Package ‘agricolaeplotr’

July 20, 2023

Type Package

Title Visualization of Design of Experiments from the ‘agricolae’ Package

Version 0.3.1

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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

RoxygenNote 7.2.3

Language en-US

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

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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citations

**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

**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

```r
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
```

Description

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

Usage

```r
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,
  shift_x = 0,
  shift_y = 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

shift\_x 
numeric indicates the shift in units in x-axis.

shift\_y 
numeric indicates the shift in units for the y-axis.

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)
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

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",
Description

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

Usage

```r
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

```r
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

```r
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

```r
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**

```r
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
## plot_cyclic

**Description**

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

**Usage**

```r
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`: A design object from `design.cyclic`.
- `y`: A `character` string indicating that `y` should be categorical.
- `factor_name`: A `character` string indicating the name of the factor.
- `labels`: A `character` string indicating the labels.
- `width`: A numeric value indicating the space between plots in term of width.
- `height`: A numeric value indicating the space between plots in term of height.
- `space_width`: A numeric value indicating the space of the plots in term of width.
- `space_height`: A numeric value indicating the space of the plots in term of height.
- `reverse_y`: A `logical` indicating whether the plots of the experiment should be changed in reverse order in row direction. Default: `FALSE`.
- `reverse_x`: A `logical` indicating whether the plots of the experiment should be changed in reverse order in column direction. Default: `FALSE`.

### Value

`ggplot` graphic that can be modified, if wished.

### Examples

```r
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 Design of Augmented Blocks (dau)

#### Description

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

#### Arguments

- **design**: outdesign from *agricolae* package
- **y**: Describes the y coordinates of an 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

```r
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)**

---

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 an 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

<table>
<thead>
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<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>design</td>
<td>outdesign from agricolae package</td>
</tr>
<tr>
<td>ncols</td>
<td>integer value, choose the number of columns to which the experiment should be plotted</td>
</tr>
<tr>
<td>nrows</td>
<td>integer value, choose the number of rows to which the experiment should be plotted</td>
</tr>
<tr>
<td>y</td>
<td>Describes the y coordinates of a experiment design, default is row</td>
</tr>
<tr>
<td>factor_name</td>
<td>Which factor should be used for plotting, needs to be a column in outdesign$book</td>
</tr>
<tr>
<td>labels</td>
<td>string indicates the column of which the labels should be displayed</td>
</tr>
<tr>
<td>width</td>
<td>numeric value, describes the width of a plot in an experiment</td>
</tr>
<tr>
<td>height</td>
<td>numeric value, describes the height of a plot in an experiment</td>
</tr>
<tr>
<td>space_width</td>
<td>numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width</td>
</tr>
<tr>
<td>space_height</td>
<td>numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of height</td>
</tr>
<tr>
<td>reverse_y</td>
<td>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</td>
</tr>
<tr>
<td>reverse_x</td>
<td>boolean, should the plots of the experiment be changed in reverse order in column direction? default:reverse_x=FALSE</td>
</tr>
</tbody>
</table>
Value

ggplot graphic that can be modified, if wished

Examples

```r
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_lsd**

*Plot Factorial Latin Square Designs (lsd)*

Description

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

Usage

```r
plot_design.factorial_lsd(
  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
### plot_design.factorial_rcbd

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

**Usage**
```r
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
)
```

---

**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

---

**Examples**

```r
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)
```
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

```r
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)
```

Description

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

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)

Description

Plots designs from FielDHub package

Usage

plot_fieldhub(
  design,            # outdesign from FielDHub package with one of the following IDs: c(9,13,14,15,16)
  x = ”COLUMN”,     # Describes the x coordinates of a experiment design
  y = ”ROW”,        # Describes the y coordinates of a experiment design
  labels = ”PLOT”,  # string Describes the column from that the plots are taken to display them
  factor_name = ”TREATMENT”, # string Which factor should be used for plotting, needs to be a column in outdesign$book
  width = 1,        # numeric value, describes the width of a plot in experiment
  height = 1,       # numeric value, describes the height of a plot in experiment
  space_width = 0.95,# numeric value, describes the share of the space of the plots. 0=only space, 1=no space between plots in term of width
  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 a experiment design
y            # Describes the y coordinates of a 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 experiment
height       # numeric value, describes the height of a plot in 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

```r
## 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)
```
**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**

```r
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
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

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_lattice_simple

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

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_triple

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

Value
ggplot graphic that can be modified, if wished

Examples

```r
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)
```

Description

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

Usage

```r
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
)```
**plot_rcdb**

**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_rcdb(
    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 an 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)
# 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_rcdb(outdesign)
plot_rcdb(outdesign,reverse_y = TRUE,reverse_x = TRUE)
plot_split_crd

Plot Split Plot Designs (crd)

Description

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

Usage

plot_split_crd(
  design,        outdesign from agricolae package
  nrows,         Number of rows for the design
  ncols,         Number of columns for the 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
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  

```r
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)
```

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

Usage  

```r
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

```r
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)
```

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

```r
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 a Strip Plot design from agricolae design.strip

Usage

```r
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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>design</td>
<td>outdesign from agricolae package</td>
</tr>
<tr>
<td>x</td>
<td>Describes the x coordinates of a experiment design</td>
</tr>
<tr>
<td>y</td>
<td>Describes the y coordinates of a experiment design</td>
</tr>
<tr>
<td>factor_name_1</td>
<td>Which factor should be used for plotting, needs to be a column in outdesign$book</td>
</tr>
<tr>
<td>factor_name_2</td>
<td>Which factor should be used for plotting, needs to be a column in outdesign$book</td>
</tr>
<tr>
<td>labels</td>
<td>Describes the column from that the plots are taken to display them</td>
</tr>
<tr>
<td>width</td>
<td>numeric value, describes the width of a plot in an experiment</td>
</tr>
</tbody>
</table>
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

```r
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)
```

Description

Plot a Youden experiment design from agricolae design.youden

Usage

```r
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 an experiment design
- **y**: Describes the y coordinates of an 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? 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

```r
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')
```

---

**serpentine**  

**Serpentine**

Description

This function produces a serpentine array of integers beginning by one

Usage

```r
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**  
**summary of a field Layout**

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 Test if input for width and height is numeric

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
test_input_nrows(9)

description
checks if input is suitable for matrix row indication

Usage
test_input_nrows(x)

Arguments
x: input to be tested

Value
error

Examples
test_input_nrows(10)

description
Test if input is a logical

Usage
test_input_reverse(x)

Arguments
x: input to be tested

Value
error
### test_input_shift

**Examples**

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

```r
test_input_shift(0.5)
```

**Description**

Test if input is numeric for shift parameter

**Usage**

```r
test_input_shift(x)
```

**Arguments**

- `x` input to be tested

**Value**

- error

**Examples**

```r
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**

```r
test_names_design(design)
```

**Arguments**

- `design` design from agricolae package

**Value**

- error
Examples

```r
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

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

Arguments

- `x`: string input
- `design`: design from agricolae package

Value

`error`

Examples

```r
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

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

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

```r
# 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_gg(); p
```

### Description

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

### Usage

```
theme_poster()
```

### Value

ggplot2 theme

### Examples

```r
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

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

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 (significant) to be used. Negative values are allowed
... further arguments passed to or from other methods
Value

dataframe with corresponding information about the experiment

Examples

```r
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
r
```
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