

# Package: posterior (via r-universe)

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**Title** Tools for Working with Posterior Distributions

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**Description** Provides useful tools for both users and developers of packages for fitting Bayesian models or working with output from Bayesian models. The primary goals of the package are to: (a) Efficiently convert between many different useful formats of draws (samples) from posterior or prior distributions. (b) Provide consistent methods for operations commonly performed on draws, for example, subsetting, binding, or mutating draws. (c) Provide various summaries of draws in convenient formats. (d) Provide lightweight implementations of state of the art posterior inference diagnostics. References: Vehtari et al. (2021) <[doi:10.1214/20-BA1221](https://doi.org/10.1214/20-BA1221)>.

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## Description

The **posterior** package is intended to provide useful tools for both users and developers of packages for fitting Bayesian models or working with output from Bayesian models. The primary goals of the package are to:

- Efficiently convert between many different useful formats of draws (samples) from posterior or prior distributions.
- Provide consistent methods for operations commonly performed on draws, for example, sub-setting, binding, or mutating draws.
- Provide various summaries of draws in convenient formats.
- Provide lightweight implementations of state of the art posterior inference diagnostics.

## Package options

The following options are used to format and print `draws` objects, as in `print.draws_array()`, `print.draws_df()`, `print.draws_list()`, `print.draws_matrix()`, and `print.draws_rvars()`:

- `posterior.max_draws`: Maximum number of draws to print.
- `posterior.max_iterations`: Maximum number of iterations to print.
- `posterior.max_chains`: Maximum number of chains to print.
- `posterior.max_variables`: Maximum number of variables to print.

The following options are used for formatting the output of `summarize_draws`:

- `posterior.num_args`: Arguments passed to `num()` for pretty printing of summaries.

The following options are used to format and print `rvar` objects, as in `print.rvar()` and `print.draws_rvars()`:

- `posterior.rvar_summary`: What style of summary to display: "mean\_sd" displays mean  $\pm$  sd, "median\_mad" displays median  $\pm$  mad.
- `posterior.digits`: How many significant digits are displayed. This defaults to a smaller value (2) than `getOption("digits")` because `rvars` print two numbers (point summary and uncertainty) next to each other.

The following option is used to construct new `rvar` objects, as in `rfun()` and `rdo()`:

- `posterior.rvar_ndraws`: The number of draws used to construct new random variables when this number cannot be determined from existing arguments (e.g., other `rvars` passed to a function).

The following options are used to control warning messages:

- `posterior.warn_on_merge_chains`: (logical) Some operations will trigger an automatic merging of chains, for example, because chains do not match between two objects involved in a binary operation. Whether this causes a warning can be controlled by this option.

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**See Also**

Useful links:

- <https://mc-stan.org/posterior/>
- <https://discourse.mc-stan.org/>
- Report bugs at <https://github.com/stan-dev/posterior/issues>

---

as\_rvar

*Coerce to a random variable*

---

**Description**

Convert `x` to an `rvar` object.

**Usage**

```
as_rvar(x, dim = NULL, dimnames = NULL, nchains = NULL)
```

```
as_rvar_numeric(x, dim = NULL, dimnames = NULL, nchains = NULL)
```

```
as_rvar_integer(x, dim = NULL, dimnames = NULL, nchains = NULL)
```

```
as_rvar_logical(x, dim = NULL, dimnames = NULL, nchains = NULL)
```

## Arguments

x	(multiple options) An object that can be converted to an <code>rvar</code> , such as a vector, array, or an <code>rvar</code> itself.
dim	(integer vector) One or more integers giving the maximal indices in each dimension to override the dimensions of the <code>rvar</code> to be created (see <code>dim()</code> ). If NULL (the default), <code>dim</code> is determined by the input. <b>NOTE:</b> This argument controls the dimensions of the <code>rvar</code> , not the underlying array, so you cannot change the number of draws using this argument.
dimnames	(list) Character vectors giving the names in each dimension to override the names of the dimensions of the <code>rvar</code> to be created (see <code>dimnames()</code> ). If NULL (the default), this is determined by the input. <b>NOTE:</b> This argument controls the names of the dimensions of the <code>rvar</code> , not the underlying array.
nchains	(positive integer) The number of chains. The default is 1.

## Details

For objects that are already `rvars`, returns them (with modified dimensions if `dim` is not NULL).

For numeric or logical vectors or arrays, returns an `rvar` with a single draw and the same dimensions as `x`. This is in contrast to the `rvar()` constructor, which treats the first dimension of `x` as the draws dimension. As a result, `as_rvar()` is useful for creating constants.

While `as_rvar()` attempts to pick the most suitable subtype of `rvar` based on the type of `x` (possibly returning an `rvar_factor` or `rvar_ordered`), `as_rvar_numeric()`, `as_rvar_integer()`, and `as_rvar_logical()` always coerce the draws of the output `rvar` to be `numeric`, `integer`, or `logical` (respectively), and always return a base `rvar`, never a subtype.

## Value

An object of class "rvar" (or one of its subtypes) representing a random variable.

## See Also

`rvar()` to construct `rvars` directly. See `rdo()`, `rfunc()`, and `rvar_rng()` for higher-level interfaces for creating `rvars`.

## Examples

```
# You can use as_rvar() to create "constant" rvars (having only one draw):
x <- as_rvar(1)
x

# Such constants can be of arbitrary shape:
as_rvar(1:4)
as_rvar(matrix(1:10, nrow = 5))
as_rvar(array(1:12, dim = c(2, 3, 2)))

# as_rvar_numeric() coerces subtypes of rvar to the base rvar type
y <- as_rvar_factor(c("a", "b", "c"))
y
```

```
as_rvar_numeric(y)
```

---

```
as_rvar_factor      Coerce to a factor random variable
```

---

## Description

Convert `x` to an `rvar_factor` or `rvar_ordered` object.

## Usage

```
as_rvar_factor(x, dim = NULL, dimnames = NULL, nchains = NULL, ...)
```

```
as_rvar_ordered(x, dim = NULL, dimnames = NULL, nchains = NULL, ...)
```

## Arguments

<code>x</code>	(multiple options) An object that can be converted to an <code>rvar</code> , such as a vector, array, or an <code>rvar</code> itself.
<code>dim</code>	(integer vector) One or more integers giving the maximal indices in each dimension to override the dimensions of the <code>rvar</code> to be created (see <code>dim()</code> ). If <code>NULL</code> (the default), <code>dim</code> is determined by the input. <b>NOTE:</b> This argument controls the dimensions of the <code>rvar</code> , not the underlying array, so you cannot change the number of draws using this argument.
<code>dimnames</code>	(list) Character vectors giving the names in each dimension to override the names of the dimensions of the <code>rvar</code> to be created (see <code>dimnames()</code> ). If <code>NULL</code> (the default), this is determined by the input. <b>NOTE:</b> This argument controls the names of the dimensions of the <code>rvar</code> , not the underlying array.
<code>nchains</code>	(positive integer) The number of chains. The default is 1.
<code>...</code>	Arguments passed on to <code>base::factor</code>
	<code>levels</code> an optional vector of the unique values (as character strings) that <code>x</code> might have taken. The default is the unique set of values taken by <code>as.character(x)</code> , sorted into increasing order of <code>x</code> . Note that this set can be specified as smaller than <code>sort(unique(x))</code> .
	<code>labels</code> <i>either</i> an optional character vector of labels for the levels (in the same order as <code>levels</code> after removing those in <code>exclude</code> ), <i>or</i> a character string of length 1. Duplicated values in <code>labels</code> can be used to map different values of <code>x</code> to the same factor level.
	<code>exclude</code> a vector of values to be excluded when forming the set of levels. This may be factor with the same level set as <code>x</code> or should be a character.
	<code>ordered</code> logical flag to determine if the levels should be regarded as ordered (in the order given).
	<code>nmax</code> an upper bound on the number of levels; see ‘Details’.

