

Package ‘reappraised’

March 5, 2026

Title Statistical Tools for Assessing Publication Integrity of Groups of Trials

Version 0.2

Description Takes user-provided baseline data from groups of randomised controlled data and assesses whether the observed distribution of baseline p-values, numbers of participants in each group, or categorical variables are consistent with the expected distribution, as an aid to the assessment of integrity concerns in published randomised controlled trials.

References (citations in PubMed format in details of each function):

Bolland MJ, Avenell A, Gamble GD, Grey A. (2016) <[doi:10.1212/WNL.0000000000003387](https://doi.org/10.1212/WNL.0000000000003387)>.

Bolland MJ, Gamble GD, Avenell A, Grey A, Lumley T. (2019) <[doi:10.1016/j.jclinepi.2019.05.006](https://doi.org/10.1016/j.jclinepi.2019.05.006)>.

Bolland MJ, Gamble GD, Avenell A, Grey A. (2019) <[doi:10.1016/j.jclinepi.2019.03.001](https://doi.org/10.1016/j.jclinepi.2019.03.001)>.

Bolland MJ, Gamble GD, Grey A, Avenell A. (2020) <[doi:10.1111/anae.15165](https://doi.org/10.1111/anae.15165)>.

Bolland MJ, Gamble GD, Avenell A, Cooper DJ, Grey A. (2021) <[doi:10.1016/j.jclinepi.2020.11.012](https://doi.org/10.1016/j.jclinepi.2020.11.012)>.

Bolland MJ, Gamble GD, Avenell A, Grey A. (2021) <[doi:10.1016/j.jclinepi.2021.05.002](https://doi.org/10.1016/j.jclinepi.2021.05.002)>.

Bolland MJ, Gamble GD, Avenell A, Cooper DJ, Grey A. (2023) <[doi:10.1016/j.jclinepi.2022.12.018](https://doi.org/10.1016/j.jclinepi.2022.12.018)>.

Carlisle JB, Loadsman JA. (2017) <[doi:10.1111/anae.13650](https://doi.org/10.1111/anae.13650)>.

Carlisle JB. (2017) <[doi:10.1111/anae.13938](https://doi.org/10.1111/anae.13938)>.

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Encoding UTF-8

RoxygenNote 7.3.3

Imports boot, data.table, dplyr, flextable, ggplot2, ggpubr, magrittr, officer, patchwork, purrr, readxl, rlang, stats, tidyr, tidyselect, utils

Depends R (>= 3.5.0)

LazyData true

Suggests knitr, rmarkdown, kableExtra

VignetteBuilder knitr

NeedsCompilation no

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anova_fn	<i>Compares differences between baseline means using Carlisle's montecarlo anova method</i>
----------	---

Description

Creates plots of distribution of p-values for differences in baseline means calculated using Carlisle's montecarlo anova method.

Usage

```
anova_fn(
  df = anova_data,
  method = "orig",
  seed = 0,
  sims = -1,
  btsp = 500,
  title = "",
  verbose = TRUE
)
```

Arguments

df	dataframe generated from load_clean function
method	"orig" is now the only option (previously "alt" was accepted)
seed	the seed to use for random number generation, default 0 = current date and time. Specify seed to make repeatable.
sims	number of simulations, default -1 = function selects based on number of variables and sample size
btsp	number of bootstrap repeats used to generate 95% confidence interval around AUC
title	optional title for plots
verbose	TRUE or FALSE indicates whether progress bar and comments show and prints plot

Details

Method is from Carlisle JB, Loadsman JA. Evidence for non-random sampling in randomised, controlled trials by Yuhji Saitoh. *Anaesthesia*. 2017;72:17-27.

R code is in appendix to paper. This function is adapted from that code.

The results from this approach will not be identical even if the same random number seed is used because they use the generated random numbers in different orders. Any differences in p-values will be small and related to the number of simulations- more simulations = smaller differences). The code that generates the p-value for each variable from the simulated means is essentially the same.

Returns a list containing 3 objects and (if verbose = TRUE) prints the plot anova_ecdf

Value

list containing 3 objects as described

- anova_ecdf = plot of cumulative distribution of calculated p-values compared to the expected uniform distribution
- anova_pvalues = plots of distribution of calculated p-values and AUC, as for pval_cont_fn()
- anova_all_results = list containing
 - anova_data = data frame of baseline data, with calculated p-values, and studywise p-values using the Carlisle-Stouffer test
 - anova_pvals = plot of distribution of calculated p-values from anova_pvalues
 - anova_auc = plot of AUC of calculated p-values from anova_pvalues
 - graph_data_ecdf = basic data that can be used to create and modify ecdf graph
 - graph_data_pvals = basic data that can be used to create and modify anova p-value graph
 - auc_data = basic data that can be used to create and modify anova auc graph
 - sims = number of simulations

Examples

```
# load example data
anova_data <- load_clean(import= "no", file.cont = "SI_pvals_cont", anova= "yes",
format.cont = "wide")$anova_data

# run function (takes only a few seconds)
anova_fn(sims = 100, btsp = 100)$anova_ecdf

# to import an excel spreadsheet (modify using local path,
# file and sheet name, range, and format):

# get path for example files
path <- system.file("extdata", "reappraised_examples.xlsx", package = "reappraised",
                    mustWork = TRUE)
# delete file name from path
path <- sub("/[^/]+$", "", path)

# load data
anova_data <- load_clean(import= "yes", anova = "yes", dir = path,
                        file.name.cont = "reappraised_examples.xlsx", sheet.name.cont = "SI_pvals_cont",
                        range.name.cont = "A:0", format.cont = "wide")$anova_data
```

cat_all_fn	<i>Compares observed and expected distribution of all categorical (binomial) variables</i>
------------	--

