

# Package ‘rsimsum’

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**Title** Analysis of Simulation Studies Including Monte Carlo Error

**Version** 0.13.1

**Description** Summarise results from simulation studies and compute Monte Carlo standard errors of commonly used summary statistics. This package is modelled on the 'simsum' user-written command in 'Stata' (White I.R., 2010 <<https://www.stata-journal.com/article.html?article=st0200>>), further extending it with additional performance measures and functionality.

**License** GPL (>= 3)

**URL** <https://ellesenne.github.io/rsimsum/>,  
<https://github.com/ellesenne/rsimsum>

**BugReports** <https://github.com/ellesenne/rsimsum/issues>

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---

autoplot.multisimsum *autoplot method for multisimsum objects*

---

## Description

autoplot can produce a series of plot to summarise results of simulation studies. See vignette("C-plotting", package = "rsimsum") for further details.

## Usage

```
## S3 method for class 'multisimsum'
autoplot(
  object,
  par,
  type = "forest",
  stats = "nsim",
  target = NULL,
```

```

    fitted = TRUE,
    scales = "fixed",
    top = TRUE,
    density.legend = TRUE,
    zoom = 1,
    zip_ci_colours = "yellow",
    ...
  )

```

## Arguments

object	An object of class multisimsum.
par	The parameter results to plot.
type	The type of the plot to be produced. Possible choices are: forest, lolly, zip, est, se, est_ba, se_ba, est_density, se_density, est_hex, se_hex, est_ridge, se_ridge, heat, nlp, with forest being the default.
stats	Summary statistic to plot, defaults to bias. See <a href="#">summary.simsum()</a> for further details on supported summary statistics.
target	Target of summary statistic, e.g. 0 for bias. Defaults to NULL, in which case target will be inferred.
fitted	Superimpose a fitted regression line, useful when type = (est, se, est_ba, se_ba, est_density, se_density, est_hex, se_hex). Defaults to TRUE.
scales	Should scales be fixed (fixed, the default), free (free), or free in one dimension (free_x, free_y)?
top	Should the legend for a nested loop plot be on the top side of the plot? Defaults to TRUE.
density.legend	Should the legend for density and hexbin plots be included? Defaults to TRUE.
zoom	A numeric value between 0 and 1 signalling that a zip plot should <i>zoom</i> on the top x% of the plot (to ease interpretation). Defaults to 1, where the whole zip plot is displayed.
zip_ci_colours	A string with (1) a hex code to use for plotting coverage probability and its Monte Carlo confidence intervals (the default, with value zip_ci_colours = "yellow"), (2) a string vector of two hex codes denoting optimal coverage (first element) and over/under coverage (second element) or (3) a vector of three hex codes denoting optimal coverage (first), undercoverage (second), and overcoverage (third).
...	Not used.

## Value

A ggplot object.

## Examples

```

data("frailty", package = "rsimsum")
ms <- multisimsum(

```

```

data = frailty,
par = "par", true = c(trt = -0.50, fv = 0.75),
estvarname = "b", se = "se", methodvar = "model",
by = "fv_dist", x = TRUE
)

library(ggplot2)
autoplot(ms, par = "trt")
autoplot(ms, par = "trt", type = "lolly", stats = "cover")
autoplot(ms, par = "trt", type = "zip")
autoplot(ms, par = "trt", type = "est_ba")

```

---

autoplot.simsum

*autoplot method for simsum objects*


---

## Description

autoplot can produce a series of plot to summarise results of simulation studies. See `vignette("C-plotting", package = "rsimsum")` for further details.

## Usage

```

## S3 method for class 'simsum'
autoplot(
  object,
  type = "forest",
  stats = "nsim",
  target = NULL,
  fitted = TRUE,
  scales = "fixed",
  top = TRUE,
  density.legend = TRUE,
  zoom = 1,
  zip_ci_colours = "yellow",
  ...
)

```

## Arguments

object	An object of class <code>simsum</code> .
type	The type of the plot to be produced. Possible choices are: <code>forest</code> , <code>lolly</code> , <code>zip</code> , <code>est</code> , <code>se</code> , <code>est_ba</code> , <code>se_ba</code> , <code>est_ridge</code> , <code>se_ridge</code> , <code>est_density</code> , <code>se_density</code> , <code>est_hex</code> , <code>se_hex</code> , <code>heat</code> , <code>nlp</code> , with <code>forest</code> being the default.
stats	Summary statistic to plot, defaults to <code>nsim</code> (the number of replications with non-missing point estimates/SEs). See <code>summary.simsum()</code> for further details on supported summary statistics.

target	Target of summary statistic, e.g. 0 for bias. Defaults to NULL, in which case target will be inferred.
fitted	Superimpose a fitted regression line, useful when type = (est, se, est_ba, se_ba, est_density, se_density, est_hex, se_hex). Defaults to TRUE.
scales	Should scales be fixed (fixed, the default), free (free), or free in one dimension (free_x, free_y)?
top	Should the legend for a nested loop plot be on the top side of the plot? Defaults to TRUE.
density.legend	Should the legend for density and hexbin plots be included? Defaults to TRUE.
zoom	A numeric value between 0 and 1 signalling that a zip plot should <i>zoom</i> on the top x% of the plot (to ease interpretation). Defaults to 1, where the whole zip plot is displayed.
zip_ci_colours	A string with (1) a hex code to use for plotting coverage probability and its Monte Carlo confidence intervals (the default, with value zip_ci_colours = "yellow"), (2) a string vector of two hex codes denoting optimal coverage (first element) and over/under coverage (second element) or (3) a vector of three hex codes denoting optimal coverage (first), undercoverage (second), and overcoverage (third).
...	Not used.

## Value

A ggplot object.