**Details**

For objects that are already `rvars`, returns them (with modified dimensions if `dim` is not `NULL`), possibly adding levels using the unique values of the draws of the `rvar` (if the object is not already factor-like).

For numeric, logical, factor, or character vectors or arrays, returns an `rvar_factor` or `rvar_ordered` with a single draw and the same dimensions as `x`. This is in contrast to the `rvar_factor()` and `rvar_ordered()` constructors, which treats the first dimension of `x` as the draws dimension. As a result, `as_rvar_factor()` and `as_rvar_ordered()` are useful for creating constants.

**Value**

An object of class `"rvar_factor"` or `"rvar_ordered"` representing a random variable.

**See Also**

`rvar()`, `rvar_factor()`, and `rvar_ordered()` to construct `rvars` directly. See `rdo()`, `rfun()`, and `rvar_rng()` for higher-level interfaces for creating `rvars`.

**Examples**

```
# You can use as_rvar_factor() to create "constant" rvars (having only one draw):
x <- as_rvar_factor("a")
x

# Such constants can be of arbitrary shape:
as_rvar_factor(letters[1:4])
as_rvar_ordered(matrix(letters[1:10], nrow = 5))
as_rvar_factor(array(letters[1:12], dim = c(2, 3, 2)))
```

---

 bind\_draws

*Bind draws objects together*


---

**Description**

Bind multiple `draws` objects together to form a single draws object.

**Usage**

```
bind_draws(x, ...)

## S3 method for class 'draws_matrix'
bind_draws(x, ..., along = "variable")

## S3 method for class 'draws_array'
bind_draws(x, ..., along = "variable")
```



```
## S3 method for class 'draws_df'
bind_draws(x, ..., along = "variable")

## S3 method for class 'draws_list'
bind_draws(x, ..., along = "variable")

## S3 method for class 'draws_rvars'
bind_draws(x, ..., along = "variable")
```

### Arguments

x	(draws) A <a href="#">draws</a> object. The draws format of x will define the format of the returned draws object.
...	(draws) Additional <a href="#">draws</a> objects to bind to x.
along	(string) The dimension along which draws objects should be bound together. Possible values are "variable" (the default), "chain", "iteration", and "draw". Not all options are supported for all input formats.

### Value

A draws object of the same class as x.

### Examples

```
x1 <- draws_matrix(alpha = rnorm(5), beta = rnorm(5))
x2 <- draws_matrix(alpha = rnorm(5), beta = rnorm(5))
ndraws(x1)
ndraws(x2)
x3 <- bind_draws(x1, x2, along = "draw")
ndraws(x3)

x4 <- draws_matrix(theta = rexp(5))
x5 <- bind_draws(x1, x4, along = "variable")
variables(x5)
```

---

chol.rvar

*Cholesky decomposition of random matrix*

---

### Description

Cholesky decomposition of an [rvar](#) containing a matrix.

### Usage

```
## S3 method for class 'rvar'
chol(x, ...)
```

**Arguments**

`x` (rvar) A 2-dimensional [rvar](#).  
`...` Additional parameters passed on to `chol.tensor()`

**Value**

An [rvar](#) containing the upper triangular factor of the Cholesky decomposition, i.e., the matrix  $R$  such that  $R'R = x$ .

---

diag,rvar-method      *Matrix diagonals (including for random variables)*

---

**Description**

Extract the diagonal of a matrix or construct a matrix, including random matrices (2-dimensional [rvars](#)). Makes `base::diag()` generic.

**Usage**

```
## S4 method for signature 'rvar'
diag(x = 1, nrow, ncol, names = TRUE)
```

**Arguments**

`x` (numeric,rvar) a matrix, vector, 1D array, missing, or a 1- or 2-dimensional [rvar](#).  
`nrow, ncol` optional dimensions for the result when `x` is not a matrix.  
`names` (when `x` is a matrix) logical indicating if the resulting vector, the diagonal of `x`, should inherit [names](#) from `dimnames(x)` if available.

**Details**

Makes `base::diag()` into a generic function. See that function's documentation for usage with [numerics](#) and for usage of `diag<-`, which is also supported by [rvar](#).

**Value**

For [rvars](#), has two modes:

1. `x` is a matrix-like [rvar](#): it returns the diagonal as a vector-like [rvar](#)
2. `x` is a vector-like [rvar](#): it returns a matrix-like [rvar](#) with `x` as the diagonal and zero for off-diagonal entries.

**See Also**

[base::diag\(\)](#)

**Examples**

```
# Sigma is a 3x3 covariance matrix
Sigma <- as_draws_rvars(example_draws("multi_normal"))$Sigma
Sigma

diag(Sigma)

diag(Sigma) <- 1:3
Sigma

diag(as_rvar(1:3))
```

---

diagnostics

*List of available convergence diagnostics*


---

**Description**

A list of available diagnostics and links to their individual help pages.

**Details**

<b>Function</b>	<b>Description</b>
<a href="#">ess_basic()</a>	Basic version of effective sample size
<a href="#">ess_bulk()</a>	Bulk effective sample size
<a href="#">ess_tail()</a>	Tail effective sample size
<a href="#">ess_quantile()</a>	Effective sample sizes for quantiles
<a href="#">ess_sd()</a>	Effective sample sizes for standard deviations
<a href="#">mcse_mean()</a>	Monte Carlo standard error for the mean
<a href="#">mcse_quantile()</a>	Monte Carlo standard error for quantiles
<a href="#">mcse_sd()</a>	Monte Carlo standard error for standard deviations
<a href="#">pareto_khat()</a>	Pareto khat diagnostic for tail(s)
<a href="#">pareto_diags()</a>	Additional diagnostics related to Pareto khat
<a href="#">rhat_basic()</a>	Basic version of Rhat
<a href="#">rhat()</a>	Improved, rank-based version of Rhat
<a href="#">rhat_nested()</a>	Rhat for use with many short chains
<a href="#">rstar()</a>	R* diagnostic

**Value**

See individual functions for a description of return types.

dissent

*Dissention***Description**

Dissention, for measuring dispersion in draws from ordinal distributions.