Description

Creates plots of observed to expected numbers and ratios for the binomial variables
Reference: Bolland MJ, Gamble GD, Avenell A, Cooper DJ, Grey A. Distributions of baseline categorical variables were different from the expected distributions in randomized trials with integrity concerns. *J Clin Epidemiol.* 2023;154:117-124

Usage

```
cat_all_fn(
  df = cat_all_data,
  two_levels = "no",
  del.disparate = "yes",
  excl.level = "yes",
  seed = 0,
  title = "",
  verbose = TRUE,
  binom = "deprecated",
  comp.pvals = "deprecated"
)
```

Arguments

df	data frame generated from load_clean function
two_levels	"yes" or "no" indicator whether variables with more than 2 levels should be collapsed to 2 levels
del.disparate	if yes, data in which the absolute difference between group sizes is >20% are deleted
excl.level	"yes" or "no" indicator whether one level of a variable should be deleted. Deleted level is chosen randomly using seed parameter. This is to avoid double counting of rows.
seed	seed for random number generator, default 0 = random. Specify seed to make repeatable.
title	title name for plots (optional)
verbose	TRUE or FALSE indicates whether progress bar and comments show and plot is printed
binom	no longer used
comp.pvals	deprecated because this function shifted to baseline p_val_cat function

Details

Returns a list containing objects described below and (if verbose = TRUE) prints graph cat_all_graph

Value

list containing 8 objects as described

- cat_all_graph = plot of observed to expected numbers and differences between groups, top panels are the absolute numbers, bottom panels are the differences between trial arms in two arm studies
- cat_all_graph_pc = plot of observed to expected numbers expressed as percentages and differences between groups, top panels are the percentages, bottom panels are the differences between trial arms in two arm studies
- cat_all_data_abs = data frame of data for absolute numbers
- cat_all_data_df = data frame of data for difference between groups in two arm studies
- cat_all_dataset_abs = data frame of dataset used for all trials
- cat_all_dataset_df = data frame of dataset used for two arm trials
- cat_all_all_graphs list containing
 - abs = plot for absolute numbers only
 - df = plot for difference between groups in two arm studies only
 - pc = plot for percentages only
 - all = composite of absolute, percentages, and differences
 - individual_graphs list of 6 individual plots making up composite figures
- cat_all_graph_data lists of data used to create and modify the respective graphs

Examples

```

# load example data
cat_all_data <- load_clean(import= "no", file.cat = "SI_cat_all", cat_all= "yes",
format.cat = "wide")$cat_all_data

# run function (takes only a few seconds)
cat_all_fn (excl.level = "yes")$cat_all_graph

# to import an excel spreadsheet (modify using local path,
# file and sheet name, range, and format):

# get path for example files
path <- system.file("extdata", "reappraised_examples.xlsx", package = "reappraised",
                    mustWork = TRUE)
# delete file name from path
path <- sub("/[^/]+$", "", path)

# load data
cat_all_data <- load_clean(import= "yes", cat_all = "yes", dir = path,
file.name.cat = "reappraised_examples.xlsx", sheet.name.cat = "SI_cat_all",
range.name.cat = "A:N", format.cat = "wide")$cat_all_data

```

cat_fn	<i>Compares observed and expected distribution of a categorical (binomial) variable</i>
--------	---

Description

Creates plots of observed to expected numbers and ratios for the specified binomial variable

Usage

```

cat_fn(
  df = cat_data,
  x_title = "",
  prefix = "",
  del.disparate = "yes",
  title = "",
  verbose = TRUE
)

```

Arguments

df	data frame generated from load_clean function
x_title	name of the variable for use on the x-axis

prefix	letter for variable columns in data frame
del.disparate	if yes, data in which the absolute difference between group sizes is >20% are deleted
title	title name for plots (optional)
verbose	TRUE or FALSE indicates whether to print plot

Details

An example is for trial withdrawals in Bolland 2021

Bolland MJ, Gamble GD, Avenell A, Cooper DJ, Grey A. Participant withdrawals were unusually distributed in randomized trials with integrity concerns: a statistical investigation. *J Clin Epidemiol* 2021;131:22-29.

Returns a list containing 4 objects and (if verbose = TRUE) prints the plot cat_graph

Value

list containing 5 objects as described

- cat_graph = plot of observed to expected numbers and differences between groups, top panels are the absolute numbers, bottom panels are the differences between trial arms in two arm studies
- cat_data_abs = data frame of data for absolute numbers
- cat_data_df = data frame of data for difference between groups in two arm studies
- cat_all_graphs = list containing
 - abs = plot for absolute numbers only
 - df = plot for difference between groups in two arm studies only
 - individual_graphs list of 4 individual plots making up composite figures
- cat_graph_data lists of data used to create and modify the respective graphs

Examples

```
# load example data
cat_data <- load_clean(import= "no", file.cat = "SI_cat", cat= "yes",
  format.cat = "wide", cat.names = c("n", "w"))$cat_data

# run function (takes only a few seconds)
cat_fn(x_title= "withdrawals", prefix="w", del.disparate = "yes")$cat_graph

# to import an excel spreadsheet (modify using local path,
# file and sheet name, range, and format):

# get path for example files
path <- system.file("extdata", "reappraised_examples.xlsx", package = "reappraised",
  mustWork = TRUE)
# delete file name from path
path <- sub("/[^/]+$", "", path)
```

```
# load data
cat_data <- load_clean(import= "yes", cat = "yes", dir = path,
  file.name.cat = "reappraised_examples.xlsx", sheet.name.cat = "SI_cat",
  range.name.cat = "A:G", cat.names = c("n", "w"), format.cat = "wide")$cat_data
```

cohort_fn	<i>Compares proportions of matching summary statistics in different cohorts</i>
-----------	---

