

Package ‘scifigure’

July 23, 2025

Title Visualize 'Reproducibility' and 'Replicability' in a Comparison of Scientific Studies

Version 0.2

Description Users may specify what fundamental qualities of a new study have or have not changed in an attempt to reproduce or replicate an original study. A comparison of the differences is visualized. Visualization approach follows 'Patil', 'Peng', and 'Leek' (2016) <[doi:10.1101/066803](https://doi.org/10.1101/066803)>.

Depends R (>= 3.0)

License MIT + file LICENSE

Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

Imports grid

Suggests knitr, rmarkdown, covr, testthat, png

VignetteBuilder knitr

NeedsCompilation no

Author Prasad Patil [aut, cre],
Gehlenborg Nils [ctb],
Muschelli John [ctb],
Leek Jeff [aut]

Maintainer Prasad Patil <prpatil42@gmail.com>

Repository CRAN

Date/Publication 2019-03-05 21:40:03 UTC

Contents

icons	2
icons_diff	2
init_experiments	3
replicate_figure	4

2

icons_diff

reproduce_figure 4

sci_figure 5

Index 7

icons	<i>scifigure icons</i>
-------	------------------------

Description

A dataset containing icon images used to render all figures in the scifigure package.

Usage

icons

Format

A list of length 44, with each item a 75x75x4 bitmap

icons_diff	<i>repfigure icons_diff</i>
------------	-----------------------------

Description

A dataset containing icon images showing difference rather than entity used to render all difference figures in the scifigure package.

Usage

icons_diff

Format

A list of length 44, with each item a 75x75x4 bitmap

init_experiments	<i>Initialize a skeleton data frame to create a figure with sci_figure</i>
------------------	--

Description

init_experiments generates a dataframe with the proper row and column headers for user manipulation before calling sci_figure

Usage

```
init_experiments(nexp = 3, exp_names = paste0("Exp", 1:nexp),
  stage_names = c("population", "question", "hypothesis",
    "experimental_design", "experimenter", "data", "analysis_plan",
    "analyst", "code", "estimate", "claim"))
```

Arguments

nexp	The number of scientific experiments to be represented in the data frame, i.e. number of columns.
exp_names	The names of each experiment, i.e. column names. Default: "Exp1, Exp2, ..."
stage_names	The names of each step in the process, i.e. row names. Defaults match Patil et al.

See Also

[sci_figure](#)

Examples

```
# Generate the default data frame of three experiments
init_experiments()

init_experiments(nexp = 5,
  exp_names = c("Run_16_01", "Run_16_04", "Run_16_07",
    "Run_16_09", "Run_16_12"))
testthat::expect_error({
  init_experiments(nexp = 2, exp_names = names)
})
```

replicate_figure	Create a figure depicting replicability
------------------	---

Description

replicate_figure is a wrapper around the sci_figure function to illustrate replicability in a two-experiment setting. Options for sci_figure are accepted, but this may be run as is.

Usage

```
replicate_figure(...)
```

Arguments

... Additional arguments passed to sci_figure.

See Also

[sci_figure](#) for additional arguments.

reproduce_figure	Create a figure depicting reproducibility
------------------	---

Description

reproduce_figure is a wrapper around the sci_figure function to illustrate reproducibility in a two-experiment setting. Options for sci_figure are accepted, but this may be run as is.

Usage

```
reproduce_figure(...)
```

Arguments

... Additional arguments passed to sci_figure.

See Also

[sci_figure](#) for additional arguments.

sci_figure	<i>Create a figure depicting reproducibility/replicability of a set of scientific experiments</i>
------------	---

Description

sci_figure creates a graphical representation of changes in a set of subsequent studies or reproduction attempts as compared to an original study.

Usage

```
sci_figure(experiments, custom_icons = NULL,
  stage_names = c("Population", "Question", "Hypothesis", "Exp. Design",
    "Experimenter", "Data", "Analysis Plan", "Analyst", "Code", "Estimate",
    "Claim"), hide_stages = NULL, diff = FALSE, showlegend = TRUE,
  cols = c("#D20000", "#007888", "#CDCDCD", "black"),
  leg_text = c("Incorrect", "Different", "Unobserved", "Original"))
```

Arguments

experiments	A data frame, which can be initialized with <code>init_experiments()</code> , whose row-names are the predefined stages of a scientific experiments, columnnames are the names of each experiment, and cell values represent the state of each stage in each experiment (states described below).
custom_icons	(optional) A list of bitmap matrices of custom icon images of length matching experiments input. Bitmap icons must be 75 x 75 pixels. See vignette for detailed instructions and specifications. Default NULL, indicating that default icons will be used.
stage_names	Character vector of names of stages. Default names match Patil et. al. If set to NULL, all names will be suppressed. Use <code>hide_stages</code> (below) to suppress specific stage names.
hide_stages	(optional) A character vector with the names of the stages in the scientific experiment, i.e. rownames of experiments, which the user wishes to suppress from the figure output. The default value of <code>hide_stages</code> is NULL, indicating that all stages will be displayed.
diff	(optional) A Boolean flag to indicate whether the rendering of the figure should emphasize the differences between the experiments ("difference mode"). The difference mode uses a set of four symbols that are semantically close to the scenarios that they are encoding. The default value is FALSE.
showlegend	Do you want the legend to be shown?
cols	colors to use for the specific scenarios when <code>diff = T</code> or <code>custom_icons</code> used.
leg_text	text for legend keys corresponding to the specific colors.

Note

For the parameter experiments, the four values any cell may take are: observed, different, unobserved, incorrect.

See Also

[init_experiments](#)

Examples

```
# Initialize the default experiments data frame
exps <- init_experiments()
sci_figure(exps)
sci_figure(exps, hide_stages = c("population", "analyst"))

# Do some manual manipulation to the experiments

exps["analyst", "Exp2"] <- "different"
exps["code", c("Exp2", "Exp3")] <- "unobserved"
sci_figure(exps, showlegend = FALSE)

# Create the same figure using the difference mode

sci_figure(exps, diff=TRUE)
too_many = init_experiments(nexp = 30)

testthat::expect_warning({
  sci_figure(too_many)
}, "showing the first")

exp2 = exps
exp2[,1] = "bad"
testthat::expect_error({
  sci_figure(exp2)
}, "Invalid cell")
```

Index

* datasets

icons, [2](#)

icons_diff, [2](#)

icons, [2](#)

icons_diff, [2](#)

init_experiments, [3](#), [6](#)

replicate_figure, [4](#)

reproduce_figure, [4](#)

sci_figure, [3](#), [4](#), [5](#)