**Usage**

```
dissent(x)

## Default S3 method:
dissent(x)

## S3 method for class 'rvar'
dissent(x)
```

**Arguments**

`x` (multiple options) A vector to be interpreted as draws from an ordinal distribution, such as:

- A [factor](#)
- A [numeric](#) (should be [integer](#) or integer-like)
- An [rvar](#), [rvar\\_factor](#), or [rvar\\_ordered](#)

**Details**

Calculates Tastle and Wierman's (2007) *dissention* measure:

$$-\sum_{i=1}^n p_i \log_2 \left( 1 - \frac{|x_i - E(x)|}{\max(x) - \min(x)} \right)$$

This ranges from 0 (all probability in one category) through 0.5 (uniform) to 1 (bimodal: all probability split equally between the first and last category).

**Value**

If `x` is a [factor](#) or [numeric](#), returns a length-1 numeric vector with a value between 0 and 1 (inclusive) giving the dissention of `x`.

If `x` is an [rvar](#), returns an array of the same shape as `x`, where each cell is the dissention of the draws in the corresponding cell of `x`.

**References**

William J. Tastle, Mark J. Wierman (2007). Consensus and dissention: A measure of ordinal dispersion. *International Journal of Approximate Reasoning*. 45(3), 531–545. doi:10.1016/j.ijar.2006.06.024.

## Examples

```
set.seed(1234)

levels <- c("lowest", "low", "neutral", "high", "highest")

# a bimodal distribution: high dissention
x <- ordered(
  sample(levels, 4000, replace = TRUE, prob = c(0.45, 0.04, 0.02, 0.04, 0.45)),
  levels = levels
)
dissent(x)

# a unimodal distribution: low dissention
y <- ordered(
  sample(levels, 4000, replace = TRUE, prob = c(0.95, 0.02, 0.015, 0.01, 0.005)),
  levels = levels
)
dissent(y)

# both together, as an rvar
xy <- c(rvar(x), rvar(y))
xy
dissent(xy)
```

---

draws	<i>Transform to draws objects</i>
-------	-----------------------------------

---

## Description

Try to transform an R object to a format supported by the **posterior** package.

## Usage

```
as_draws(x, ...)
```

```
is_draws(x)
```

## Arguments

x (draws) A draws object or another R object for which the method is defined.  
... Arguments passed to individual methods (if applicable).

## Details

The class "draws" is the parent class of all supported formats, which also have their own subclasses of the form "draws\_{format}" (e.g. "draws\_array").

**Value**

If possible, a draws object in the closest supported format to `x`. The formats are linked to in the **See Also** section below.

**See Also**

Other formats: [draws\\_array\(\)](#), [draws\\_df\(\)](#), [draws\\_list\(\)](#), [draws\\_matrix\(\)](#), [draws\\_rvars\(\)](#)

**Examples**

```
# create some random draws
x <- matrix(rnorm(30), nrow = 10)
colnames(x) <- c("a", "b", "c")
str(x)

# transform to a draws object
y <- as_draws(x)
str(y)

# remove the draws classes from the object
class(y) <- class(y)[-1:2]
str(y)
```

---

draws-index

*Index draws objects*

---

**Description**

Index iterations, chains, and draws of [draws](#) objects.

**Usage**

```
iteration_ids(x)

chain_ids(x)

draw_ids(x)

niterations(x)

nchains(x)

ndraws(x)
```

**Arguments**

`x` (draws) A draws object or another R object for which the method is defined.

**Details**

The methods `iteration_ids()`, `chain_ids()`, and `draw_ids()` return vectors of all iterations, chains, and draws, respectively. In contrast, the methods `niterations()`, `nchains()`, and `ndraws()` return the number of variables, iterations, chains, and draws, respectively.

**Value**

For `iteration_ids()`, `chain_ids()`, and `draw_ids()`, an integer vector.

For `niterations()`, `nchains()`, and `ndraws()`, a scalar integer.

**See Also**

[variables](#), [rename\\_variables](#)

**Examples**

```
x <- example_draws()

iteration_ids(x)
niterations(x)

chain_ids(x)
nchains(x)

draw_ids(x)
ndraws(x)
```

---

draws\_array

*The draws\_array format*

---

**Description**

The `as_draws_array()` methods convert objects to the `draws_array` format. The `draws_array()` function creates an object of the `draws_array` format based on a set of numeric vectors. See **Details**.

**Usage**

```
as_draws_array(x, ...)

## Default S3 method:
as_draws_array(x, ...)

## S3 method for class 'draws_array'
as_draws_array(x, ...)

## S3 method for class 'draws_matrix'
```

```

as_draws_array(x, ...)

## S3 method for class 'draws_df'
as_draws_array(x, ...)

## S3 method for class 'draws_list'
as_draws_array(x, ...)

## S3 method for class 'draws_rvars'
as_draws_array(x, ...)

## S3 method for class 'mcmc'
as_draws_array(x, ...)

## S3 method for class 'mcmc.list'
as_draws_array(x, ...)

draws_array(..., .nchains = 1)

is_draws_array(x)

```

### Arguments

<code>x</code>	An object to convert to a <code>draws_array</code> object.
<code>...</code>	For <code>as_draws_array()</code> : Arguments passed to individual methods (if applicable). For <code>draws_array()</code> : Named arguments containing numeric vectors each defining a separate variable.
<code>.nchains</code>	(positive integer) The number of chains. The default is 1.

### Details

Objects of class "draws\_array" are 3-D arrays with dimensions "iteration", "chain", and "variable". See **Examples**.

### Value

A `draws_array` object, which has classes `c("draws_array", "draws", "array")`.

### See Also

Other formats: [draws](#), [draws\\_df\(\)](#), [draws\\_list\(\)](#), [draws\\_matrix\(\)](#), [draws\\_rvars\(\)](#)

### Examples

```

x1 <- as_draws_array(example_draws())
class(x1)
print(x1)
str(x1)

```



```
x2 <- draws_array(a = rnorm(10), b = rnorm(10), c = 1)
class(x2)
print(x2)
str(x2)
```

---

draws\_df

*The draws\_df format*


---

## Description

The `as_draws_df()` methods convert objects to the `draws_df` format. The `draws_df()` function creates an object of the `draws_df` format based on a set of numeric vectors. See **Details**.

## Usage

```
as_draws_df(x, ...)
```

## Default S3 method:  
`as_draws_df(x, ...)`

## S3 method for class 'data.frame'  
`as_draws_df(x, ...)`

## S3 method for class 'draws\_df'  
`as_draws_df(x, ...)`

## S3 method for class 'draws\_matrix'  
`as_draws_df(x, ...)`

## S3 method for class 'draws\_array'  
`as_draws_df(x, ...)`

## S3 method for class 'draws\_list'  
`as_draws_df(x, ...)`

## S3 method for class 'draws\_rvars'  
`as_draws_df(x, ...)`

## S3 method for class 'mcmc'  
`as_draws_df(x, ...)`

## S3 method for class 'mcmc.list'  
`as_draws_df(x, ...)`

```
draws_df(..., .nchains = 1)
```

```
is_draws_df(x)
```

**Arguments**

<code>x</code>	An object to convert to a <code>draws_df</code> object.
<code>...</code>	For <code>as_draws_df()</code> : Arguments passed to individual methods (if applicable). For <code>draws_df()</code> : Named arguments containing numeric vectors each defining a separate variable.
<code>.nchains</code>	(positive integer) The number of chains. The default is 1.