## Examples

```
data("MIsim", package = "rsimsum")
s <- rsimsum::simsum(
  data = MIsim, estvarname = "b", true = 0.5, se = "se",
  methodvar = "method", x = TRUE
)

library(ggplot2)
autoplot(s)
autoplot(s, type = "lolly")
autoplot(s, type = "est_hex")
autoplot(s, type = "zip", zoom = 0.5)

# Nested loop plot:
data("nlp", package = "rsimsum")
s1 <- rsimsum::simsum(
  data = nlp, estvarname = "b", true = 0, se = "se",
  methodvar = "model", by = c("baseline", "ss", "esigma")
)
autoplot(s1, stats = "bias", type = "nlp")
```

---

 autoplot.summary.multisimsum

*autoplot method for summary.multisimsum objects*


---

## Description

autoplot method for summary.multisimsum objects

## Usage

```
## S3 method for class 'summary.multisimsum'
autoplot(
  object,
  par,
  type = "forest",
  stats = "nsim",
  target = NULL,
  fitted = TRUE,
  scales = "fixed",
  top = TRUE,
  density.legend = TRUE,
  zoom = 1,
  zip_ci_colours = "yellow",
  ...
)
```

## Arguments

object	An object of class <code>summary.multisimsum</code> .
par	The parameter results to plot.
type	The type of the plot to be produced. Possible choices are: <code>forest</code> , <code>lolly</code> , <code>zip</code> , <code>est</code> , <code>se</code> , <code>est_ba</code> , <code>se_ba</code> , <code>est_density</code> , <code>se_density</code> , <code>est_hex</code> , <code>se_hex</code> , <code>est_ridge</code> , <code>se_ridge</code> , <code>heat</code> , <code>nlp</code> , with <code>forest</code> being the default.
stats	Summary statistic to plot, defaults to <code>bias</code> . See <a href="#">summary.simsum()</a> for further details on supported summary statistics.
target	Target of summary statistic, e.g. 0 for <code>bias</code> . Defaults to <code>NULL</code> , in which case target will be inferred.
fitted	Superimpose a fitted regression line, useful when <code>type = (est, se, est_ba, se_ba, est_density, se_density, est_hex, se_hex)</code> . Defaults to <code>TRUE</code> .
scales	Should scales be fixed ( <code>fixed</code> , the default), free ( <code>free</code> ), or free in one dimension ( <code>free_x</code> , <code>free_y</code> )?
top	Should the legend for a nested loop plot be on the top side of the plot? Defaults to <code>TRUE</code> .
density.legend	Should the legend for density and hexbin plots be included? Defaults to <code>TRUE</code> .

zoom	A numeric value between 0 and 1 signalling that a zip plot should <i>zoom</i> on the top x% of the plot (to ease interpretation). Defaults to 1, where the whole zip plot is displayed.
zip_ci_colours	A string with (1) a hex code to use for plotting coverage probability and its Monte Carlo confidence intervals (the default, with value zip_ci_colours = "yellow"), (2) a string vector of two hex codes denoting optimal coverage (first element) and over/under coverage (second element) or (3) a vector of three hex codes denoting optimal coverage (first), undercoverage (second), and overcoverage (third).
...	Not used.

**Value**

A ggplot object.

**Examples**

```
data("frailty", package = "rsimsum")
ms <- multisimsum(
  data = frailty,
  par = "par", true = c(trt = -0.50, fv = 0.75),
  estvarname = "b", se = "se", methodvar = "model",
  by = "fv_dist", x = TRUE
)
sms <- summary(ms)

library(ggplot2)
autoplot(sms, par = "trt")
```

---

autoplot.summary.simsun

*autoplot method for summary.simsun objects*

---

**Description**

autoplot method for summary.simsun objects

**Usage**

```
## S3 method for class 'summary.simsun'
autoplot(
  object,
  type = "forest",
  stats = "nsim",
  target = NULL,
  fitted = TRUE,
  scales = "fixed",
  top = TRUE,
```

```

density.legend = TRUE,
zoom = 1,
zip_ci_colours = "yellow",
...
)

```

## Arguments

object	An object of class <code>summary.simsum</code> .
type	The type of the plot to be produced. Possible choices are: <code>forest</code> , <code>lolly</code> , <code>zip</code> , <code>est</code> , <code>se</code> , <code>est_ba</code> , <code>se_ba</code> , <code>est_ridge</code> , <code>se_ridge</code> , <code>est_density</code> , <code>se_density</code> , <code>est_hex</code> , <code>se_hex</code> , <code>heat</code> , <code>nlp</code> , with <code>forest</code> being the default.
stats	Summary statistic to plot, defaults to <code>nsim</code> (the number of replications with non-missing point estimates/SEs). See <code>summary.simsum()</code> for further details on supported summary statistics.
target	Target of summary statistic, e.g. 0 for bias. Defaults to <code>NULL</code> , in which case target will be inferred.
fitted	Superimpose a fitted regression line, useful when <code>type = (est, se, est_ba, se_ba, est_density, se_density, est_hex, se_hex)</code> . Defaults to <code>TRUE</code> .
scales	Should scales be fixed ( <code>fixed</code> , the default), free ( <code>free</code> ), or free in one dimension ( <code>free_x</code> , <code>free_y</code> )?
top	Should the legend for a nested loop plot be on the top side of the plot? Defaults to <code>TRUE</code> .
density.legend	Should the legend for density and hexbin plots be included? Defaults to <code>TRUE</code> .
zoom	A numeric value between 0 and 1 signalling that a zip plot should <i>zoom</i> on the top x% of the plot (to ease interpretation). Defaults to 1, where the whole zip plot is displayed.
zip_ci_colours	A string with (1) a hex code to use for plotting coverage probability and its Monte Carlo confidence intervals (the default, with value <code>zip_ci_colours = "yellow"</code> ), (2) a string vector of two hex codes denoting optimal coverage (first element) and over/under coverage (second element) or (3) a vector of three hex codes denoting optimal coverage (first), undercoverage (second), and overcoverage (third).
...	Not used.

## Value

A `ggplot` object.

## Examples

```

data("MIsim", package = "rsimsum")
s <- rsimsum::simsum(
  data = MIsim, estvarname = "b", true = 0.5, se = "se",
  methodvar = "method", x = TRUE
)

```

```
ss <- summary(s)

library(ggplot2)
autoplot(ss)
autoplot(ss, type = "lolly")
```

---

dropbig

*Identify replications with large point estimates, standard errors*

---

## Description

dropbig is useful to identify replications with large point estimates or standard errors. Large values are defined as standardised values above a given threshold, as defined when calling dropbig. Regular standardisation using mean and standard deviation is implemented, as well as robust standardisation using median and inter-quartile range. Further to that, the standardisation process is stratified by data-generating mechanism if by factors are defined.