Description

Creates flextable of probability of matching mean, SD, and mean and SD for each variable in different cohorts in the specified number of simulations

Usage

```
cohort_fn(
  df = cohort_data,
  seed = 0,
  sims = -1,
  n_vars = 10,
  popn = "",
  title = "",
  verbose = TRUE
)
```

Arguments

df	data frame generated from load_clean function
seed	the seed to use for random number generation, default 0 = current date and time. Specify seed to make repeatable.
sims	number of simulations, default -1 = function selects based on number of variables and sample size.
n_vars	restrict analyses to variables in at least (\geq) this number of cohorts, default = 10 (ie variable has mean in 10 or more cohorts).
popn	if dataset contains studies in different sub-populations, code this in cohort_data\$population and studies are subsetted if match in this variable. 'All' overrides this and uses all data regardless of information in this variable.
title	title name for plots (optional)
verbose	TRUE or FALSE indicates whether progress bar and comments show and flextable is printed

Details

Reference data is from Bolland 2021

Bolland MJ, Gamble GD, Avenell A, Grey A. Identical summary statistics were uncommon in randomized trials and cohort studies. *J Clin Epidemiol* 2021;136:180-188.

Returns a list containing 6 objects and (if verbose = TRUE) prints the flextable cohort_ft

Value

list containing 6 objects as described

- cohort_ft = flextable of results
- cohort_graph = plot of observed to expected numbers of matches per cohort for mean; SD; and mean and SD
- all_graphs = list containing
 - all_graphs = all plots on single plot
 - both_graphs = list of 3 plots row by row used to form all_graphs
 - individual_graphs = list of 6 individual plots used to form all_graphs
- cohort_cohort_data = data frame used to generate results data
- cohort_prob_data = data frame used to make flextable
- cohort_oe_data = data frame used to make observed to expected plots

Examples

```
# load example data
cohort_data <- load_clean(import= "no", file.cont = "SI_cohort", cohort= "yes",
format.cont = "long")$cohort_data

# run function (takes only a few seconds)
cohort_fn(sims = 100)$cohort_ft

# to import an excel spreadsheet (modify using local path,
# file and sheet name, range, and format):

# get path for example files
path <- system.file("extdata", "reappraised_examples.xlsx", package = "reappraised",
                    mustWork = TRUE)
# delete file name from path
path <- sub("/[^/]+$", "", path)

# load data
cohort_data <- load_clean(import= "yes", cohort = "yes", dir = path,
file.name.cont = "reappraised_examples.xlsx", sheet.name.cont = "SI_cohort",
range.name.cont = "A1:F101", format.cont = "long")$cohort_data
```

final_digit_fn	<i>Compares proportions of final digits from summary statistics</i>
----------------	---

Description

Creates graph of proportion of final digits for summary statistics of specified variables

Usage

```
final_digit_fn(
  df = generic_data,
  vars = "",
  dec.pl = "no",
  dec.pl.vars = "",
  title = "",
  verbose = TRUE
)
```

Arguments

df	data frame generated from load_clean function
vars	vector of the summary statistics to be used (a single letter eg m,c("m","s"))
dec.pl	"yes" or "no" indicator whether columns for decimal places are included (yes) or should be calculated (no). No is the default and uses the decimal places calculated in load clean which, for the example of the prefix "m", will be in the form dpm, or dpm1, dpm2... If overriding that specific the decimal place variables in dec.pl.vars. The calculated decimal places (dpx) are removed automatically.
dec.pl.vars	vector of the names of the columns for decimal places for each statistic eg for the statistic "m", use dp_m if all dec places are the same, or dp_m1, dp_m2 etc. For multiple statistics, as an example use c("dp_m", "dp_s") with suffixes as needed.
title	title name for plots (optional)
verbose	TRUE or FALSE indicates whether print plot

Details

This approach is still in development and needs validation and discussion about its place in integrity assessment.

Requires data frame containing columns for study, variable (named var), summary statistic(s) (named with single letter eg m or s), and optional columns for decimal places for each statistic (named dp_* eg dp_m, dp_s). Data can be imported using the generic option of load_clean function

Returns a list containing 6 objects and prints the plot digit_graph

Value

list containing 5 objects as described

- digit_graph = plot of proportions of final digits
- digit_ft = flextable of results
- digit_table = data frame of results
- digit_dataset = data frame of data set used to generate results data
- digit_data = results of analyses used to generate results data
- digit_graph_data = lists of data used to create and modify the respective graphs

Examples

```
# load example data
generic_data <- load_clean(import= "no", file.cont = "SI_pvals_cont", generic= "yes",
gen.vars.del = c("p"), format.cont = "wide")$generic_data

# run function (takes only a few seconds)
final_digit_fn(vars = c("m","s"), dec.pl = "n")$digit_graph

# to import an excel spreadsheet (modify using local path,
# file and sheet name, range, and format):

# get path for example files
path <- system.file("extdata", "reappraised_examples.xlsx", package = "reappraised",
                    mustWork = TRUE)
# delete file name from path
path <- sub("/[^/]+$", "", path)

# load data
generic_data <- load_clean(import= "yes", generic = "yes", dir = path,
                          file.name.cont = "reappraised_examples.xlsx", sheet.name.cont = "SI_pvals_cont",
                          range.name.cont = "A1:O51", gen.vars.del = c("p"),
                          format.cont = "wide")$generic_data
```

graph_maker_fn

Creates graphs for functions in package

Description

Creates plots from the data in the results of the various functions

Usage

```
graph_maker_fn(data, graph_type = NULL)
```

Arguments

data list exported from the function
graph_type optional can specify the graph type ("pval", "auc", "rr", or "cat")