**Details**

Objects of class "draws\_df" are [tibble](#) data frames. They have one column per variable as well as additional metadata columns ".iteration", ".chain", and ".draw". The difference between the ".iteration" and ".draw" columns is that the former is relative to the MCMC chain while the latter ignores the chain information and has all unique values. See **Examples**.

If a data.frame-like object is supplied to `as_draws_df` that contains columns named ".iteration" or ".chain", they will be treated as iteration and chain indices, respectively. See **Examples**.

**Value**

A `draws_df` object, which has classes `c("draws_df", "draws", class(tibble::tibble()))`.

**See Also**

Other formats: [draws](#), [draws\\_array\(\)](#), [draws\\_list\(\)](#), [draws\\_matrix\(\)](#), [draws\\_rvars\(\)](#)

**Examples**

```
x1 <- as_draws_df(example_draws())
class(x1)
print(x1)
str(x1)

x2 <- draws_df(a = rnorm(10), b = rnorm(10), c = 1)
class(x2)
print(x2)
str(x2)

# the difference between iteration and draw is clearer when contrasting
# the head and tail of the data frame
print(head(x1, reserved = TRUE, max_variables = 2))
print(tail(x1, reserved = TRUE, max_variables = 2))

# manually supply chain information
xnew <- data.frame(mu = rnorm(10), .chain = rep(1:2, each = 5))
xnew <- as_draws_df(xnew)
print(xnew)
```

---

draws_list	<i>The draws_list format</i>
------------	------------------------------

---

### Description

The `as_draws_list()` methods convert objects to the `draws_list` format. The `draws_list()` function creates an object of the `draws_list` format based on a set of numeric vectors. See **Details**.

### Usage

```
as_draws_list(x, ...)

## Default S3 method:
as_draws_list(x, ...)

## S3 method for class 'draws_list'
as_draws_list(x, ...)

## S3 method for class 'draws_matrix'
as_draws_list(x, ...)

## S3 method for class 'draws_array'
as_draws_list(x, ...)

## S3 method for class 'draws_df'
as_draws_list(x, ...)

## S3 method for class 'draws_rvars'
as_draws_list(x, ...)

## S3 method for class 'mcmc'
as_draws_list(x, ...)

## S3 method for class 'mcmc.list'
as_draws_list(x, ...)

draws_list(..., .nchains = 1)

is_draws_list(x)
```

### Arguments

<code>x</code>	An object to convert to a <code>draws_list</code> object.
<code>...</code>	For <code>as_draws_list()</code> : Arguments passed to individual methods (if applicable). For <code>draws_list()</code> : Named arguments containing numeric vectors each defining a separate variable.
<code>.nchains</code>	(positive integer) The number of chains. The default is 1.

**Details**

Objects of class "draws\_list" are lists with one element per MCMC chain. Each of these elements is itself a named list of numeric vectors with one vector per variable. The length of each vector is equal to the number of saved iterations per chain. See **Examples**.

**Value**

A draws\_list object, which has classes c("draws\_list", "draws", "list").

**See Also**

Other formats: [draws](#), [draws\\_array\(\)](#), [draws\\_df\(\)](#), [draws\\_matrix\(\)](#), [draws\\_rvars\(\)](#)

**Examples**

```
x1 <- as_draws_list(example_draws())
class(x1)
print(x1)
str(x1)

x2 <- draws_list(a = rnorm(10), b = rnorm(10), c = 1)
class(x2)
print(x2)
str(x2)
```

---

draws\_matrix

*The draws\_matrix format*

---

**Description**

The `as_draws_matrix()` methods convert objects to the `draws_matrix` format. The `draws_matrix()` function creates an object of the `draws_matrix` format based on a set of numeric vectors. See **Details**.

**Usage**

```
as_draws_matrix(x, ...)

## Default S3 method:
as_draws_matrix(x, ...)

## S3 method for class 'draws_matrix'
as_draws_matrix(x, ...)

## S3 method for class 'draws_array'
as_draws_matrix(x, ...)

## S3 method for class 'draws_df'
```

```

as_draws_matrix(x, ...)

## S3 method for class 'draws_list'
as_draws_matrix(x, ...)

## S3 method for class 'draws_rvars'
as_draws_matrix(x, ...)

## S3 method for class 'mcmc'
as_draws_matrix(x, ...)

## S3 method for class 'mcmc.list'
as_draws_matrix(x, ...)

draws_matrix(..., .nchains = 1)

is_draws_matrix(x)

```

### Arguments

<code>x</code>	An object to convert to a <code>draws_matrix</code> object.
<code>...</code>	For <code>as_draws_matrix()</code> : Arguments passed to individual methods (if applicable). For <code>draws_matrix()</code> : Named arguments containing numeric vectors each defining a separate variable.
<code>.nchains</code>	(positive integer) The number of chains. The default is 1.

### Details

Objects of class `"draws_matrix"` are matrices (2-D arrays) with dimensions `"draw"` and `"variable"`. See **Examples**.

### Value

A `draws_matrix` object, which has classes `c("draws_matrix", "draws", "matrix")`.

### See Also

Other formats: [draws](#), [draws\\_array\(\)](#), [draws\\_df\(\)](#), [draws\\_list\(\)](#), [draws\\_rvars\(\)](#)

### Examples

```

x1 <- as_draws_matrix(example_draws())
class(x1)
print(x1)
str(x1)

x2 <- draws_matrix(a = rnorm(10), b = rnorm(10), c = 1)
class(x2)
print(x2)
str(x2)

```

---

draws_of	<i>Get/set array of draws underlying a random variable</i>
----------	--

---

### Description

Gets/sets the array-representation that backs an `rvar`. Should be used rarely.

### Usage

```
draws_of(x, with_chains = FALSE)
draws_of(x, with_chains = FALSE) <- value
```

### Arguments

<code>x</code>	( <code>rvar</code> ) An <code>rvar</code> object.
<code>with_chains</code>	(logical) Should the array of draws include a dimension for chains? If <code>FALSE</code> (the default), chains are not included and the array has dimension <code>c(ndraws(x), dim(x))</code> . If <code>TRUE</code> , chains are included and the array has dimension <code>c(niterations(x), nchains(x), dim(x))</code> .
<code>value</code>	(array) An array of values to use as the backing array of <code>x</code> .

### Details

While `rvars` implement fast versions of basic math operations (including [matrix multiplication](#)), sometimes you may need to bypass the `rvar` abstraction to do what you need to do more efficiently. `draws_of()` allows you to get / set the underlying array of draws in order to do that.

`rvars` represent draws internally using arrays of arbitrary dimension, which is returned by `draws_of(x)` and can be set using `draws_of(x) <- value`. The **first** dimension of these arrays is the index of the draws. If `with_chains = TRUE`, then the dimensions of the returned array are modified so that the first dimension is the index of the iterations and the second dimension is the index of the chains.

### Value

If `with_chains = FALSE`, an array with dimensions `c(ndraws(x), dim(x))`.

If `with_chains = TRUE`, an array with dimensions `c(niterations(x), nchains(x), dim(x))`.