## Usage

```
dropbig(
  data,
  estvarname,
  se = NULL,
  methodvar = NULL,
  by = NULL,
  max = 10,
  semax = 100,
  robust = TRUE
)
```

## Arguments

data	A data.frame in which variable names are interpreted. It has to be in tidy format, e.g. each variable forms a column and each observation forms a row.
estvarname	The name of the variable containing the point estimates.
se	The name of the variable containing the standard errors of the point estimates.
methodvar	The name of the variable containing the methods to compare. For instance, methods could be the models compared within a simulation study. Can be NULL.
by	A vector of variable names to compute performance measures by a list of factors. Factors listed here are the (potentially several) data-generating mechanisms used to simulate data under different scenarios (e.g. sample size, true distribution of a variable, etc.). Can be NULL.
max	Specifies the maximum acceptable absolute value of the point estimates, after standardisation. Defaults to 10.
semax	Specifies the maximum acceptable absolute value of the standard error, after standardisation. Defaults to 100.

`robust` Specifies whether to use robust standardisation (using median and inter-quartile range) rather than normal standardisation (using mean and standard deviation). Defaults to TRUE.

### Value

The same `data.frame` given as input with an additional column named `.dropbig` identifying rows that are classified as large (`.dropbig = TRUE`) according to the specified criterion.

### Examples

```
data("frailty", package = "rsimsum")
frailty2 <- subset(frailty, par == "fv")

# Using low values of max, semax for illustration purposes:
dropbig(
  data = frailty2, estvarname = "b", se = "se",
  methodvar = "model", by = "fv_dist", max = 2, semax = 2
)

# Using regular standardisation:
dropbig(
  data = frailty2, estvarname = "b", se = "se",
  methodvar = "model", by = "fv_dist", max = 2, semax = 2, robust = FALSE
)
```

---

frailty

*Example of a simulation study on frailty survival models*

---

### Description

A dataset from a simulation study comparing frailty flexible parametric models fitted using penalised likelihood to semiparametric frailty models. Both models are fitted assuming a Gamma and a log-Normal frailty. One thousand datasets were simulated, each containing a binary treatment variable with a log-hazard ratio of -0.50. Clustered survival data was simulated assuming 50 clusters of 50 individuals each, with a mixture Weibull baseline hazard function and a frailty following either a Gamma or a Log-Normal distribution. The comparison involves estimates of the log-treatment effect, and estimates of heterogeneity (i.e. the estimated frailty variance).

### Usage

frailty

frailty2

**Format**

A data frame with 16,000 rows and 6 variables:

- *i* Simulated dataset number.
- *b* Point estimate.
- *se* Standard error of the point estimate.
- *par* The estimand. *trt* is the log-treatment effect, *fv* is the variance of the frailty.
- *fv\_dist* The true frailty distribution.
- *model* Method used (Cox, Gamma, Cox, Log-Normal, RP(P), Gamma, or RP(P), Log-Normal).

An object of class `data.frame` with 16000 rows and 7 columns.

**Note**

`frailty2` is a version of the same dataset with the `model` column split into two columns, `m_baseline` and `m_frailty`.

**Examples**

```
data("frailty", package = "rsimsum")
data("frailty2", package = "rsimsum")
```

---

`get_data`

*get\_data*

---

**Description**

Extract data slots from an object of class `simsum`, `summary.simsum`, `multisimsum`, or `summary.multisimsum`.

**Usage**

```
get_data(x, stats = NULL, ...)
```

**Arguments**

- |                    |  |
|--------------------|--|
| <code>x</code>     | An object of class <code>simsum</code> .   |
| <code>stats</code> | Summary statistics to include; can be a scalar value or a vector. Possible choices are: <ul style="list-style-type: none"> <li>• <code>nsim</code>, the number of replications with non-missing point estimates and standard error.</li> <li>• <code>thetamean</code>, average point estimate.</li> <li>• <code>thetamedian</code>, median point estimate.</li> <li>• <code>se2mean</code>, average standard error.</li> <li>• <code>se2median</code>, median standard error.</li> <li>• <code>bias</code>, bias in point estimate.</li> </ul> |

- empse, empirical standard error.
  - mse, mean squared error.
  - relprec, percentage gain in precision relative to the reference method.
  - modelse, model-based standard error.
  - relerror, relative percentage error in standard error.
  - cover, coverage of a nominal level\
  - becover, bias-eliminated coverage of a nominal level\
  - power, power of a (1 - level)\ Defaults to NULL, in which case all summary statistics are returned.
- ... Ignored.

**Value**

A data.frame containing summary statistics from a simulation study.

**Examples**

```
data(MIsim)
x <- simsum(
  data = MIsim, estvarname = "b", true = 0.5, se = "se",
  methodvar = "method"
)
get_data(x)

# Extracting only bias and coverage:
get_data(x, stats = c("bias", "cover"))

xs <- summary(x)
get_data(xs)
```

---

is.multisimsum

*is.multisimsum*


---

**Description**

Reports whether x is a multisimsum object

**Usage**

```
is.multisimsum(x)
```

**Arguments**

x An object to test.

---

is.simsum	<i>is.simsum</i>
-----------	------------------

---

**Description**

Reports whether x is a simsum object

**Usage**

```
is.simsum(x)
```

**Arguments**

x	An object to test.
---	--------------------

---

is.summary.multisimsum	<i>is.summary.multisimsum</i>
------------------------	-------------------------------

---

**Description**

Reports whether x is a summary.multisimsum object

**Usage**

```
is.summary.multisimsum(x)
```

**Arguments**

x	An object to test.
---	--------------------

---

is.summary.simsum	<i>is.summary.simsum</i>
-------------------	--------------------------

---

**Description**

Reports whether x is a summary.simsum object

**Usage**

```
is.summary.simsum(x)
```

**Arguments**

x	An object to test.
---	--------------------

---

kable.simsum            *Create 'kable's*

---

## Description

Create tables in LaTeX, HTML, Markdown, or reStructuredText from objects of class `simsum`, `summary.simsum`, `multisimsum`, `summary.multisimsum`.

## Usage

```
## S3 method for class 'simsum'  
kable(x, stats = NULL, digits = max(3, getOption("digits") - 3), ...)  
  
## S3 method for class 'summary.simsum'  
kable(x, stats = NULL, digits = max(3, getOption("digits") - 3), ...)  
  
## S3 method for class 'multisimsum'  
kable(x, stats = NULL, digits = max(3, getOption("digits") - 3), ...)  
  
## S3 method for class 'summary.multisimsum'  
kable(x, stats = NULL, digits = max(3, getOption("digits") - 3), ...)  
  
kable(x, ...)
```

## Arguments

`x`                    An object of class `simsum`, `summary.simsum`, `multisimsum`, `summary.multisimsum`;  
`stats`                Summary statistics to include. See `tidy()` for more details;  
`digits`                Maximum number of digits for numeric columns;  
`...`                 Further arguments passed to `knitr::kable()`.