Details

Returns a list containing the graphs from the respective function

Value

A list containing the outputted graphs

Examples

```
# load example data
pval_cont_data <- load_clean(import= "no", file.cont = "SI_pvals_cont", pval_cont= "yes",
format.cont = "wide")$pval_cont_data

# run function (takes only a few seconds)
graph <- pval_cont_fn(btsp=100, verbose= FALSE, sims=100)$all_results$graph_data_calc
graph_maker_fn(graph) [[2]]
```

load_clean

Load data then clean and format it

Description

Function loads and cleans data for the nine functions

Usage

```
load_clean(
  import = "yes",
  file.cont = "",
  file.cat = "",
  dir = "",
  file.name = "",
  pval_cont = "no",
  match = "no",
  cohort = "no",
  anova = "no",
  dir.cont = "",
  file.name.cont = "",
  sheet.name.cont = "Sheet1",
  range.name.cont = "",
```

```

format.cont = "wide",
cat = "no",
sr = "no",
cat_all = "no",
pval_cat = "no",
cat.names = c("n"),
dir.cat = "",
file.name.cat = "",
sheet.name.cat = "Sheet1",
range.name.cat = "",
format.cat = "wide",
generic = "",
gen.vars.keep = "",
gen.vars.del = "",
verbose = TRUE
)

```

Arguments

import	'yes' indicates import excel file. 'no' indicates takes dataset already loaded into R as data frame
file.cont	If import = 'no', name of data frame containing continuous data
file.cat	If import = 'no', name of data frame containing categorical data
dir	If import = 'yes', path to location of excel file for continuous and categorical data
file.name	If import = 'yes', file name of excel file containing continuous and categorical data
pval_cont	'yes'/'no' indicating if data will be used for pval_cont_fn. Only data for 1 continuous data function can be loaded with each run of this function.
match	'yes'/'no' indicating if data will be used for match_fn. Only data for 1 continuous data function can be loaded with each run of this function.
cohort	'yes'/'no' indicating if data will be used for cohort_fn. Only data for 1 continuous data function can be loaded with each run of this function.
anova	'yes'/'no' indicating if data will be used for anova_fn. Only data for 1 continuous data function can be loaded with each run of this function.
dir.cont	If import = 'yes', path to location of excel file for continuous data
file.name.cont	If import = 'yes', file name of excel file containing continuous data
sheet.name.cont	Sheet name containing continuous data
range.name.cont	Range of cells containing continuous data. Can be in format 'a1:b20' or 'a:b'
format.cont	'wide'/'long' indicating continuous data is in wide or long format
cat	'yes'/'no' indicating if data will be used for cat_fn. Only data for 1 categorical data function can be loaded with each run of this function.

sr	'yes'/'no' indicating if data will be used for sr_fn. Only data for 1 categorical data function can be loaded with each run of this function.
cat_all	'yes'/'no' indicating if data will be used for cat_all_fn. Only data for 1 categorical data function can be loaded with each run of this function.
pval_cat	'yes'/'no' indicating if data will be used for cat_all_fn. Only data for 1 categorical data function can be loaded with each run of this function.
cat.names	names of variables to be used in cat_fn and sr_fn
dir.cat	If import = 'yes', path to location of excel file for categorical data
file.name.cat	If import = 'yes', file name of excel file containing categorical data
sheet.name.cat	Sheet name containing categorical data
range.name.cat	Range of cells containing categorical. Can be in format 'a1:b20' or 'a:b'
format.cat	'wide'/'long' indicating categorical data is in wide or long format
generic	'yes'/'no' indicating if data to be loaded for generic use
gen.vars.keep	Vector of variables in data to keep
gen.vars.del	Vector of variables in data to delete
verbose	TRUE/FALSE TRUE indicates comments will be printed during loading

Details

Function can load continuous or categorical data. Continuous data can be used for comparison of baseline p-values (pval_cont_fn), matching summary stats within a trial (match_fn), matching summary stats in different cohorts (cohort_fn), or comparing means of baseline p-values (anova_fn). Categorical data can be used for comparisons of observed with expected distributions for single variable (cat_fn), for group numbers in trials using simple randomisation (sr_fn), for all variables (cat_all_fn), and for comparison of baseline p-values (pval_cat_fn).

There is one function in development that allows assessment of proportion of final digits in summary statistics (final_digit_fn). This function works using summary statistics but could be adapted to use on raw continuous or categorical data.

Only 1 continuous and/or 1 categorical data set allowed per load to avoid clashes

Data can be imported from a file (import = "yes") or taken from an existing data frame, import = "no"

If loading from an existing data use file.cont and file.cat

If loading from common directory or file, can use dir and file.name rather than more specific dir.cont, dir.cat, file.name.cont, or file.name.cat.

Comments about each indicator: pval_cont

loads continuous data for pval_cont_fn, outputs as list of 1 containing named data frame pval_cont_data.

format should be study, variable or var, n, m, s, p. Can be in any order. n = sample size, m = mean, s = standard deviation, p = baseline p value (can omit if not reported)

can be in wide or long format

wide: study, var, n1, n2, n3 ..., m1, m2, m3 ... s1, s2, s3..., p

long: study, var, group, m , s, n , p

group or g or grp required for long format
separators (eg n1 n_1 n.1) are stripped and replaced

match

loads continuous data for match_fn, outputs as list of 1 containing named data frame match_data

remainder is same as for pval_cont above.
only difference between pval_cont and match is that match allows for missing mean or SD whereas pval_cont does not

format should be study, variable or var, n, m, s. Can be in any order. n = sample size, m = mean, s = standard deviation

can be in wide or long format
wide: study, var, n1, n2, m1, m2, s1, s2, p
long: study, var, group, m , s, n

group or g or grp required for long format
separators (eg n1 n_1 n.1) are stripped and replaced

