2, r=5,serie=2)
plot_dau(outdesign)
plot_dau(outdesign,reverse_y = TRUE)
```

---

 plot\_design.factorial\_crd

*Plot Factorial Complete Randomized Designs (crd)*


---

### Description

Plot a design of a factorial experiment with completely randomized design (crd) from design.ab

### Usage

```
plot_design.factorial_crd(
  design,
  ncols,
  nrows,
  y = "row",
  factor_name = "A",
  labels = "plots",
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_y = FALSE,
  reverse_x = FALSE
)
```

### Arguments

design	outdesign from agricolae package
ncols	integer value, choose the number of columns to which the experiment should be plotted
nrows	integer value, choose the number of rows to which the experiment should be plotted
y	Describes the y coordinates of a experiment design, default is row
factor_name	Which factor should be used for plotting, needs to be a column in outdesign\$book
labels	string indicates the column of which the labels should be displayed
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width
space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE

**Value**

ggplot graphic that can be modified, if wished

**Examples**

```
library(agricolaeplotr)
library(agricolae)
trt<-c(3,2) # factorial 3x2
outdesign <- design.ab(trt, r=3, serie=2,design = 'crd')
plot_design.factorial_crd(outdesign,ncols = 8,nrows = 6)
plot_design.factorial_crd(outdesign,reverse_y = TRUE,ncols = 8,nrows = 6)
plot_design.factorial_crd(outdesign,reverse_y = TRUE,reverse_x = TRUE,ncols = 8,nrows = 6)
```

---

plot\_design.factorial\_1sd

*Plot Factorial Latin Square Designs (1sd)*

---

**Description**

Plot a design of a factorial experiment with latin square design (1sd) design from agricolae design.ab

**Usage**

```
plot_design.factorial_1sd(
  design,
  x = "col",
  y = "row",
  factor_name = "A",
  labels = "plots",
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_y = FALSE,
  reverse_x = FALSE
)
```

**Arguments**

design	outdesign from agricolae package
x	Describes the x coordinates of a experiment design
y	Describes the y coordinates of a experiment design
factor_name	Which factor should be used for plotting, needs to be a column in outdesign\$book
labels	Describes the column from that the plots are taken to display them
width	numeric value, describes the width of a plot in an experiment

height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width
space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE

**Value**

ggplot graphic that can be modified, if wished

**Examples**

```
library(agricolaeplotr)
library(agricolae)
trt<-c(3,2) # factorial 3x2
outdesign <-design.ab(trt, r=3, serie=2,design = 'lsd')
plot_design.factorial_lsd(outdesign,factor_name = 'B',reverse_x = TRUE)
```

---

plot\_design.factorial\_rcbd

*Plot Factorial Designs with rcbd Design*

---

**Description**

Plot a design of a factorial experiment with randomized complete block design (rcbd) from design.ab

**Usage**

```
plot_design.factorial_rcbd(
  design,
  y = "row",
  factor_name = "A",
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_x = FALSE,
  reverse_y = FALSE
)
```

**Arguments**

design	outdesign from agricolae package
y	Describes the y coordinates of a experiment design
factor_name	Which factor should be used for plotting, needs to be a column in outdesign\$book
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width
space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE

**Value**

ggplot graphic that can be modified, if wished

**Examples**

```
library(agricolaeplotr)
library(agricolae)
trt<-c(2,4)
k=6
outdesign<-design.ab(trt, r=k, serie=3,design='rcbd')
plot_design.factorial_rcbd(design=outdesign,factor_name = 'B')
plot_design.factorial_rcbd(outdesign,reverse_y = TRUE,reverse_x = TRUE)
```

---

plot\_design\_crd

*Plot Complete Randomized Design*

---

**Description**

Plot a design of a factorial experiment with randomized complete block design from agricolae design.ab



**Usage**

```
plot_design_crd(
  design,
  ncols,
  nrows,
  y = "row",
  factor_name = "trt",
  labels = "plots",
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_y = FALSE,
  reverse_x = FALSE
)
```

**Arguments**

design	outdesign from agricolae package
ncols	integer value, choose the number of columns to which the experiment should be plotted
nrows	integer value, choose the number of rows to which the experiment should be plotted
y	Describes the y coordinates of a experiment design, default is row
factor_name	Which factor should be used for plotting, needs to be a column in outdesign\$book
labels	Describes the column from that the plots are taken to display them
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width
space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE

**Value**

ggplot graphic that can be modified, if wished

**Examples**