## See Also

[knitr::kable\(\)](#)

**Description**

A dataset from a simulation study comparing different ways to handle missing covariates when fitting a Cox model (White and Royston, 2009). One thousand datasets were simulated, each containing normally distributed covariates  $x$  and  $z$  and time-to-event outcome. Both covariates have 20% of their values deleted independently of all other variables so the data became missing completely at random (Little and Rubin, 2002). Each simulated dataset was analysed in three ways. A Cox model was fit to the complete cases (CC). Then two methods of multiple imputation using chained equations (van Buuren, Boshuizen, and Knook, 1999) were used. The MI\_LOGT method multiply imputes the missing values of  $x$  and  $z$  with the outcome included as  $\log(t)$  and  $d$ , where  $t$  is the survival time and  $d$  is the event indicator. The MI\_T method is the same except that  $\log(t)$  is replaced by  $t$  in the imputation model. The results are stored in long format.

**Usage**

```
MIsim
```

```
MIsim2
```

**Format**

A data frame with 3,000 rows and 4 variables:

- dataset Simulated dataset number.
- method Method used (CC, MI\_LOGT or MI\_T).
- b Point estimate.
- se Standard error of the point estimate.

An object of class `tbl_df` (inherits from `tbl`, `data.frame`) with 3000 rows and 5 columns.

**Note**

MIsim2 is a version of the same dataset with the method column split into two columns, `m1` and `m2`.

**References**

White, I.R., and P. Royston. 2009. Imputing missing covariate values for the Cox model. *Statistics in Medicine* 28(15):1982-1998 [doi:10.1002/sim.3618](https://doi.org/10.1002/sim.3618)

**Examples**

```
data("MIsim", package = "rsimsum")  
data("MIsim2", package = "rsimsum")
```

---

multisimsum	<i>Analyses of simulation studies with multiple estimands at once, including Monte Carlo error</i>
-------------	--

---

## Description

multisimsum is an extension of `simsum()` that can handle multiple estimated parameters at once. multisimsum calls `simsum()` internally, each estimands at once. There is only one new argument that must be set when calling multisimsum: `par`, a string representing the column of data that identifies the different estimands. Additionally, with multisimsum the argument `true` can be a named vector, where names correspond to each estimand (see examples). Otherwise, constant values (or values identified by a column in data) will be utilised. See `vignette("E-custom-inputs", package = "rsimsum")` for more details.

## Usage

```
multisimsum(
  data,
  par,
  estvarname,
  se = NULL,
  true = NULL,
  methodvar = NULL,
  ref = NULL,
  by = NULL,
  ci.limits = NULL,
  df = NULL,
  dropbig = FALSE,
  x = FALSE,
  control = list()
)
```

## Arguments

<code>data</code>	A <code>data.frame</code> in which variable names are interpreted. It has to be in tidy format, e.g. each variable forms a column and each observation forms a row.
<code>par</code>	The name of the variable containing the methods to compare. Can be <code>NULL</code> .
<code>estvarname</code>	The name of the variable containing the point estimates. Note that some column names are forbidden: these are listed below in the <i>Details</i> section.
<code>se</code>	The name of the variable containing the standard errors of the point estimates. Note that some column names are forbidden: these are listed below in the <i>Details</i> section.
<code>true</code>	The true value of the parameter; this is used in calculations of bias, relative bias, coverage, and mean squared error and is required whenever these performance measures are requested. <code>true</code> can be a numeric value or a string that identifies a column in data. In the former setting, <code>simsum</code> will assume the same value for

all replications; conversely, each replication will use a distinct value for true as identified by each row of data. See `vignette("E-custom-inputs", package = "rsimsum")` for more details. Note that some column names are forbidden: these are listed below in the *Details* section.

<code>methodvar</code>	The name of the variable containing the methods to compare. For instance, methods could be the models compared within a simulation study. Can be NULL. If a vector of column names is passed to <code>simsum()</code> , those columns will be combined into a single column named <code>:methodvar</code> using the <code>base::interaction()</code> function before computing all performance measures. Note that some column names are forbidden: these are listed below in the <i>Details</i> section.
<code>ref</code>	Specifies the reference method against which relative precision will be calculated. Only useful if <code>methodvar</code> is specified.
<code>by</code>	A vector of variable names to compute performance measures by a list of factors. Factors listed here are the (potentially several) data-generating mechanisms used to simulate data under different scenarios (e.g. sample size, true distribution of a variable, etc.). Can be NULL. Note that some column names are forbidden: these are listed below in the <i>Details</i> section.
<code>ci.limits</code>	Can be used to specify the limits (lower and upper) of confidence intervals used to calculate coverage and bias-eliminated coverage. Useful for non-Wald type estimators (e.g. bootstrap). Defaults to NULL, where Wald-type confidence intervals based on the provided SEs are calculated for coverage; otherwise, it can be a numeric vector (for fixed confidence intervals) or a vector of strings that identify columns in data with replication-specific lower and upper limits. See <code>vignette("E-custom-inputs", package = "rsimsum")</code> for more details. Note that some column names are forbidden: these are listed below in the <i>Details</i> section.
<code>df</code>	Can be used to specify that a column containing the replication-specific number of degrees of freedom that will be used to calculate confidence intervals for coverage (and bias-eliminated coverage) assuming t-distributed critical values (rather than normal theory intervals). See <code>vignette("E-custom-inputs", package = "rsimsum")</code> for more details. Note that some column names are forbidden: these are listed below in the <i>Details</i> section.
<code>dropbig</code>	Specifies that point estimates or standard errors beyond the maximum acceptable values should be dropped. Defaults to FALSE.
<code>x</code>	Set to TRUE to include the data argument used to calculate summary statistics (i.e. after pre-processing the input dataset e.g. removing values deemed too large via the <code>dropbig</code> argument) as a slot. Calling <code>simsum</code> with <code>x = TRUE</code> is required to produce zipper plots. The downside is that the size of the returned object increases considerably, therefore it is set to FALSE by default.
<code>control</code>	A list of parameters that control the behaviour of <code>simsum</code> . Possible values are: <ul style="list-style-type: none"> <li><code>mcse</code>, whether to calculate Monte Carlo standard errors. Defaults to TRUE;</li> <li><code>level</code>, the significance level used for coverage, bias-eliminated coverage, and power. Defaults to 0.95;</li> <li><code>power_df</code>, whether to use robust critical values from a t distribution with <code>power_df</code> degrees of freedom when calculating power. Defaults to NULL, in which case a Gaussian distribution is used;</li> </ul>

- `na.rm`, whether to remove point estimates or standard errors where either (or both) is missing. Defaults to TRUE;
- `char.sep`, a character utilised when splitting the input dataset data. Generally, this should not be changed;
- `dropbig.max`, specifies the maximum acceptable absolute value of the point estimates, after standardisation. Defaults to 10;
- `dropbig.semax`, specifies the maximum acceptable absolute value of the standard error, after standardisation. Defaults to 100
- `dropbig.robust`, specifies whether to use robust standardisation (using median and inter-quartile range) rather than normal standardisation (using mean and standard deviation). Defaults to TRUE, in which case robust standardisation will be used for `dropbig`.