cohort

loads continuous data for cohort_fn, outputs as list of 1 containing named data frame cohort_data

same as pval_cont but allows a lookup variable for variable names

format should be study, variable or var, n, m, s, p. Can be in any order. n = sample size, m = mean, s = standard deviation

can be in wide or long format
wide: study, var, n1, n2, n3 ..., m1, m2, m3 ... s1, s2, s3...
long: study, var, group, m , s, n

group or g or grp required for long format
separators (eg n1 n_1 n.1) are stripped and replaced

lookup table is var_name_final, var_name_orig and allows you to specify a list of all variables names (var_name_orig) from all studies and a lookup table of standardised names (var_name_final) allowing different names in different studies to be standardised

has optional variable 'population' which can be used to subset the data if trials in different populations are reported

anova

loads continuous data for `anova_fn`, outputs as list of 1 containing named data frame `anova_data`

same as for `pval_cont` above but allows for optional value for decimal place

format should be study, variable or var, n, m, s, p. Can be in any order. n = sample size, m = mean, s = standard deviation, d= decimal place of mean (if omitted, this is calculated automatically in `anova_fn`)

can be in wide or long format

wide: study, var, n1, n2, n3 ..., m1, m2, m3 ... s1, s2, s3..., d

long: study, var, group, m, s, n, d

group or g or grp required for long format

separators (eg n1 n_1 n.1) are stripped and replaced

cat

loads categorical data for `cat_fn`, outputs as list of 1 containing named data frame `cat_data`

format should be study, n, v. Can be in any order, n= group size, v= number with characteristic

can be in wide or long format

wide: study, n1, n2, n3 ..., v1, v2, v3...

long: study, group, n, v

group or g or grp required for long format

use `cat.names` to name variable eg `c("n", "v")`, `c("n", "g")` ...

separators (eg n1 n_1 n.1) are stripped and replaced

sr

loads categorical data for `sr_fn`, outputs as list of 1 containing named data frame `sr_data`

as for `cat` but only requires study and n

format should be study, n. n= group size

can be in wide or long format

wide: study, n1, n2, n3 ...

long: study, group, n

group or g or grp required for long format

separators (eg n1 n_1 n.1) are stripped and replaced

cat_all

loads categorical data for `cat_all_fn`, outputs as list of 1 containing named data frame `cat_all_data`

format should be study, var or variable, n, N, level, recode. Can be in any order, n = number with characteristic, N = group size,

optional level - number for level of variable (eg y/n =1,2; high/med/low =1,2,3)

optional recode- for variables with >2 levels to tell how to recode into 2 groups

optional calculated_level - if levels have been calculated rather than reported eg if gender is reported as males n=10, N= 20, then females n=10 would be the calculated level "yes".

can be in wide or long format

wide study, var, n1, n2, n3, ... N1, N2, N3... level, recode, calculated_level

long study, var, group, n, N, level, recode, calculated_level

group or g or grp required for long format

if variable has 2 levels, only 1 required, other will be calculated.

separators (eg n1 n_1 n.1) are stripped and replaced

pval_cat

loads categorical data for pval_cat_fn, outputs as list of 1 containing named data frame pval_cat_data

as for cat_all but recode variable is not generated

format should be study, var or variable, n, N. Can be in any order, n = number with characteristic, N = group size,

optional baseline p value (can omit if not reported), can use "ns" for not significant or "<" or ">" to indicate threshold (eg "<0.05")

optional level - number for level of variable (eg y/n =1,2; high/med/low =1,2,3)

optional calculated_level - if levels have been calculated rather than reported eg if gender is reported as males n=10, N= 20, then females n=10 would be the calculated level "yes". optional stat: statistical test used for p-value : chisq - Chisquare, chisqc- Chisquare with correction, fisher- Fisher's exact, midp.exact, midp.classic, lr- likelihood ratio, mh - Mantel-Haenszel test

can be in wide or long format

wide study, var, n1, n2, n3, ... N1, N2, N3... p, stat, level, calculated_level

long study, var, group, n, N, p, stat, level, calculated_level

group or g or grp required for long format

if variable has 2 levels, only 1 required, other will be calculated.

separators (eg n1 n_1 n.1) are stripped and replaced

generic

loads data for use generic use, outputs as list of 1 containing named data frame generic_data

use cont suffixes for file details: dir.cont (or dir), file.name.cont (or file.name), sheet.name.cont, range.name.cont)

format should be study, var or variable, variable names

optional gen.vars.keep = vector of variables to keep

optional gen.vars.del = vector of variables to delete optional decimal places - can use dpm, or dpx where x=prefix of variable if one decimal place for all vars or dpm1, dpm2, dps1, dps2.....

can be in wide or long format

wide study, var, a1, a2..., b1, b2 ..., dpa1, dpa2..., dpb1, dpb2...

long study, var, group, a, b, dpa, dpb ...

group or g or grp required for long format

separators (eg n1 n_1 n.1) are stripped and replaced

no data checking or other transformations take place

Value

list containing a named data frame containing data in suitable format for appropriate function as described in Details

Examples

```
# examples of loading data for each function are given in the individual functions.
# Here is one- for pval_cont_fn():

pval_cont_data <- load_clean(import= "no", file.cont = "SI_pvals_cont", pval_cont= "yes",
format.cont = "wide")$pval_cont_data

# to import an excel spreadsheet (modify using local path,
# file and sheet name, range, and format):

# get path for example files
path <- system.file("extdata", "reappraised_examples.xlsx", package = "reappraised",
                    mustWork = TRUE)
# delete file name from path
path <- sub("/[^/]+$", "", path)

# load data
pval_cont_data <- load_clean(import= "yes", pval_cont = "yes", dir = path,
file.name.cont = "reappraised_examples.xlsx", sheet.name.cont = "SI_pvals_cont",
range.name.cont = "A1:O51", format.cont = "wide")$pval_cont_data
```

match_fn	<i>Compares proportions of matching summary statistics within randomised trials</i>
----------	---