### Examples

```
x <- rvar(1:10, nchains = 2)
x

# draws_of() without arguments will return the array of draws without
# chain information (first dimension is draw)
draws_of(x)

# draws_of() with with_chains = TRUE will reshape the returned array to
```

```

# include chain information in the second dimension
draws_of(x, with_chains = TRUE)

# you can also set draws using draws_of(). When with_chains = FALSE the
# existing chain information will be retained ...
draws_of(x) <- 2:11
x

# when with_chains = TRUE the chain information will be set by the
# second dimension of the assigned array
draws_of(x, with_chains = TRUE) <- array(2:11, dim = c(2,5))
x

```

---

draws\_rvars

*The draws\_rvars format*


---

## Description

The `as_draws_rvars()` methods convert objects to the `draws_rvars` format. The `draws_rvars()` function creates an object of the `draws_rvars` format based on a set of numeric vectors. See **Details**.

## Usage

```

as_draws_rvars(x, ...)

## Default S3 method:
as_draws_rvars(x, ...)

## S3 method for class 'draws_rvars'
as_draws_rvars(x, ...)

## S3 method for class 'list'
as_draws_rvars(x, ...)

## S3 method for class 'draws_matrix'
as_draws_rvars(x, ...)

## S3 method for class 'draws_array'
as_draws_rvars(x, ...)

## S3 method for class 'draws_df'
as_draws_rvars(x, ...)

## S3 method for class 'draws_list'
as_draws_rvars(x, ...)

```

```
## S3 method for class 'mcmc'
as_draws_rvars(x, ...)

## S3 method for class 'mcmc.list'
as_draws_rvars(x, ...)

draws_rvars(..., .nchains = 1)

is_draws_rvars(x)
```

### Arguments

x	An object to convert to a draws_rvars object.
...	For as_draws_rvars(): Arguments passed to individual methods (if applicable). For draws_rvars(): Named arguments containing numeric vectors each defining a separate variable.
.nchains	(positive integer) The number of chains. The default is 1.

### Details

Objects of class "draws\_rvars" are lists of [rvar](#) objects. See **Examples**.

### Value

A draws\_rvars object, which has classes c("draws\_rvars", "draws", "list").

### See Also

Other formats: [draws](#), [draws\\_array\(\)](#), [draws\\_df\(\)](#), [draws\\_list\(\)](#), [draws\\_matrix\(\)](#)

### Examples

```
x1 <- as_draws_rvars(example_draws())
class(x1)
print(x1)
str(x1)

x2 <- draws_rvars(a = rnorm(10), b = rnorm(10), c = 1)
class(x2)
print(x2)
str(x2)
```



---

draws_summary	<i>Summaries of draws objects</i>
---------------	-----------------------------------

---

## Description

The `summarise_draws()` (and `summarize_draws()`) methods provide a quick way to get a table of summary statistics and diagnostics. These methods will convert an object to a draws object if it isn't already. For convenience, a `summary()` method for draws and rvar objects are also provided as an alias for `summarise_draws()` if the input object is a draws or rvar object.

## Usage

```
summarise_draws(.x, ...)

summarize_draws(.x, ...)

## S3 method for class 'draws'
summarise_draws(
  .x,
  ...,
  .args = list(),
  .num_args = getOption("posterior.num_args", list()),
  .cores = 1
)

## S3 method for class 'draws'
summary(object, ...)

## S3 method for class 'rvar'
summarise_draws(.x, ...)

## S3 method for class 'rvar'
summary(object, ...)

default_summary_measures()

default_convergence_measures()

default_mcse_measures()
```

## Arguments

<code>.x, object</code>	(draws) A draws object or one coercible to a draws object.
<code>...</code>	Name-value pairs of summary or <a href="#">diagnostic</a> functions. The provided names will be used as the names of the columns in the result <i>unless</i> the function returns a named vector, in which case the latter names are used. The functions can be specified in any format supported by <a href="#">as_function()</a> . See <b>Examples</b> .

<code>.args</code>	(named list) Optional arguments passed to the summary functions.
<code>.num_args</code>	(named list) Optional arguments passed to <code>num()</code> for pretty printing of summaries. Can be controlled globally via the posterior <code>.num_args</code> <a href="#">option</a> .
<code>.cores</code>	(positive integer) The number of cores to use for computing summaries for different variables in parallel. Coerced to integer if possible, otherwise errors. The default is <code>.cores = 1</code> , in which case no parallelization is implemented. By default, a socket cluster is used on Windows and forks otherwise.

## Details

The default summary functions used are the ones specified by `default_summary_measures()` and `default_convergence_measures()`:

`default_summary_measures()`

- `mean()`
- `median()`
- `sd()`
- `mad()`
- `quantile2()`

`default_convergence_measures()`

- `rhat()`
- `ess_bulk()`
- `ess_tail()`

The `var()` function should not be used to compute variances due to its inconsistent behavior with matrices. Instead, please use `distributional::variance()`.

## Value

The `summarise_draws()` methods return a [tibble](#) data frame. The first column ("variable") contains the variable names and the remaining columns contain summary statistics and diagnostics.

The functions `default_summary_measures()`, `default_convergence_measures()`, and `default_mcse_measures()` return character vectors of names of the default measures.

## See Also

[diagnostics](#) for a list of available diagnostics and links to their individual help pages.

## Examples

```
x <- example_draws("eight_schools")
class(x)
str(x)

summarise_draws(x)
summarise_draws(x, "mean", "median")
```

```

summarise_draws(x, mean, mcse = mcse_mean)
summarise_draws(x, ~quantile(.x, probs = c(0.4, 0.6)))

# using default_*_measures()
summarise_draws(x, default_summary_measures())
summarise_draws(x, default_convergence_measures())
summarise_draws(x, default_mcse_measures())

# compute variance of variables
summarise_draws(x, var = distributional::variance)

# illustrate use of '.args'
ws <- rexp(ndraws(x))
summarise_draws(x, weighted.mean, .args = list(w = ws))

# adjust how numerical summaries are printed
summarise_draws(x, .num_args = list(sigfig = 2, notation = "dec"))

```

---

drop,rvar-method

*Drop redundant dimensions*


---

## Description

Delete the dimensions of an [rvar](#) which are of size one. See [base::drop\(\)](#)

## Usage

```
## S4 method for signature 'rvar'
drop(x)
```

## Arguments

x (rvar) an [rvar](#).

## Value

An [rvar](#) with the same length as x, but where any entry equal to 1 in `dim(x)` has been removed. The exception is if `dim(x) == 1`, in which case `dim(drop(x)) == 1` as well (this is because [rvars](#), unlike [numerics](#), never have NULL dimensions).

## Examples

```

# Sigma is a 3x3 covariance matrix
Sigma <- as_draws_rvars(example_draws("multi_normal"))$Sigma
Sigma

Sigma[1, ]

drop(Sigma[1, ])

```

```
# equivalently ...
Sigma[1, drop = TRUE]
```

---

entropy	<i>Normalized entropy</i>
---------	---------------------------

---

## Description

Normalized entropy, for measuring dispersion in draws from categorical distributions.