### Details

The following names are not allowed for `estvarname`, `se`, `methodvar`, `by`, `par`: `stat`, `est`, `mcse`, `lower`, `upper`, `:methodvar`.

### Value

An object of class `multisimsum`.

### Examples

```
data("frailty", package = "rsimsum")
ms <- multisimsum(
  data = frailty,
  par = "par", true = c(trt = -0.50, fv = 0.75),
  estvarname = "b", se = "se", methodvar = "model",
  by = "fv_dist"
)
ms
```

---

nlp

*Example of a simulation study on survival modelling*

---

### Description

A dataset from a simulation study with 150 data-generating mechanisms, useful to illustrate nested loop plots. This simulation study aims to compare the Cox model and flexible parametric models in a variety of scenarios: different baseline hazard functions, sample size, and varying amount of heterogeneity unaccounted for in the model (simulated as white noise with a given variance). A Cox model and a Royston-Parmar model with 5 degrees of freedom are fit to each replication.

### Usage

nlp

**Format**

A data frame with 30,000 rows and 10 variables:

- `dgm` Data-generating mechanism, 1 to 150.
- `i` Simulated dataset number.
- `model` Method used, with 1 the Cox model and 2 the RP(5) model.
- `b` Point estimate for the log-hazard ratio.
- `se` Standard error of the point estimate.
- `baseline` Baseline hazard function of the simulated dataset.
- `ss` Sample size of the simulated dataset.
- `esigma` Standard deviation of the white noise.
- `pars` (Ancillary) Parameters of the baseline hazard function.

**Note**

Further details on this simulation study can be found in the R script used to generate this dataset, available on GitHub: <https://github.com/ellesenne/rsimsum/blob/master/data-raw/nlp-data.R>

**References**

- Cox D.R. 1972. Regression models and life-tables. *Journal of the Royal Statistical Society, Series B (Methodological)* 34(2):187-220. doi:10.1007/9781461243809\_37
- Royston, P. and Parmar, M.K. 2002. Flexible parametric proportional-hazards and proportional-odds models for censored survival data, with application to prognostic modelling and estimation of treatment effects. *Statistics in Medicine* 21(15):2175-2197 doi:10.1002/sim.1203
- Rücker, G. and Schwarzer, G. 2014. Presenting simulation results in a nested loop plot. *BMC Medical Research Methodology* 14:129 doi:10.1186/1471228814129

**Examples**

```
data("nlp", package = "rsimsum")
```

---

nsim

*Compute number of simulations required*

---

**Description**

The function `nsim` computes the number of simulations  $B$  to perform based on the accuracy of an estimate of interest, using the following equation:

$$B = \left( \frac{(Z_{1-\alpha/2} + Z_{1-\theta})\sigma}{\delta} \right)^2,$$

where  $\delta$  is the specified level of accuracy of the estimate of interest you are willing to accept (i.e. the permissible difference from the true value  $\beta$ ),  $Z_{1-\alpha/2}$  is the  $(1 - \alpha/2)$  quantile of the standard normal distribution,  $Z_{1-\theta}$  is the  $(1 - \theta)$  quantile of the standard normal distribution with  $(1 - \theta)$  being the power to detect a specific difference from the true value as significant, and  $\sigma^2$  is the variance of the parameter of interest.

### Usage

```
nsim(alpha, sigma, delta, power = 0.5)
```

### Arguments

alpha	Significance level. Must be a value between 0 and 1.
sigma	Variance for the parameter of interest. Must be greater than 0.
delta	Specified level of accuracy of the estimate of interest you are willing to accept. Must be greater than 0.
power	Power to detect a specific difference from the true value as significant. Must be a value between 0 and 1. Defaults to 0.5, e.g. a power of 50%.

### Value

A scalar value  $B$  representing the number of simulations to perform based on the accuracy required.

### References

Burton, A., Douglas G. Altman, P. Royston. et al. 2006. The design of simulation studies in medical statistics. *Statistics in Medicine* 25: 4279-4292 [doi:10.1002/sim.2673](https://doi.org/10.1002/sim.2673)

### Examples

```
# Number of simulations required to produce an estimate to within 5%
# accuracy of the true coefficient of 0.349 with a 5% significance level,
# assuming the variance of the estimate is 0.0166 and 50% power:
nsim(alpha = 0.05, sigma = sqrt(0.0166), delta = 0.349 * 5 / 100, power = 0.5)

# Number of simulations required to produce an estimate to within 1%
# accuracy of the true coefficient of 0.349 with a 5% significance level,
# assuming the variance of the estimate is 0.0166 and 50% power:
nsim(alpha = 0.05, sigma = sqrt(0.0166), delta = 0.349 * 1 / 100, power = 0.5)
```

---

```
print.multisimsum      print.multisimsum
```

---

### Description

Print method for multisimsum objects

**Usage**

```
## S3 method for class 'multisimsum'  
print(x, ...)
```

**Arguments**

x                    An object of class multisimsum.  
...                   Ignored.

**Examples**

```
data(frailty)  
ms <- multisimsum(  
  data = frailty, par = "par", true = c(  
    trt = -0.50,  
    fv = 0.75  
  ), estvarname = "b", se = "se", methodvar = "model",  
  by = "fv_dist"  
)  
ms  
  
data("frailty", package = "rsimsum")  
frailty$true <- ifelse(frailty$par == "trt", -0.50, 0.75)  
ms <- multisimsum(data = frailty, par = "par", estvarname = "b", true = "true")  
ms
```

---

print.simsum                    *print.simsum*

---

**Description**

Print method for simsum objects

**Usage**

```
## S3 method for class 'simsum'  
print(x, ...)
```

**Arguments**

x                    An object of class simsum.  
...                   Ignored.