```
library(agricolaeplotr)
library(agricolae)
trt = c(2,3,4,5,6)
outdesign1 <-design.crd(trt,r=5,serie=2,2543,'Mersenne-Twister')
plot_design_crd(outdesign1,ncols = 13,nrows = 3)
```

---

plot\_fieldhub

*Plot FieldHub Design*


---

**Description**

Plots designs from FieldHub package

**Usage**

```
plot_fieldhub(
  design,
  x = "COLUMN",
  y = "ROW",
  labels = "PLOT",
  factor_name = "TREATMENT",
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_y = FALSE,
  reverse_x = FALSE,
  shift_x = 0,
  shift_y = 0
)
```

**Arguments**

design	outdesign from FieldHub package with one of the following IDs: c(9,13,14,15,16)
x	Describes the x coordinates of an experiment design
y	Describes the y coordinates of an experiment design
labels	string Describes the column from that the plots are taken to display them
factor_name	string Which factor should be used for plotting, needs to be a column in outdesign\$book
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width

space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE
shift_x	numeric indicates the shift in units in x-axis.
shift_y	numeric indicates the shift in units for the y-axis.

### Value

ggplot graphic that can be modified, if wished

### Examples

```
## Not run:
library(agricolaeplotr)
library(FieldHub)
H <- paste("H", 1:4, sep = "")
V <- paste("V", 1:5, sep = "")

strip1 <- FieldHub::strip_plot(Hplots = H,
                              Vplots = V,
                              b = 1,
                              l = 1,
                              plotNumber = 101,
                              planter = "serpentine",
                              locationNames = "A",
                              seed = 333)

strip1$fieldBook$ROW <- as.numeric(ordered(strip1$fieldBook$VSTRIP,
                                           levels = unique(strip1$fieldBook$VSTRIP)))
strip1$fieldBook$COLUMN <- as.numeric(ordered(strip1$fieldBook$HSTRIP,
                                              levels = unique(strip1$fieldBook$HSTRIP)))

plot_fieldhub(strip1,
              x = "ROW",
              y = "COLUMN",
              labels = "HSTRIP",
              factor_name = "HSTRIP",
              width = 12,
              height = 10,
              reverse_y = FALSE,
              reverse_x = FALSE)

## End(Not run)
```

---

 plot\_graeco

*Plot Graeco Latin Square Design*


---

### Description

Plot a design of an experiment with an Graeco - latin square design from agricolae design.graeco

### Usage

```
plot_graeco(
  design,
  x = "col",
  y = "row",
  factor_name = "T1",
  labels = "plots",
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_y = FALSE,
  reverse_x = FALSE
)
```

### Arguments

design	outdesign from agricolae package
x	Describes the x coordinates of a experiment design
y	Describes the y coordinates of a experiment design
factor_name	Which factor should be used for plotting, needs to be a column in outdesign\$book
labels	Describes the column from that the plots are taken to display them
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width
space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE

### Value

ggplot graphic that can be modified, if wished

**Examples**

```

library(agricolaeplotr)
library(agricolae)
T1<-c('a','b','c','d')
T2<-c('v','w','x','y','z','zz')
outdesign <- design.graeco(trt1=T1, trt2=T2, serie = 2,
  seed = 0, kinds = 'Super-Duper',randomization=TRUE)
plot_graeco(outdesign, factor_name = 'T2',reverse_y = TRUE)
plot_graeco(outdesign, factor_name = 'T2',reverse_x = TRUE)

```

---

plot\_latin\_square      *Plot Latin Square Design*

---

**Description**

Plot a design of a factorial experiment with a latin square design from agricolae design.lsd

**Usage**

```

plot_latin_square(
  design,
  x = "col",
  y = "row",
  factor_name = "trt",
  labels = "plots",
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_y = FALSE,
  reverse_x = FALSE
)

```

**Arguments**

design	outdesign from agricolae package
x	Describes the x coordinates of a experiment design
y	Describes the y coordinates of a experiment design
factor_name	Which factor should be used for plotting, needs to be a column in outdesign\$book
labels	Describes the column from that the plots are taken to display them
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width

space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE

**Value**

ggplot graphic that can be modified, if wished

**Examples**