Description

Creates flextable of matching summary statistics by significant figures with Reference data

Usage

```
match_fn(
  df = match_data,
  calc_refp = "y",
  seed = 0,
  sims = -1,
  verbose = TRUE,
  title = ""
)
```

Arguments

df	data frame generated from load_clean function
calc_refp	calculate reference distribution for p-values empirically from simulations using seed and sims ("yes") or use reference published dataset (Anaesthesia 2020, see references) ("no")
seed	the seed to use for random number generation, default 0 = current date and time. Specify seed to make repeatable.
sims	number of simulations, default -1 = function selects based on number of variables and sample size.
verbose	TRUE or FALSE indicates whether to print flextable
title	optional title for plots

Details

Reference data is from Bolland 2021

Bolland MJ, Gamble GD, Avenell A, Grey A. Identical summary statistics were uncommon in randomized trials and cohort studies. *J Clin Epidemiol* 2021;136:180-188.

Returns a list containing 11 objects and (if verbose = TRUE) prints the flextable match_ft_all

Value

list containing 11 objects as described

- match_ft_all = flextable of matches with reference data
- match_ft = flextable of matches (no reference data)

- ref_match_ft = flextable of reference data
- match_match_data = data frame of results used in calculations
- match_table = data frame of matches used to make flextable
- ref_table = data frame of reference data used to make flextable
- match_probbystudy = data frame of observed and expected matches and probability of no matches by study
- match_probbystudy.diff.fmt = same as probbystudy but in wide format
- match_obsexp_all = data frame of data for observed to expected matches for entire group of studies
- match_obsexpbystudy = same as obsexp_all but by study
- match_graphs = list of graphs
 - comp = figure of 6 graphs of observed to expected data and ratios for mean matches, sd matches, and both mean and sd matches
 - individ = 3 lists of individual figures and data for mean, sd, and both mean and sd matches that make up the composite figure
 - match_graph_data = 6 lists of data used to create and modify the respective graphs

Examples

```
# load example data
match_data <- load_clean(import= "no", file.cont = "SI_pvals_cont", match= "yes",
format.cont = "wide")$match_data

# run function (takes only a few seconds)
match_fn(sims=100)$match_ft_all

# to import an excel spreadsheet (modify using local path,
# file and sheet name, range, and format):

# get path for example files
path <- system.file("extdata", "reappraised_examples.xlsx", package = "reappraised",
                    mustWork = TRUE)
# delete file name from path
path <- sub("/[^/]+$", "", path)

# load data
match_data <- load_clean(import= "yes", match = "yes", dir = path,
                        file.name.cont = "reappraised_examples.xlsx", sheet.name.cont = "SI_pvals_cont",
                        range.name.cont = "A:0", format.cont = "wide")$match_data
```

pval_cat_fn	<i>Compares observed and expected distribution of p-values for categorical variables</i>
-------------	--

Description

Creates plots of calculated p-value distribution and AUC (area under curve) and compares reported and calculated p-values

Usage

```
pval_cat_fn(
  df = pval_cat_data,
  match_pvals = "yes",
  miss_data_explain = "yes",
  seed = 0,
  sims = -1,
  btsp = 500,
  title = "",
  stat = "chi_midp.exact",
  stat.override = "no",
  fisher.sim = "y",
  fish.n.sims = 2000,
  method = "sm",
  verbose = TRUE
)
```

Arguments

df	data frame generated from load_clean function
match_pvals	"yes" or "no" indicator to compare reported p-value with range of calculated p-values from summary data
miss_data_explain	"yes" or "no" indicator to check whether missing data might explain differences in reported and calculated p-values
seed	the seed to use for random number generation, default 0 = current date and time. Specify seed to make repeatable.
sims	number of simulations, default -1 = function selects based on number of variables.
btsp	number of bootstrap repeats used to generate 95% confidence interval around AUC
title	optional title for plots
stat	statistical test to be used 'chisq', 'fisher', 'midp' or 'midp.exact', 'midp.classic', or combinations -if chisq is not appropriate because expected cells<5, use second test: 'chi_fish', 'chi_midp.exact' or 'chi_midp.classic'

stat.override	if 'yes' then test specified in stat will be used rather than values for stat in data frame
fisher.sim	"yes" or "no" indicator whether to allow fisher test to simulate p-values for >2*2 tables
fish.n.sims	number of simulations to use in Fisher test, default 2,000
method	no longer available automatically uses equivalent of 'sm'
verbose	TRUE or FALSE indicates whether progress bar and comments show and prints plot

Details

See also Bolland MJ, Gamble GD, Avenell A, Grey A, Lumley T. Baseline P value distributions in randomized trials were uniform for continuous but not categorical variables. *J Clin Epidemiol* 2019;112:67-76.