## Usage

```
entropy(x)

## Default S3 method:
entropy(x)

## S3 method for class 'rvar'
entropy(x)
```

## Arguments

**x** (multiple options) A vector to be interpreted as draws from a categorical distribution, such as:

- A [factor](#)
- A [numeric](#) (should be [integer](#) or integer-like)
- An [rvar](#), [rvar\\_factor](#), or [rvar\\_ordered](#)

## Details

Calculates the normalized Shannon entropy of the draws in **x**. This value is the entropy of **x** divided by the maximum entropy of a distribution with *n* categories, where *n* is `length(unique(x))` for numeric vectors and `length(levels(x))` for factors:

$$-\frac{\sum_{i=1}^n p_i \log(p_i)}{\log(n)}$$

This scales the output to be between 0 (all probability in one category) and 1 (uniform). This form of normalized entropy is referred to as  $H_{REL}$  in Wilcox (1967).

## Value

If **x** is a [factor](#) or [numeric](#), returns a length-1 numeric vector with a value between 0 and 1 (inclusive) giving the normalized Shannon entropy of **x**.

If **x** is an [rvar](#), returns an array of the same shape as **x**, where each cell is the normalized Shannon entropy of the draws in the corresponding cell of **x**.

## References

Allen R. Wilcox (1967). *Indices of Qualitative Variation* (No. ORNL-TM-1919). Oak Ridge National Lab., Tenn.

## Examples

```
set.seed(1234)

levels <- c("a", "b", "c", "d", "e")

# a uniform distribution: high normalized entropy
x <- factor(
  sample(levels, 4000, replace = TRUE, prob = c(0.2, 0.2, 0.2, 0.2, 0.2)),
  levels = levels
)
entropy(x)

# a unimodal distribution: low normalized entropy
y <- factor(
  sample(levels, 4000, replace = TRUE, prob = c(0.95, 0.02, 0.015, 0.01, 0.005)),
  levels = levels
)
entropy(y)

# both together, as an rvar
xy <- c(rvar(x), rvar(y))
xy
entropy(xy)
```

---

ess\_basic

*Basic version of the effective sample size*

---

## Description

Compute the basic effective sample size (ESS) estimate for a single variable as described in Gelman et al. (2013) with some changes according to Vehtari et al. (2021). For practical applications, we strongly recommend the improved ESS convergence diagnostics implemented in [ess\\_bulk\(\)](#) and [ess\\_tail\(\)](#). See Vehtari (2021) for an in-depth comparison of different effective sample size estimators.

## Usage

```
ess_basic(x, ...)

## Default S3 method:
ess_basic(x, split = TRUE, ...)

## S3 method for class 'rvar'
ess_basic(x, split = TRUE, ...)
```

## Arguments

<code>x</code>	(multiple options) One of: <ul style="list-style-type: none"> <li>• A matrix of draws for a single variable (iterations x chains). See <a href="#">extract_variable_matrix()</a>.</li> <li>• An <a href="#">rvar</a>.</li> </ul>
<code>...</code>	Arguments passed to individual methods (if applicable).
<code>split</code>	(logical) Should the estimate be computed on split chains? The default is TRUE.

## Value

If the input is an array, returns a single numeric value. If any of the draws is non-finite, that is, NA, NaN, Inf, or -Inf, the returned output will be (numeric) NA. Also, if all draws within any of the chains of a variable are the same (constant), the returned output will be (numeric) NA as well. The reason for the latter is that, for constant draws, we cannot distinguish between variables that are supposed to be constant (e.g., a diagonal element of a correlation matrix is always 1) or variables that just happened to be constant because of a failure of convergence or other problems in the sampling process.

If the input is an [rvar](#), returns an array of the same dimensions as the [rvar](#), where each element is equal to the value that would be returned by passing the draws array for that element of the [rvar](#) to this function.

## References

Andrew Gelman, John B. Carlin, Hal S. Stern, David B. Dunson, Aki Vehtari and Donald B. Rubin (2013). *Bayesian Data Analysis, Third Edition*. Chapman and Hall/CRC.

Aki Vehtari, Andrew Gelman, Daniel Simpson, Bob Carpenter, and Paul-Christian Bürkner (2021). Rank-normalization, folding, and localization: An improved R-hat for assessing convergence of MCMC (with discussion). *Bayesian Analysis*. 16(2), 667–718. doi:10.1214/20-BA1221

Aki Vehtari (2021). Comparison of MCMC effective sample size estimators. Retrieved from [https://avehtari.github.io/rhat\\_ess/ess\\_comparison.html](https://avehtari.github.io/rhat_ess/ess_comparison.html)

## See Also

Other diagnostics: [ess\\_bulk\(\)](#), [ess\\_quantile\(\)](#), [ess\\_sd\(\)](#), [ess\\_tail\(\)](#), [mcse\\_mean\(\)](#), [mcse\\_quantile\(\)](#), [mcse\\_sd\(\)](#), [pareto\\_diags\(\)](#), [pareto\\_khat\(\)](#), [rhat\(\)](#), [rhat\\_basic\(\)](#), [rhat\\_nested\(\)](#), [rstar\(\)](#)

## Examples

```
mu <- extract_variable_matrix(example_draws(), "mu")
ess_basic(mu)

d <- as_draws_rvars(example_draws("multi_normal"))
ess_basic(d$Sigma)
```

---

ess_bulk	<i>Bulk effective sample size (bulk-ESS)</i>
----------	--

---

### Description

Compute a bulk effective sample size estimate (bulk-ESS) for a single variable. Bulk-ESS is useful as a diagnostic for the sampling efficiency in the bulk of the posterior. It is defined as the effective sample size for rank normalized values using split chains. For the tail effective sample size see [ess\\_tail\(\)](#). See Vehtari (2021) for an in-depth comparison of different effective sample size estimators.

### Usage

```
ess_bulk(x, ...)  
  
## Default S3 method:  
ess_bulk(x, ...)  
  
## S3 method for class 'rvar'  
ess_bulk(x, ...)
```

### Arguments

`x` (multiple options) One of:

- A matrix of draws for a single variable (iterations x chains). See [extract\\_variable\\_matrix\(\)](#).
- An [rvar](#).

`...` Arguments passed to individual methods (if applicable).

### Value

If the input is an array, returns a single numeric value. If any of the draws is non-finite, that is, NA, NaN, Inf, or -Inf, the returned output will be (numeric) NA. Also, if all draws within any of the chains of a variable are the same (constant), the returned output will be (numeric) NA as well. The reason for the latter is that, for constant draws, we cannot distinguish between variables that are supposed to be constant (e.g., a diagonal element of a correlation matrix is always 1) or variables that just happened to be constant because of a failure of convergence or other problems in the sampling process.

If the input is an [rvar](#), returns an array of the same dimensions as the [rvar](#), where each element is equal to the value that would be returned by passing the draws array for that element of the [rvar](#) to this function.