**Examples**

```

data("MIsim")
x <- simsum(
  data = MIsim, estvarname = "b", true = 0.5, se = "se",
  methodvar = "method"
)
x

MIsim$true <- 0.5
x <- simsum(data = MIsim, estvarname = "b", true = "true", se = "se")
x

```

---

```

print.summary.multisimsum
      print.summary.multisimsum

```

---

**Description**

Print method for `summary.multisimsum` objects

**Usage**

```

## S3 method for class 'summary.multisimsum'
print(x, digits = 4, mcse = TRUE, ...)

```

**Arguments**

<code>x</code>	An object of class <code>summary.multisimsum</code> .
<code>digits</code>	Number of significant digits used for printing. Defaults to 4.
<code>mcse</code>	Should Monte Carlo standard errors be reported? If <code>mcse = FALSE</code> , confidence intervals based on Monte Carlo standard errors will be reported instead, see <a href="#">summary.multisimsum()</a> . If a <code>NULL</code> value is passed, only point estimates are printed regardless of whether Monte Carlo standard errors were computed or not. Defaults to <code>TRUE</code> .
<code>...</code>	Ignored.

**Examples**

```

data(frailty)
ms <- multisimsum(
  data = frailty, par = "par", true = c(
    trt = -0.50,
    fv = 0.75
  ), estvarname = "b", se = "se", methodvar = "model",
  by = "fv_dist"
)
sms <- summary(ms, stats = c("bias", "cover", "mse"))

```

```
sms

# Printing less significant digits:
print(sms, digits = 3)

# Printing confidence intervals:
print(sms, digits = 3, mcse = FALSE)

# Printing values only:
print(sms, mcse = NULL)
```

---

```
print.summary.simsum  print.summary.simsum
```

---

## Description

Print method for `summary.simsum` objects

## Usage

```
## S3 method for class 'summary.simsum'
print(x, digits = 4, mcse = TRUE, ...)
```

## Arguments

<code>x</code>	An object of class <code>summary.simsum</code> .
<code>digits</code>	Number of significant digits used for printing. Defaults to 4.
<code>mcse</code>	Should Monte Carlo standard errors be reported? If <code>mcse = FALSE</code> , confidence intervals based on Monte Carlo standard errors will be reported instead, see <a href="#">summary.simsum()</a> . If a <code>NULL</code> value is passed, only point estimates are printed regardless of whether Monte Carlo standard errors were computed or not. Defaults to <code>TRUE</code> .
<code>...</code>	Ignored.

## Examples

```
data("MIsim")
x <- simsum(
  data = MIsim, estvarname = "b", true = 0.5, se = "se",
  methodvar = "method"
)
xs <- summary(x)
xs

# Printing less significant digits:
print(xs, digits = 2)

# Printing confidence intervals:
```

```
print(xs, mcse = FALSE)

# Printing values only:
print(xs, mcse = NULL)
```

---

relhaz

*Example of a simulation study on survival modelling*

---

## Description

A dataset from a simulation study assessing the impact of misspecifying the baseline hazard in survival models on regression coefficients. One thousand datasets were simulated, each containing a binary treatment variable with a log-hazard ratio of -0.50. Survival data was simulated for two different sample sizes, 50 and 250 individuals, and under two different baseline hazard functions, exponential and Weibull. Consequently, a Cox model (Cox, 1972), a fully parametric exponential model, and a Royston-Parmar (Royston and Parmar, 2002) model with two degrees of freedom were fit to each simulated dataset. See `vignette("B-relhaz", package = "rsimsum")` for more information.

## Usage

```
relhaz
```

## Format

A data frame with 1,200 rows and 6 variables:

- `dataset` Simulated dataset number.
- `n` Sample size of the simulate dataset.
- `baseline` Baseline hazard function of the simulated dataset.
- `model` Method used (Cox, Exp, or RP(2)).
- `theta` Point estimate for the log-hazard ratio.
- `se` Standard error of the point estimate.

## References

- Cox D.R. 1972. Regression models and life-tables. *Journal of the Royal Statistical Society, Series B (Methodological)* 34(2):187-220. doi:[10.1007/9781461243809\\_37](https://doi.org/10.1007/9781461243809_37)
- Royston, P. and Parmar, M.K. 2002. Flexible parametric proportional-hazards and proportional-odds models for censored survival data, with application to prognostic modelling and estimation of treatment effects. *Statistics in Medicine* 21(15):2175-2197 doi:[10.1002/sim.1203](https://doi.org/10.1002/sim.1203)

## Examples

```
data("relhaz", package = "rsimsum")
```

## Description

`simsum()` computes performance measures for simulation studies in which each simulated data set yields point estimates by one or more analysis methods. Bias, relative bias, empirical standard error and precision relative to a reference method can be computed for each method. If, in addition, model-based standard errors are available then `simsum()` can compute the average model-based standard error, the relative error in the model-based standard error, the coverage of nominal confidence intervals, the coverage under the assumption that there is no bias (bias-eliminated coverage), and the power to reject a null hypothesis. Monte Carlo errors are available for all estimated quantities.

## Usage

```
simsum(  
  data,  
  estvarname,  
  se = NULL,  
  true = NULL,  
  methodvar = NULL,  
  ref = NULL,  
  by = NULL,  
  ci.limits = NULL,  
  df = NULL,  
  dropbig = FALSE,  
  x = FALSE,  
  control = list()  
)
```

## Arguments

<code>data</code>	A <code>data.frame</code> in which variable names are interpreted. It has to be in tidy format, e.g. each variable forms a column and each observation forms a row.
<code>estvarname</code>	The name of the variable containing the point estimates. Note that some column names are forbidden: these are listed below in the <i>Details</i> section.
<code>se</code>	The name of the variable containing the standard errors of the point estimates. Note that some column names are forbidden: these are listed below in the <i>Details</i> section.
<code>true</code>	The true value of the parameter; this is used in calculations of bias, relative bias, coverage, and mean squared error and is required whenever these performance measures are requested. <code>true</code> can be a numeric value or a string that identifies a column in <code>data</code> . In the former setting, <code>simsum</code> will assume the same value for all replications; conversely, each replication will use a distinct value for <code>true</code> as identified by each row of <code>data</code> . See <code>vignette("E-custom-inputs", package</code>

= "rsimsum") for more details. Note that some column names are forbidden: these are listed below in the *Details* section.