```
library(agricolaeplotr)
library(agricolae)
trt<-LETTERS[1:9]
outdesign<- design.lsd(trt,serie=2)
plot_latin_square(outdesign, reverse_y = TRUE)
```

---

plot\_lattice\_simple *Plot Simple Lattice Design*

---

**Description**

Plot a design of a factorial experiment with a lattice design from agricolae design.lattice with r=2

**Usage**

```
plot_lattice_simple(
  design,
  y = "block",
  factor_name = "trt",
  labels = "plots",
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_y = FALSE,
  reverse_x = FALSE
)
```

**Arguments**

design	outdesign from agricolae package
y	Describes the y coordinates of a experiment design
factor_name	Which factor should be used for plotting, needs to be a column in outdesign\$book

labels	Describes the column from that the plots are taken to display them
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width
space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE

**Value**

ggplot graphic that can be modified, if wished

**Examples**

```
library(agricolaeplotr)
library(agricolae)
trt<-1:100
outdesign<-design.lattice(trt,r=2,serie=3) # simple lattice design, 10x10
plot_lattice_simple(outdesign,width = 2, height = 1)
```

---

plot\_lattice\_triple    *Plot Triple Lattice Design*

---

**Description**

Plot a design of a factorial experiment with a latin square design from agricolae design.lattice with r=3

**Usage**

```
plot_lattice_triple(
  design,
  y = "block",
  factor_name = "trt",
  labels = "plots",
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_y = FALSE,
  reverse_x = FALSE
)
```

**Arguments**

design	outdesign from agricolae package
y	Describes the y coordinates of a experiment design
factor_name	Which factor should be used for plotting, needs to be a column in outdesign\$book
labels	Describes the column from that the plots are taken to display them
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width
space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE

**Value**

ggplot graphic that can be modified, if wished

**Examples**

```
library(agricolaeplotr)
library(agricolae)
trt<-LETTERS[1:9]
outdesign<-design.lattice(trt,r=3,serie=2)
plot_lattice_triple(design=outdesign,reverse_x=TRUE)
```

---

plot\_longest\_diagonal *Plot the longest diagonal of a field*

---

**Description**

This function takes a field and plots the longest diagonal of the field. The field is divided into segments and points are sampled from these segments.



**Usage**

```
plot_longest_diagonal(  
  field,  
  n = 8,  
  type = "random",  
  n_segments = 2,  
  distance_field_boundary = 3,  
  width_diagonal_path = 2  
)
```

**Arguments**

field	An object of class <code>sf</code> representing the field.
n	Integer, the number of sample points along the longest diagonal.
type	Type of sampling. Default is "random".
n_segments	Numeric, the number of segments to divide the longest diagonal (default is 2).
distance_field_boundary	Numeric, the distance to buffer the field for creating the boundary (default is 3.0).
width_diagonal_path	Numeric, the width to buffer the diagonal path (default is 2.0).

**Value**

- `p`: A `ggplot` object showing the field, the buffered field, the buffered line, and the sample points.
- `buffered_line`: A `sf` object representing the buffered line.
- `my_line`: A `sf` object representing the longest diagonal of the field.
- `sample_points`: A `sf` object representing the sampled points.
- `length`: A numeric value, representing the length of the longest line.

**Examples**

```
library(sf)  
my_sf <- st_read(system.file("shape/gfn_schlaege.shp", package="agricolaeplotr"))  
st_crs(my_sf) <- 25832  
field <- my_sf[my_sf$SCHLAG_NR == 170,]  
plot_longest_diagonal(field)
```

---

 plot\_rcbd

*Plot randomized complete block designs*


---

### Description

Plot a design of an experiment with randomized complete block design (rcbd) design from agricolae design.rcbd

### Usage

```
plot_rcbd(
  design,
  y = "block",
  factor_name = "trt",
  labels = "plots",
  treatment_label = "trt",
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  label_width = 10,
  reverse_y = FALSE,
  reverse_x = FALSE
)
```

### Arguments

design	outdesign from agricolae package
y	Describes the y coordinates of a experiment design
factor_name	Which factor should be used for plotting, needs to be a column in outdesign\$book
labels	Describes the column from that the plots are taken to display them
treatment_label	Describes the column(s) from the treatments the plots are taken to display them as a label text
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width
space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
label_width	numeric value, describes the maximum width of a label
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE

**Value**

ggplot graphic that can be modified, if wished

**Examples**