Returns a list containing 6 objects and (if verbose = TRUE) prints the plot pval_cat_calculated_pvalues

Value

list containing 6 objects as described

- pval_cat_calculated_pvalues = plots of calculated p-value distribution and AUC
- pval_cat_reported_pvalues = plots of reported p-value distribution and AUC (if p-values were reported)
- pval_cat_check = data frame of comparison between reported and calculated p-values from a range of tests
- pval_cat_ft_diff_calc_rep_p = flextable of distribution of differences in calculated and reported results
- pval_cat_diff_results = dataset with data for flextable
- all_results = list containing
 - pval_cat_baseline_pvalues_data = data frame of all results used in calculations with reported and calculated p-values
 - pval_cat_reported_pvalues = plot of reported p-value distribution
 - pval_cat_auc_reported_pvalues = AUC of reported p-values
 - pval_cat_calculated_pvalues = plot of calculated p-value distribution
 - pval_cat_auc_calculated_pvalues = AUC of calculated p-values
 - pval_cat_diff_calc_rep_p = data frame of differences between reported and calculated p-values
 - pval_cat_diff_calc_rep_p_summary = summary table of differences between reported and calculated p-values
 - sims = number of simulations used in generating reference data
 - graph_data_calc = basic data that can be used to create and modify calculated p-value graph
 - graph_data_rep = basic data that can be used to create and modify reported p-value graph
 - auc_data_calc = basic data that can be used to create and modify calculated AUC graph
 - auc_data_rep = basic data that can be used to create and modify reported AUC graph

Examples

```

# load example data
pval_cat_data <- load_clean(import= "no", file.cat = "SI_cat_all", pval_cat= "yes",
format.cont = "wide")$pval_cat_data

# run function (takes a few seconds)
pval_cat_fn(sims = 50, btsp = 100)$pval_cat_calculated_pvalues

# to import an excel spreadsheet (modify using local path,
# file and sheet name, range, and format):

# get path for example files
path <- system.file("extdata", "reappraised_examples.xlsx", package = "reappraised",
                    mustWork = TRUE)
# delete file name from path
path <- sub("/[^/]+$", "", path)

# load data
pval_cat_data <- load_clean(import= "yes", pval_cat = "yes", dir = path,
file.name.cat = "reappraised_examples.xlsx", sheet.name.cat = "SI_cat_all",
range.name.cat = "A:n", format.cat = "wide")$pval_cat_data

```

pval_cont_fn	<i>Compares observed and expected distribution of p-values for continuous variables</i>
--------------	---

Description

Creates plots of calculated p-value distribution and AUC (area under curve)

Usage

```

pval_cont_fn(
  df = pval_cont_data,
  calc_refp = "y",
  seed = 0,
  sims = -1,
  btsp = 500,
  title = "",
  verbose = TRUE
)

```

Arguments

df data frame generated from load_clean function

calc_refp	calculate reference distribution for p-values empirically from simulations using seed and sims ("yes") or use reference published dataset (Anaesthesia 2020, see references) ("no")
seed	the seed to use for random number generation, default 0 = random. Specify seed to make repeatable.
sims	number of simulations, default -1 = function selects based on number of variables and sample size.
btsp	number of bootstrap repeats used to generate 95% confidence interval around AUC. Default =500
title	optional title for plots
verbose	TRUE or FALSE indicates whether progress bar and comments show and prints plot

Details

Reference data is from (Carlisle 2017, Bolland 2021)

Carlisle JB . Data fabrication and other reasons for non-random sampling in 5087 randomised, controlled trials in anaesthetic and general medical journals. *Anaesthesia* 2017;72:944–52 .2017

Bolland MJ, Gamble GD, Grey A, Avenell A. Empirically generated reference proportions for baseline p values from rounded summary statistics. *Anaesthesia* 2020;75:1685-1687.

See also Bolland MJ, Gamble GD, Avenell A, Grey A, Lumley T. Baseline P value distributions in randomized trials were uniform for continuous but not categorical variables. *J Clin Epidemiol* 2019;112:67-76.

and Bolland MJ, Gamble GD, Avenell A, Grey A. Rounding, but not randomization method, non-normality, or correlation, affected baseline P-value distributions in randomized trials. *J Clin Epidemiol* 2019;110:50-62.

Returns a list containing 6 objects and (if verbose = TRUE) prints the plot pval_cont_calculated_pvalues

Value

list containing 6 objects as described

- pval_cont_calculated_pvalues = plots of calculated p-value distribution and AUC
- pval_cont_reported_pvalues = plots of reported p-value distribution and AUC (if p-values were reported)
- pval_cont_ft_diff_calc_rep_p = flextable of distribution of differences in calculated and reported results
- pval_cont_results = dataset with results used in calculations, including Carlisle studywise p-value on reported p-values (see anova function)
- pval_cont_check = dataset of reported p-value, min and max possible p-value calculated from maximally rounded summary stats and flag if outside this range
- all_results = list containing
 - pval_cont_baseline_pvalues_data = data frame of all results used in calculations
 - pval_cont_diff_calc_rep_p = data frame of differences between calculated and reported p-values

- pval_cont_diff_calc_rep_p_summary = table of raw differences between calculated and reported p-values
- pval_cont_reported_pvalues= plot of reported p-value distribution
- pval_cont_auc_reported_pvalues = AUC of reported p-values
- pval_cont_calculated_pvalues = plot of calculated p-value distribution
- pval_cont_auc_calculated_pvalues= AUC of calculated p-values
- sims = number of simulations if not specified and calc_refp = yes
- graph_data_rep = basic data that can be used to create and modify reported p-value graph
- graph_data_calc = basic data that can be used to create and modify calculated p-value graph
- auc_data_rep = basic data that can be used to create and modify reported auc graph
- auc_data_calc = basic data that can be used to create and modify calculated auc graph

Examples

```
# load example data
pval_cont_data <- load_clean(import= "no", file.cont = "SI_pvals_cont", pval_cont= "yes",
format.cont = "wide")$pval_cont_data

# run function (takes only a few seconds)
pval_cont_fn(btsp=100, sims=100)$pval_cont_calculated_pvalues

# to import an excel spreadsheet (modify using local path,
# file and sheet name, range, and format):

# get path for example files
path <- system.file("extdata", "reappraised_examples.xlsx", package = "reappraised",
                    mustWork = TRUE)
# delete file name from path
path <- sub("/[^/]+$", "", path)

# load data
pval_cont_data <- load_clean(import= "yes", pval_cont = "yes", dir = path,
                             file.name.cont = "reappraised_examples.xlsx", sheet.name.cont = "SI_pvals_cont",
                             range.name.cont = "A1:O51", format.cont = "wide")$pval_cont_data
```

SI_cat

Example of 20 observations for categorical analysis

Description

Sample from Sato/Iwamoto dataset of 35 studies with withdrawal data
see Bolland MJ, Gamble GD, Avenell A, Cooper DJ, Grey A. Participant withdrawals were unusually distributed in randomized trials with integrity concerns: a statistical investigation. J Clin Epidemiol 2021;131:22-29.