methodvar	The name of the variable containing the methods to compare. For instance, methods could be the models compared within a simulation study. Can be NULL. If a vector of column names is passed to <code>simsum()</code> , those columns will be combined into a single column named <code>:methodvar</code> using the <code>base::interaction()</code> function before computing all performance measures. Note that some column names are forbidden: these are listed below in the <i>Details</i> section.
ref	Specifies the reference method against which relative precision will be calculated. Only useful if <code>methodvar</code> is specified.
by	A vector of variable names to compute performance measures by a list of factors. Factors listed here are the (potentially several) data-generating mechanisms used to simulate data under different scenarios (e.g. sample size, true distribution of a variable, etc.). Can be NULL. Note that some column names are forbidden: these are listed below in the <i>Details</i> section.
ci.limits	Can be used to specify the limits (lower and upper) of confidence intervals used to calculate coverage and bias-eliminated coverage. Useful for non-Wald type estimators (e.g. bootstrap). Defaults to NULL, where Wald-type confidence intervals based on the provided SEs are calculated for coverage; otherwise, it can be a numeric vector (for fixed confidence intervals) or a vector of strings that identify columns in data with replication-specific lower and upper limits. See <code>vignette("E-custom-inputs", package = "rsimsum")</code> for more details. Note that some column names are forbidden: these are listed below in the <i>Details</i> section.
df	Can be used to specify that a column containing the replication-specific number of degrees of freedom that will be used to calculate confidence intervals for coverage (and bias-eliminated coverage) assuming t-distributed critical values (rather than normal theory intervals). See <code>vignette("E-custom-inputs", package = "rsimsum")</code> for more details. Note that some column names are forbidden: these are listed below in the <i>Details</i> section.
dropbig	Specifies that point estimates or standard errors beyond the maximum acceptable values should be dropped. Defaults to FALSE.
x	Set to TRUE to include the data argument used to calculate summary statistics (i.e. after pre-processing the input dataset e.g. removing values deemed too large via the <code>dropbig</code> argument) as a slot. Calling <code>simsum</code> with <code>x = TRUE</code> is required to produce zipper plots. The downside is that the size of the returned object increases considerably, therefore it is set to FALSE by default.
control	A list of parameters that control the behaviour of <code>simsum</code> . Possible values are: <ul style="list-style-type: none"> <li>• <code>mcse</code>, whether to calculate Monte Carlo standard errors. Defaults to TRUE;</li> <li>• <code>level</code>, the significance level used for coverage, bias-eliminated coverage, and power. Defaults to 0.95;</li> <li>• <code>power_df</code>, whether to use robust critical values from a t distribution with <code>power_df</code> degrees of freedom when calculating power. Defaults to NULL, in which case a Gaussian distribution is used;</li> <li>• <code>na.rm</code>, whether to remove point estimates or standard errors where either (or both) is missing. Defaults to TRUE;</li> </ul>

- `char.sep`, a character utilised when splitting the input dataset data. Generally, this should not be changed;
- `dropbig.max`, specifies the maximum acceptable absolute value of the point estimates, after standardisation. Defaults to 10;
- `dropbig.semax`, specifies the maximum acceptable absolute value of the standard error, after standardisation. Defaults to 100
- `dropbig.robust`, specifies whether to use robust standardisation (using median and inter-quartile range) rather than normal standardisation (using mean and standard deviation). Defaults to TRUE, in which case robust standardisation will be used for `dropbig`.

### Details

The following names are not allowed for any column in data that is passed to `simsum()`: `stat`, `est`, `mcse`, `lower`, `upper`, `:methodvar`, `:true`.

### Value

An object of class `simsum`.

### References

White, I.R. 2010. `simsum`: Analyses of simulation studies including Monte Carlo error. The Stata Journal 10(3): 369-385. <https://www.stata-journal.com/article.html?article=st0200>

Morris, T.P., White, I.R. and Crowther, M.J. 2019. *Using simulation studies to evaluate statistical methods*. Statistics in Medicine, [doi:10.1002/sim.8086](https://doi.org/10.1002/sim.8086)

Gasparini, A. 2018. `rsimsum`: Summarise results from Monte Carlo simulation studies. Journal of Open Source Software 3(26):739, [doi:10.21105/joss.00739](https://doi.org/10.21105/joss.00739)

### Examples

```
data("MIsim", package = "rsimsum")
s <- simsum(data = MIsim, estvarname = "b", true = 0.5, se = "se", methodvar = "method", ref = "CC")
# If 'ref' is not specified, the reference method is inferred
s <- simsum(data = MIsim, estvarname = "b", true = 0.5, se = "se", methodvar = "method")
```

---

summary.multisimsum     *Summarising multisimsum objects*

---

### Description

The `summary()` method for objects of class `multisimsum` returns confidence intervals for performance measures based on Monte Carlo standard errors.

### Usage

```
## S3 method for class 'multisimsum'
summary(object, ci_level = 0.95, df = NULL, stats = NULL, ...)
```

**Arguments**

object	An object of class multisimsum.
ci_level	Significance level for confidence intervals based on Monte Carlo standard errors. Ignored if a multisimsum object with control parameter mcse = FALSE is passed.
df	Degrees of freedom of a t distribution that will be used to calculate confidence intervals based on Monte Carlo standard errors. If NULL (the default), quantiles of a Normal distribution will be used instead.
stats	Summary statistics to include; can be a scalar value or a vector (for multiple summary statistics at once). Possible choices are: <ul style="list-style-type: none"> <li>• nsim, the number of replications with non-missing point estimates and standard error.</li> <li>• thetamean, average point estimate.</li> <li>• thetamedian, median point estimate.</li> <li>• se2mean, average standard error.</li> <li>• se2median, median standard error.</li> <li>• bias, bias in point estimate.</li> <li>• rbias, relative (to the true value) bias in point estimate.</li> <li>• empse, empirical standard error.</li> <li>• mse, mean squared error.</li> <li>• relprec, percentage gain in precision relative to the reference method.</li> <li>• modelse, model-based standard error.</li> <li>• relerror, relative percentage error in standard error.</li> <li>• cover, coverage of a nominal level\</li> <li>• becover, bias corrected coverage of a nominal level\</li> <li>• power, power of a (1 - level)\ Defaults to NULL, in which case all possible summary statistics are included.</li> </ul>
...	Ignored.

**Value**

An object of class summary.multisimsum.