### References

Aki Vehtari, Andrew Gelman, Daniel Simpson, Bob Carpenter, and Paul-Christian Bürkner (2021). Rank-normalization, folding, and localization: An improved R-hat for assessing convergence of MCMC (with discussion). *Bayesian Analysis*. 16(2), 667–718. doi:10.1214/20-BA1221

Aki Vehtari (2021). Comparison of MCMC effective sample size estimators. Retrieved from [https://avehtari.github.io/rhat\\_ess/ess\\_comparison.html](https://avehtari.github.io/rhat_ess/ess_comparison.html)

### See Also

Other diagnostics: [ess\\_basic\(\)](#), [ess\\_quantile\(\)](#), [ess\\_sd\(\)](#), [ess\\_tail\(\)](#), [mcse\\_mean\(\)](#), [mcse\\_quantile\(\)](#), [mcse\\_sd\(\)](#), [pareto\\_diags\(\)](#), [pareto\\_khat\(\)](#), [rhat\(\)](#), [rhat\\_basic\(\)](#), [rhat\\_nested\(\)](#), [rstar\(\)](#)

### Examples

```
mu <- extract_variable_matrix(example_draws(), "mu")
ess_bulk(mu)

d <- as_draws_rvars(example_draws("multi_normal"))
ess_bulk(d$Sigma)
```

---

ess\_mean

*Effective sample size for the mean*

---

### Description

Compute an effective sample size estimate for a mean (expectation) estimate of a single variable.

### Usage

```
ess_mean(x, ...)

## S3 method for class 'rvar'
ess_mean(x, ...)
```

### Arguments

`x` (multiple options) One of:

- A matrix of draws for a single variable (iterations x chains). See [extract\\_variable\\_matrix\(\)](#).
- An [rvar](#).

`...` Arguments passed to individual methods (if applicable).

### Value

If the input is an array, returns a single numeric value. If any of the draws is non-finite, that is, NA, NaN, Inf, or -Inf, the returned output will be (numeric) NA. Also, if all draws within any of the chains of a variable are the same (constant), the returned output will be (numeric) NA as well. The reason for the latter is that, for constant draws, we cannot distinguish between variables that are supposed to be constant (e.g., a diagonal element of a correlation matrix is always 1) or variables that just happened to be constant because of a failure of convergence or other problems in the sampling process.



If the input is an `rvar`, returns an array of the same dimensions as the `rvar`, where each element is equal to the value that would be returned by passing the draws array for that element of the `rvar` to this function.

## References

Andrew Gelman, John B. Carlin, Hal S. Stern, David B. Dunson, Aki Vehtari and Donald B. Rubin (2013). *Bayesian Data Analysis, Third Edition*. Chapman and Hall/CRC.

## Examples

```
mu <- extract_variable_matrix(example_draws(), "mu")
ess_mean(mu)

d <- as_draws_rvars(example_draws("multi_normal"))
ess_mean(d$Sigma)
```

---

ess_quantile	<i>Effective sample sizes for quantiles</i>
--------------	---

---

## Description

Compute effective sample size estimates for quantile estimates of a single variable.

## Usage

```
ess_quantile(x, probs = c(0.05, 0.95), ...)
```

## Default S3 method:

```
ess_quantile(x, probs = c(0.05, 0.95), names = TRUE, ...)
```

## S3 method for class 'rvar'

```
ess_quantile(x, probs = c(0.05, 0.95), names = TRUE, ...)
```

```
ess_median(x, ...)
```

## Default S3 method:

```
ess_mean(x, ...)
```

## Arguments

x	(multiple options) One of: <ul style="list-style-type: none"> <li>• A matrix of draws for a single variable (iterations x chains). See <code>extract_variable_matrix()</code>.</li> <li>• An <code>rvar</code>.</li> </ul>
probs	(numeric vector) Probabilities in $[0, 1]$ .
...	Arguments passed to individual methods (if applicable).
names	(logical) Should the result have a names attribute? The default is TRUE, but use FALSE for improved speed if there are many values in probs.

**Value**

If the input is an array, returns a numeric vector with one element per quantile. If any of the draws is non-finite, that is, NA, NaN, Inf, or -Inf, the returned output will be a vector of (numeric) NA values. Also, if all draws of a variable are the same (constant), the returned output will be a vector of (numeric) NA values as well. The reason for the latter is that, for constant draws, we cannot distinguish between variables that are supposed to be constant (e.g., a diagonal element of a correlation matrix is always 1) or variables that just happened to be constant because of a failure of convergence or other problems in the sampling process.

If the input is an `rvar` and `length(probs) == 1`, returns an array of the same dimensions as the `rvar`, where each element is equal to the value that would be returned by passing the draws array for that element of the `rvar` to this function. If `length(probs) > 1`, the first dimension of the result indexes the input probabilities; i.e. the result has dimension `c(length(probs), dim(x))`.

**References**

Aki Vehtari, Andrew Gelman, Daniel Simpson, Bob Carpenter, and Paul-Christian Bürkner (2021). Rank-normalization, folding, and localization: An improved R-hat for assessing convergence of MCMC (with discussion). *Bayesian Analysis*. 16(2), 667–718. doi:10.1214/20-BA1221

**See Also**

Other diagnostics: `ess_basic()`, `ess_bulk()`, `ess_sd()`, `ess_tail()`, `mcse_mean()`, `mcse_quantile()`, `mcse_sd()`, `pareto_diags()`, `pareto_khat()`, `rhat()`, `rhat_basic()`, `rhat_nested()`, `rstar()`

**Examples**

```
mu <- extract_variable_matrix(example_draws(), "mu")
ess_quantile(mu, probs = c(0.1, 0.9))

d <- as_draws_rvars(example_draws("multi_normal"))
ess_quantile(d$mu, probs = c(0.1, 0.9))
```

---

 ess\_sd

*Effective sample size for the standard deviation*


---

**Description**

Compute an effective sample size estimate for the standard deviation (SD) estimate of a single variable. This is defined as the effective sample size estimate for the absolute deviation from mean.

**Usage**

```
ess_sd(x, ...)
```

## Default S3 method:

```
ess_sd(x, ...)
```

```
## S3 method for class 'rvar'
ess_sd(x, ...)
```

### Arguments

**x** (multiple options) One of:

- A matrix of draws for a single variable (iterations x chains). See [extract\\_variable\\_matrix\(\)](#).
- An [rvar](#).

**...** Arguments passed to individual methods (if applicable).

### Value

If the input is an array, returns a single numeric value. If any of the draws is non-finite, that is, NA, NaN, Inf, or -Inf, the returned output will be (numeric) NA. Also, if all draws within any of the chains of a variable are the same (constant), the returned output will be (numeric) NA as well. The reason for the latter is that, for constant draws, we cannot distinguish between variables that are supposed to be constant (e.g., a diagonal element of a correlation matrix is always 1) or variables that just happened to be constant because of a failure of convergence or other problems in the sampling process.

If the input is an [rvar](#), returns an array of the same dimensions as the [rvar](#), where each element is equal to the value that would be returned by passing the draws array for that element of the [rvar](#) to this function.