```
library(agricolaeplotr)
library(agricolae)
# 5 treatments and 6 blocks
trt<-c('A','B','C','D','E')
outdesign <-design.rcbd(trt,6,serie=2,986,'Wichmann-Hill') # seed = 986
plot_rcbd(outdesign)
plot_rcbd(outdesign,reverse_y = TRUE,reverse_x = TRUE)
```

---

plot_split_crd	<i>Plot Split Plot Designs (crd)</i>
----------------	--------------------------------------

---

**Description**

Plot a design of a split plot experiment with a complete randomized design (crd) from design.split

**Usage**

```
plot_split_crd(
  design,
  nrows,
  ncols,
  factor_name_1 = "T1",
  factor_name_2 = "T2",
  labels = "plots",
  subplots = TRUE,
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_y = FALSE,
  reverse_x = FALSE
)
```

**Arguments**

design	outdesign from agricolae package
nrows	Number of rows for the design
ncols	Number of columns for the design
factor_name_1	string Which factor should be used for plotting, needs to be a column in outdesign\$book

factor_name_2	string Which factor should be used for plotting, needs to be a column in outdesign\$book
labels	string Describes the column from that the plots are taken to display them
subplots	should the plot function return the subplots (default) or main plots?
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width
space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE

### Value

ggplot graphic that can be modified, if wished

### Examples

```
library(agricolaeplotr)
library(agricolae)
T1<-c('a','b','c','d','e','f','g')
T2<-c('v','w','x','y','zzz')
r <- 4
outdesign2 <- design.split(trt1=T1, trt2=T2, r=r,
serie = 2, seed = 0, kinds = 'Super-Duper',
randomization=TRUE,first=TRUE,design = 'crd')
plot_split_crd(outdesign2,ncols = 6,nrows=5)

outdesign2 <- design.split(trt1=T1, trt2=T2, r=r,
serie = 2, seed = 0, kinds = 'Super-Duper',
randomization=FALSE,first=TRUE,design = 'crd')
plot_split_crd(outdesign2,ncols = 6,nrows=5)
```

---

plot\_split\_lsd

*Plot Split Plot Design lsd*

---

### Description

Plot a design of a split plot experiment with latin squared design (lsd) from design.split

**Usage**

```
plot_split_lsd(
  design,
  factor_name_1 = "T1",
  factor_name_2 = "T2",
  labels = "plots",
  subplots = TRUE,
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_y = FALSE,
  reverse_x = FALSE
)
```

**Arguments**

design	outdesign from agricolae package
factor_name_1	string Which factor should be used for plotting, needs to be a column in outdesign\$book
factor_name_2	string Which factor should be used for plotting, needs to be a column in outdesign\$book
labels	string Describes the column from that the plots are taken to display them
subplots	should the plot function return the subplots (default) or main plots?
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width
space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE

**Value**

ggplot graphic that can be modified, if wished

**Examples**

```
library(agricolaeplotr)
library(agricolae)
T1<-c('a','b','c','d','e')
T2<-c('v','w','x','y')
```

```

outdesign2 <- design.split(trt1=T1, trt2=T2, r=r, serie = 2,
                          seed = 0, kinds = 'Super-Duper',
                          randomization=TRUE, first=TRUE, design = 'lsd')
plot_split_lsd(outdesign2,width = 4,height = 4)

```

---

plot\_split\_rcbd

*Plot Split Plot Designs with rcdb*


---

### Description

Plot a design of a split plot experiment with randomized complete blocks design (rcbd) from design.split

### Usage

```

plot_split_rcbd(
  design,
  y = "block",
  factor_name_1 = "T1",
  factor_name_2 = "T2",
  subplots = TRUE,
  labels = "plots",
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_y = FALSE,
  reverse_x = FALSE
)

```

### Arguments

design	outdesign from agricolae package
y	string defines the block
factor_name_1	string Which factor should be used for plotting, needs to be a column in outdesign\$book
factor_name_2	string Which factor should be used for plotting, needs to be a column in outdesign\$book
subplots	should the plot function return the subplots (default) or main plots?
labels	string Describes the column from that the plots are taken to display them
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width

space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE

**Value**

ggplot graphic that can be modified, if wished

**Examples**