**See Also**

[multisimsum\(\)](#), [print.summary.multisimsum\(\)](#)

**Examples**

```
data(frailty)
ms <- multisimsum(
  data = frailty, par = "par", true = c(
    trt = -0.50,
    fv = 0.75
  ), estvarname = "b", se = "se", methodvar = "model",
  by = "fv_dist"
```

```
)
sms <- summary(ms)
sms
```

---

summary.simsum

*Summarising simsum objects*


---

## Description

The `summary()` method for objects of class `simsum` returns confidence intervals for performance measures based on Monte Carlo standard errors.

## Usage

```
## S3 method for class 'simsum'
summary(object, ci_level = 0.95, df = NULL, stats = NULL, ...)
```

## Arguments

<code>object</code>	An object of class <code>simsum</code> .
<code>ci_level</code>	Significance level for confidence intervals based on Monte Carlo standard errors. Ignored if a <code>simsum</code> object with control parameter <code>mcse = FALSE</code> is passed.
<code>df</code>	Degrees of freedom of a t distribution that will be used to calculate confidence intervals based on Monte Carlo standard errors. If <code>NULL</code> (the default), quantiles of a Normal distribution will be used instead. However, using Z-based or t-based confidence intervals is valid only for summary statistics such as bias and coverage. Confidence intervals for other quantities may not be appropriate, therefore their usage is not recommended.
<code>stats</code>	Summary statistics to include; can be a scalar value or a vector (for multiple summary statistics at once). Possible choices are: <ul style="list-style-type: none"> <li>• <code>nsim</code>, the number of replications with non-missing point estimates and standard error.</li> <li>• <code>thetamean</code>, average point estimate.</li> <li>• <code>thetamedian</code>, median point estimate.</li> <li>• <code>se2mean</code>, average variance.</li> <li>• <code>se2median</code>, median variance.</li> <li>• <code>bias</code>, bias in point estimate.</li> <li>• <code>rbias</code>, relative (to the true value) bias in point estimate.</li> <li>• <code>empse</code>, empirical standard error.</li> <li>• <code>mse</code>, mean squared error.</li> <li>• <code>relprec</code>, percentage gain in precision relative to the reference method.</li> <li>• <code>modelse</code>, model-based standard error.</li> <li>• <code>relerror</code>, relative percentage error in standard error.</li> <li>• <code>cover</code>, coverage of a nominal level\</li> </ul>

- becover, bias corrected coverage of a nominal level\
- power, power of a (1 - level)\

Defaults to NULL, in which case all possible summary statistics are included.

... Ignored.

### Value

An object of class `summary.simsum`.

### See Also

[simsum\(\)](#), [print.summary.simsum\(\)](#)

### Examples

```
data("MIsim")
object <- simsum(
  data = MIsim, estvarname = "b", true = 0.5, se = "se",
  methodvar = "method"
)
xs <- summary(object)
xs
```

---

<code>tidy.simsum</code>	<i>Turn an object into a tidy dataset</i>
--------------------------	---

---

### Description

Extract a tidy dataset with results from an object of class `simsum`, `summary.simsum`, `multisimsum`, or `summary.multisimsum`.

### Usage

```
## S3 method for class 'simsum'
tidy(x, stats = NULL, ...)

## S3 method for class 'summary.simsum'
tidy(x, stats = NULL, ...)

## S3 method for class 'multisimsum'
tidy(x, stats = NULL, ...)

## S3 method for class 'summary.multisimsum'
tidy(x, stats = NULL, ...)
```

**Arguments**

<code>x</code>	An object of class <code>simsum</code> .
<code>stats</code>	Summary statistics to include; can be a scalar value or a vector. Possible choices are: <ul style="list-style-type: none"> <li>• <code>nsim</code>, the number of replications with non-missing point estimates and standard error.</li> <li>• <code>thetamean</code>, average point estimate.</li> <li>• <code>thetamedian</code>, median point estimate.</li> <li>• <code>se2mean</code>, average standard error.</li> <li>• <code>se2median</code>, median standard error.</li> <li>• <code>bias</code>, bias in point estimate.</li> <li>• <code>rbias</code>, relative (to the true value) bias in point estimate.</li> <li>• <code>empse</code>, empirical standard error.</li> <li>• <code>mse</code>, mean squared error.</li> <li>• <code>relprec</code>, percentage gain in precision relative to the reference method.</li> <li>• <code>modelse</code>, model-based standard error.</li> <li>• <code>releror</code>, relative percentage error in standard error.</li> <li>• <code>cover</code>, coverage of a nominal level\</li> <li>• <code>becover</code>, bias-eliminated coverage of a nominal level\</li> <li>• <code>power</code>, power of a (1 - level)\ Defaults to NULL, in which case all summary statistics are returned.</li> </ul>
<code>...</code>	Ignored.

**Value**

A `data.frame` containing summary statistics from a simulation study.

**Examples**

```
data(MIsim)
x <- simsum(
  data = MIsim, estvarname = "b", true = 0.5, se = "se",
  methodvar = "method"
)
tidy(x)

# Extracting only bias and coverage:
tidy(x, stats = c("bias", "cover"))

xs <- summary(x)
tidy(xs)
```

---

`tt`*Example of a simulation study on the t-test*

---

**Description**

A dataset from a simulation study with 4 data-generating mechanisms, useful to illustrate custom input of confidence intervals to calculate coverage probability. This simulation study aims to compare the t-test assuming pooled or unpooled variance in violation (or not) of the t-test assumptions: normality of data, and equality (or not) or variance between groups. The true value of the difference between groups is -1.

**Usage**`tt`**Format**

A data frame with 4,000 rows and 8 variables:

- `diff` The difference in mean between groups estimated by the t-test;
- `se` Standard error of the estimated difference;
- `conf.low`, `conf.high` Confidence interval for the difference in mean as reported by the t-test;
- `df` The number of degrees of freedom assumed by the t-test;
- `repno` Identifies each replication, between 1 and 500;
- `dgm` Identifies each data-generating mechanism: 1 corresponds to normal data with equal variance between the groups, 2 is normal data with unequal variance, 3 and 4 are skewed data (simulated from a Gamma distribution) with equal and unequal variance between groups, respectively;
- `method` Analysis method: 1 represents the t-test with pooled variance, while 2 represents the t-test with unpooled variance.

**Note**

Further details on this simulation study can be found in the R script used to generate this dataset, available on GitHub: <https://github.com/ellessenne/rsimsum/blob/master/data-raw/tt-data.R>

**Examples**

```
data("tt", package = "rsimsum")
```

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