Usage

SI_cat

Format

A data frame with 20 rows and 8 variables:

study study ID

n1, n2, n3 number of participants in each group

w1, w2, w3 number of withdrawals in each group

SI_cat_all	<i>Example of 50 variables from different studies for categorical (cat_all_fn) analysis</i>
------------	---

Description

Sample from Sato/Iwamoto dataset of 31 studies with categorical data

Usage

SI_cat_all

Format

A data frame with 106 rows and 14 variables:

study study ID

var variable

level level of variable

recode value to recode level two if collapsing variable to two levels

levels_no total number of levels for each variable

group number of trial arms

n1, n2, n3 number of participants with characteristic in each group

N1, N2, N3 number of participants in each group

p reported p-value

stat reported statistical test used to calculate p-value

`SI_cohort`*Example of 100 observations for cohort analysis*

Description

Sample from Sato/Iwamoto dataset of 226 baseline variables in 34 cohorts see Bolland MJ, Gamble GD, Avenell A, Grey A. Identical summary statistics were uncommon in randomized trials and cohort studies. *J Clin Epidemiol* 2021;136:180-188.

Usage`SI_cohort`**Format**

A data frame with 100 rows and 6 variables:

study study ID

var variable name

n number of participants in group

m mean of variable

s sd of variable

group number of group

`SI_pvals_cont`*Example of 50 observations for p-value analysis*

Description

Sample from Sato/Iwamoto dataset of 500 baseline variables in 41 trials for details see Bolland MJ, Avenell A, Gamble GD, Grey A. Systematic review and statistical analysis of the integrity of 33 randomized controlled trials. *Neurology* 2016;87:2391-2402.

Usage`SI_pvals_cont`

Format

A data frame with 50 rows and 15 variables:

study study ID

var variable name

n1,n2,n3,n4 size of group 1, 2, 3, 4

m1,m2,m3,m4 mean of variable for group 1, 2, 3, 4

s1,s2,s3,s4 sd of variable for group 1, 2, 3, 4

p reported p-value

sr_fn	<i>Compares observed and expected distribution of difference in numbers of participants between groups in two-arm randomised trials</i>
-------	---

Description

Creates plot of observed to expected numbers and ratios for differences in numbers of participants between trial groups

Usage

```
sr_fn(
  df = sr_data,
  br = "no",
  block = data.frame(study = "", fbsz = "", n_fb = "", df = ""),
  title = "",
  verbose = TRUE
)
```

Arguments

df	data frame generated from load_clean function
br	block randomisation: 'yes' or 'no'. If 'no' runs function as if all trials used simple randomisation. If 'yes' performs simple calculations as if block randomised
block	an additional option for studies using block randomisation. block is a data frame containing columns named study (for study id); fbsz (for the final block size); n_fb (for number of participants in the final block); df (the difference between groups)
title	title name for plots (optional)
verbose	TRUE or FALSE indicates whether progress bar and comments in block randomisation function show and whether to print plot

Details

An example is for Sato and Iwamoto trials in Bolland 2016

Bolland MJ, Avenell A, Gamble GD, Grey A. Systematic review and statistical analysis of the integrity of 33 randomized controlled trials. *Neurology* 2016;87:2391-2402.

Returns a list containing 4 objects and (if verbose = TRUE) prints the plot sr_graph

Value

list containing 5 objects as described

- sr_graph = plot of observed to expected numbers for differences between numbers of participants in trial groups
- sr_graph = plot of observed to expected numbers and ratios for differences between numbers of participants in trial groups
- sr_individual_graphs = list containing 2 plots making up composite figure
- sr_data = data frame containing data for plots
- sr_graph_data lists of data used to create and modify the respective graphs

Examples

```
# load example data
sr_data <- load_clean(import= "no", file.cat = "SI_cat", sr= "yes",
format.cat = "wide")$sr_data

# run function (takes only a few seconds)
sr_fn()$sr_graph

# to import an excel spreadsheet (modify using local path,
# file and sheet name, range, and format):

# get path for example files
path <- system.file("extdata", "reappraised_examples.xlsx", package = "reappraised",
                    mustWork = TRUE)
# delete file name from path
path <- sub("/[^/]+$", "", path)

# load data
sr_data <- load_clean(import= "yes", sr = "yes", dir = path,
file.name.cat = "reappraised_examples.xlsx", sheet.name.cat = "SI_cat",
range.name.cat = "A:D", format.cat = "wide")$sr_data

# function has an additional option for block randomisation.
# If studies are block randomised and the final block size is known,
# the number of participants in the final block can be determined.
# The distribution of differences between groups for the final block
# can be compared to the expected distribution
#
# Few studies provide all these details so it seems unlikely this function
# would get used often
```

```
# Example takes only a few seconds to run

sr_fn(br = "yes", block = data.frame(study = c(1,2,3,4,5,6,7,8,9,10),
  fb_sz= c(2,4,6,8,10,12,8,8,6,14), n_fb = c(1,1,4,5,7,8,4,6,2,10),
  df=c(1,1,0,1,3,4,2,2,0,0)))$sr_graph
```

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