```
library(agricolaeplotr)
library(agricolae)
T1<-c('a','b','c','d','e')
T2<-c('v','w','x','y','z','zz')
r = 3
outdesign2 <- design.split(trt1=T1, trt2=T2, r=r,serie = 2,
  seed = 0, kinds = 'Super-Duper',randomization=TRUE,
  first=TRUE,design = 'rcbd')
plot_split_rcbd(outdesign2,width = 1,height = 1)
plot_split_rcbd(outdesign2,width = 1,height = 1,reverse_y = TRUE)
plot_split_rcbd(outdesign2,width = 1,height = 1,reverse_x = TRUE,reverse_y = TRUE)
```

---

plot\_strip

*Plot Strip Design*

---

**Description**

Plot a design of an experiment with an Strip Plot design from agricolae design.strip

**Usage**

```
plot_strip(
  design,
  x = "col",
  y = "row",
  factor_name_1 = "T1",
  factor_name_2 = "T2",
  labels = "plots",
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_y = FALSE,
  reverse_x = FALSE
)
```

**Arguments**

design	outdesign from agricolae package
x	Describes the x coordinates of a experiment design
y	Describes the y coordinates of a experiment design
factor_name_1	Which factor should be used for plotting, needs to be a column in outdesign\$book
factor_name_2	Which factor should be used for plotting, needs to be a column in outdesign\$book
labels	Describes the column from that the plots are taken to display them
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width
space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE

**Value**

ggplot graphic that can be modified, if wished

**Examples**

```
library(agricolaeplotr)
library(agricolae)
T1<-c('a','b','c','d')
T2<-c('v','w','x','y','z')
r = 3
outdesign <- design.strip(trt1=T1, trt2=T2, r=r,serie = 2,
  seed = 0, kinds = 'Super-Duper',randomization=TRUE)
plot_strip(outdesign,factor_name_1 = "T1",factor_name_2="T2")
plot_strip(outdesign,factor_name_1 = "T1",factor_name_2="T2",reverse_x = TRUE)
```

---

plot\_youden

*Plot Youden Design*

---

**Description**

Plot a Youden experiment design from agricolae design.youden



**Usage**

```
plot_youden(
  design,
  x = "col",
  y = "row",
  factor_name = "varieties",
  labels = "plots",
  width = 1,
  height = 1,
  space_width = 0.95,
  space_height = 0.85,
  reverse_y = FALSE,
  reverse_x = FALSE
)
```

**Arguments**

design	outdesign from agricolae package
x	Describes the x coordinates of a experiment design
y	Describes the y coordinates of a experiment design
factor_name	string Which factor should be used for plotting, needs to be a column in outdesign\$book
labels	string Describes the column from that the plots are taken to display them.
width	numeric value, describes the width of a plot in an experiment
height	numeric value, describes the height of a plot in an experiment
space_width	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width
space_height	numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height
reverse_y	boolean, should the plots of the experiment be changed in reverse order in Row direction? Use reverse_y=TRUE to have same sketch as in agricolae. default:reverse_y=FALSE
reverse_x	boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE

**Value**

ggplot graphic that can be modified, if wished

**Examples**

```
library(agricolaeplotr)
library(agricolae)
varieties<-c('perricholi','yungay','maria bonita','tomasa')
outdesign <-design.youden(varieties,r=2,serie=2,seed=23)
plot_youden(outdesign, labels = 'varieties')
```

---

protective_layers	<i>Create Protective Layers for Design of Experiments (DOEs)</i>
-------------------	--

---

## Description

This function generates protective layers around the polygons of an experiment. These layers can be used to plot boundaries, for example, to protect agricultural on-farm experiments from accidental harvesting.

## Usage

```
protective_layers(design, borders = c(0, 3, 5, 10))
```

## Arguments

design	An sf object containing the polygons of the experiment. The coordinate reference system (crs) of the data needs to be in metric distance, not degrees.
borders	A numeric vector specifying the distances (in meters) for which protective layers should be created. The layers will be created with decreasing distances, starting from the largest.

## Value

An sf object representing the protective layers around the experiment polygons.

## Examples

```
library(agricolaeplotr)
library(sf)
library(ggplot2)
example("make_polygons")
polygo <- make_polygons(plt, north = 13454206.89, east = 7939183.21)
polygo <- st_transform(polygo, 25832)
pl <- protective_layers(polygo)
# plot experiment shape
ggplot(pl) + geom_sf(fill=c("black","orange","blue","red"))+ theme_minimal()
# write them to kml for Google Maps
# st_write(pl, "boundaries2.kml", append = FALSE)
```

---

sample_locations	<i>Sample Locations</i>
------------------	-------------------------

---

### Description

Returns locations to sample for each plot.

### Usage

```
sample_locations(design, n, plot = TRUE, ...)
```

### Arguments

design	Your experiment design of plot layouts.
n	Number of samples per plot (integer).
plot	Logical, indicating whether to visualize the sample locations as a ggplot2-based map.
...	further options for ‘st_sample’ and ‘make_polygons’

### Details

This function takes an experiment design (plot layout) and returns random sample locations within each plot. The function uses the ‘sf’ package to generate spatial polygons for the plots and then samples points within each polygon. Optionally, it can also display the sample locations as a ggplot2-based map.

### Value

An ‘sf’ object containing the sample locations within each plot.

### Examples

```
library(agricolaeplotr)
library(agricolae)
library(ggplot2)
trt <- c('A', 'B', 'C', 'D')
k <- 3
outdesign <- design.bib(trt, k, serie = 2, seed = 41, kinds = 'Super-Duper')
plot_bib(outdesign)
p <- plot_bib(outdesign)
sample_locations(p, 3, TRUE, projection_output = 25832)
```

---

serpentine	<i>Serpentine</i>
------------	-------------------

---

**Description**

This function produces a serpentine array of integers beginning by one

**Usage**

```
serpentine(n, times, m = 1)
```

**Arguments**

n	integer value indicating the upper cap of a numeric sequence
times	integer number of replications
m	integer value indicating the lower cap of a numeric sequence

**Value**

vector containing the serpentine sequence

**Examples**

```
serpentine(n=20,times = 15)
serpentine(n=20,times = 15,m=4)
```

---

summary	<i>summary of a field Layout</i>
---------	----------------------------------

---

**Description**

print a summary of a FieldLayout object

**Usage**

```
summary(object, unit = "m", part = "net_plot", ...)
```

**Arguments**

object	an object, created by DOE_obj with a FieldLayout class
unit	a string that corresponds to measure unit (default is m)
part	which part of the summary are you interested? Choose one of the following: "net_plot", "gross_plot", "field", "experiment", "all"
...	further arguments passed to or from other methods

**Examples**

```
library(agricolaeplotr)
library(agricolae)
varieties<-c('perricholi','yungay','maria bonita','tomasa')
outdesign <-design.youden(varieties,r=2,serie=2,seed=23)
p <- plot_youden(outdesign, labels = 'varieties')
stats <- DOE_obj(p)
# print plot summary for net plot (plots without space)
summary(stats, part = "net_plot")
# print plot summary for gross plot (plots with space)
summary(stats, part = "gross_plot")
# print plot summary for entire field
summary(stats, part = "field")
# print plot summary for design summary
summary(stats, part = "experiment")
# print plot summary for all information shown above in one output
summary(stats, part = "all")
```

---

test_input_extend	<i>Test if input for width and height is numeric</i>
-------------------	--

---

**Description**

Test if input is numeric for field width and height

**Usage**

```
test_input_extend(x)
```

**Arguments**

x                   input to be tested

**Value**

error

**Examples**

```
library(agricolaeplotr)
test_input_extend(3)
```

test\_input\_ncols      *checks matrix column input*

---

**Description**

checks if input is suitable for matrix column indication

**Usage**

```
test_input_ncols(x)
```

**Arguments**

x                    input to be tested

**Value**

error

**Examples**

```
library(agricolaeplotr)
test_input_ncols(9)
```

---

test\_input\_nrows      *checks matrix rows input*

---

**Description**

checks if input is suitable for matrix row indication

**Usage**

```
test_input_nrows(x)
```

**Arguments**

x                    input to be tested

**Value**

error

**Examples**

```
library(agricolaeplotr)
test_input_nrows(10)
```

---

test\_input\_reverse      *Test if input is a logical*

---

**Description**

Test if input is a logical

**Usage**

```
test_input_reverse(x)
```

**Arguments**

x                      input to be tested

**Value**

error

**Examples**

```
library(agricolaeplotr)
test_input_reverse(TRUE)
```

---

test\_input\_shift      *Test if input for shift parameter is numeric*

---

**Description**

Test if input is numeric for shift parameter

**Usage**

```
test_input_shift(x)
```

**Arguments**

x                      input to be tested

**Value**

error

**Examples**

```
library(agricolaeplotr)
test_input_shift(0.5)
```

---

test\_names\_design      *Test of experimental design*

---

**Description**

Test if the outdesign file contains book and parameter list

**Usage**

```
test_names_design(design)
```

**Arguments**

design                  design from agricolae package

**Value**

error

**Examples**

```
library(agricolaeplotr)
library(agricolae)
trt<-c(2,4)
k=6
outdesign<-design.ab(trt, r=k, serie=3,design='rcbd')
test_names_design(outdesign)
```

---

test\_name\_in\_column      *Test if input column names*

---

**Description**

Test if input is in column names of a table

**Usage**

```
test_name_in_column(x, design)
```

**Arguments**

x                        string input  
design                    design from agricolae package

**Value**

error



**Examples**

```
library(agricolaeplotr)
library(agricolae)
trt<-c(2,4)
k=6
outdesign<-design.ab(trt, r=k, serie=3,design='rcbd')
test_name_in_column('B',outdesign)
```

---

test_string	<i>Test if input is a string</i>
-------------	----------------------------------

---

**Description**

Test if input is a string

**Usage**

```
test_string(x)
```

**Arguments**

x                   input to be tested

**Value**

error

**Examples**

```
library(agricolaeplotr)
test_string('smallstring')
```

---

theme_gi	<i>theme_gi</i>
----------	-----------------

---

**Description**

Creates a theme for 'ggplot' based graphics to ensure to meet formal requirements for conferences of the Gesellschaft fuer Informatik

**Usage**

```
theme_gi()
```

**Value**

a 'ggplot' graph with a modified theme

## Examples

```
# example borrowed from ggplot2
library(ggplot2)
df <- data.frame(
  gp = factor(rep(letters[1:3], each = 10)),
  y = rnorm(30))

p <- ggplot() +
  geom_point(data = df, aes(gp, y))
p <- p + theme_gi();p
```

---

theme\_poster

*ggplot2 theme for poster presentation*

---

## Description

This theme is designed to increase font size to ensure readability on poster presentations

## Usage

```
theme_poster()
```

## Value

ggplot2 theme

## Examples

```
library(agricolaeplotr)
library(agricolae)
T1<-c('a','b','c','d','e','f','g')
T2<-c('v','w','x','y','z')
r <- 4
outdesign2 <- design.split(trt1=T1, trt2=T2, r=r,
  serie = 2, seed = 0, kinds = 'Super-Duper',
  randomization=FALSE,first=TRUE,design = 'crd')
plot_split_crd(outdesign2,ncols = 6,nrows=5)+
  theme_poster()
```

---

theme_pres	<i>ggplot2 theme for outdoor presentation</i>
------------	---

---

**Description**

This theme is designed to increase font size to ensure readability on outdoor used devices

**Usage**

```
theme_pres()
```

**Value**

ggplot2 theme

**Examples**

```
library(agricolaeplotr)
library(agricolae)
T1<-c('a','b','c','d','e','f','g')
T2<-c('v','w','x','y','z')
r <- 4
outdesign2 <- design.split(trt1=T1, trt2=T2, r=r,
  serie = 2, seed = 0, kinds = 'Super-Duper',
  randomization=FALSE,first=TRUE,design = 'crd')
plot_split_crd(outdesign2,ncols = 6,nrows=5)+
  theme_pres()
```

---

to_table	<i>to_table</i>
----------	-----------------

---

**Description**

Write field experiment information to a dataframe.

**Usage**

```
to_table(object, part = "net_plot", unit = "m", digits = 3, ...)
```

**Arguments**

object	an object, created by DOE_obj with a FieldLayout class
part	which part of the summary are you interested? Choose one of the following: "net_plot", "gross_plot", "field", "experiment"
unit	a string that corresponds to measure unit (default is m)
digits	integer indicating the number of decimal places (round) or significant digits (signif) to be used. Negative values are allowed
...	further arguments passed to or from other methods

**Value**

dataframe with corresponding information about the experiment

**Examples**

```
library(agricolaeplotr)
library(agricolae)
varieties<-c('perricholi','yungay','maria bonita','tomasa')
outdesign <-design.youden(varieties,r=2,serie=2,seed=23)
p <- plot_youden(outdesign, labels = 'varieties', width=4, height=3)
stats <- DOE_obj(p)
r <- to_table(stats,part = "net_plot", digits = 2)
r
r <- to_table(stats,part = "gross_plot", digits = 2)
r
r <- to_table(stats,part = "field", digits = 2)
r
r <- to_table(stats,part = "experiment", digits = 2)
r
r <- to_table(stats,part = "all", digits = 2)
r
```

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