### References

Aki Vehtari, Andrew Gelman, Daniel Simpson, Bob Carpenter, and Paul-Christian Bürkner (2021). Rank-normalization, folding, and localization: An improved R-hat for assessing convergence of MCMC (with discussion). *Bayesian Analysis*. 16(2), 667–718. doi:10.1214/20-BA1221

### See Also

Other diagnostics: [ess\\_basic\(\)](#), [ess\\_bulk\(\)](#), [ess\\_quantile\(\)](#), [ess\\_tail\(\)](#), [mcse\\_mean\(\)](#), [mcse\\_quantile\(\)](#), [mcse\\_sd\(\)](#), [pareto\\_diags\(\)](#), [pareto\\_khat\(\)](#), [rhat\(\)](#), [rhat\\_basic\(\)](#), [rhat\\_nested\(\)](#), [rstar\(\)](#)

### Examples

```
mu <- extract_variable_matrix(example_draws(), "mu")
ess_sd(mu)

d <- as_draws_rvars(example_draws("multi_normal"))
ess_sd(d$Sigma)
```

---

 ess\_tail

*Tail effective sample size (tail-ESS)*


---

### Description

Compute a tail effective sample size estimate (tail-ESS) for a single variable. Tail-ESS is useful as a diagnostic for the sampling efficiency in the tails of the posterior. It is defined as the minimum of the effective sample sizes for 5% and 95% quantiles. For the bulk effective sample size see [ess\\_bulk\(\)](#). See Vehtari (2021) for an in-depth comparison of different effective sample size estimators.

### Usage

```
ess_tail(x, ...)

## Default S3 method:
ess_tail(x, ...)

## S3 method for class 'rvar'
ess_tail(x, ...)
```

### Arguments

`x` (multiple options) One of:

- A matrix of draws for a single variable (iterations x chains). See [extract\\_variable\\_matrix\(\)](#).
- An [rvar](#).

`...` Arguments passed to individual methods (if applicable).

### Value

If the input is an array, returns a single numeric value. If any of the draws is non-finite, that is, NA, NaN, Inf, or -Inf, the returned output will be (numeric) NA. Also, if all draws within any of the chains of a variable are the same (constant), the returned output will be (numeric) NA as well. The reason for the latter is that, for constant draws, we cannot distinguish between variables that are supposed to be constant (e.g., a diagonal element of a correlation matrix is always 1) or variables that just happened to be constant because of a failure of convergence or other problems in the sampling process.

If the input is an [rvar](#), returns an array of the same dimensions as the [rvar](#), where each element is equal to the value that would be returned by passing the draws array for that element of the [rvar](#) to this function.

### References

Aki Vehtari, Andrew Gelman, Daniel Simpson, Bob Carpenter, and Paul-Christian Bürkner (2021). Rank-normalization, folding, and localization: An improved R-hat for assessing convergence of MCMC (with discussion). *Bayesian Analysis*. 16(2), 667–718. doi:10.1214/20-BA1221

Aki Vehtari (2021). Comparison of MCMC effective sample size estimators. Retrieved from [https://avehtari.github.io/rhat\\_ess/ess\\_comparison.html](https://avehtari.github.io/rhat_ess/ess_comparison.html)

### See Also

Other diagnostics: [ess\\_basic\(\)](#), [ess\\_bulk\(\)](#), [ess\\_quantile\(\)](#), [ess\\_sd\(\)](#), [mcse\\_mean\(\)](#), [mcse\\_quantile\(\)](#), [mcse\\_sd\(\)](#), [pareto\\_diags\(\)](#), [pareto\\_khat\(\)](#), [rhat\(\)](#), [rhat\\_basic\(\)](#), [rhat\\_nested\(\)](#), [rstar\(\)](#)

### Examples

```
mu <- extract_variable_matrix(example_draws(), "mu")
ess_tail(mu)

d <- as_draws_rvars(example_draws("multi_normal"))
ess_tail(d$Sigma)
```

---

example_draws	<i>Example draws objects</i>
---------------	------------------------------

---

### Description

Objects for use in examples, vignettes, and tests.

### Usage

```
example_draws(example = "eight_schools")
```

### Arguments

`example` (string) The name of the example draws object. See **Details** for available options.

### Details

The following example draws objects are available.

**eight\_schools**: A [draws\\_array](#) object with 100 iterations from each of 4 Markov chains obtained by fitting the eight schools model described in Gelman et al. (2013) with **Stan**. The variables are:

- `mu`: Overall mean of the eight schools
- `tau`: Standard deviation between schools
- `theta`: Individual means of each of the eight schools

**multi\_normal**: A [draws\\_array](#) object with 100 iterations from each of the 4 Markov chains obtained by fitting a 3-dimensional multivariate normal model to 100 simulated observations. The variables are:

- `mu`: Mean parameter vector of length 3
- `Sigma`: Covariance matrix of dimension 3 x 3

**Value**

A draws object.

**Note**

These objects are only intended to be used in demonstrations and tests. They contain fewer iterations and chains than recommended for performing actual inference.

**References**

Andrew Gelman, John B. Carlin, Hal S. Stern, David B. Dunson, Aki Vehtari and Donald B. Rubin (2013). Bayesian Data Analysis, Third Edition. Chapman and Hall/CRC.

**Examples**

```
draws_eight_schools <- example_draws("eight_schools")
summarise_draws(draws_eight_schools)

draws_multi_normal <- example_draws("multi_normal")
summarise_draws(draws_multi_normal)
```

---

extract_variable	<i>Extract draws of a single variable</i>
------------------	---

---

**Description**

Extract a vector of draws of a single variable.

**Usage**

```
extract_variable(x, variable, ...)

## Default S3 method:
extract_variable(x, variable, ...)

## S3 method for class 'draws'
extract_variable(x, variable, ...)

## S3 method for class 'draws_df'
extract_variable(x, variable, ...)

## S3 method for class 'draws_list'
extract_variable(x, variable, ...)

## S3 method for class 'draws_rvars'
extract_variable(x, variable, ...)
```

**Arguments**

x	(draws) A draws object or another R object for which the method is defined.
variable	(string) The name of the variable to extract. Must include indices for array variables (e.g. "x[1]", "y[1,2]"). To extract all dimensions from variables with indices, use <code>extract_variable_array()</code> .
...	Arguments passed to individual methods (if applicable).

**Value**

A vector of length equal to the number of draws.

**See Also**

Other variable extraction methods: `extract_variable_array()`, `extract_variable_matrix()`

**Examples**

```
x <- example_draws()
mu <- extract_variable(x, variable = "mu")
str(mu)
```

---

extract\_variable\_array

*Extract array of a single (possibly indexed) variable*

---

**Description**

Extract an array of draws of a single variable, including any dimensions of variables with indices.

**Usage**

```
extract_variable_array(x, variable, ...)
```

```
## Default S3 method:
extract_variable_array(x, variable, ...)
```

```
## S3 method for class 'draws'
extract_variable_array(x, variable, ...)
```

**Arguments**

x	(draws) A draws object or another R object for which the method is defined.
variable	(string) The name of the variable to extract. To extract all dimensions from variables with indices (e.g. "x[1]"), provide the base variable name (e.g. "x").
...	Arguments passed to individual methods (if applicable).

**Value**

An array with dimension `niterations(x) x nchains(x) x` any remaining dimensions determined by the indices of the variable `x`.

**See Also**

Other variable extraction methods: [extract\\_variable\(\)](#), [extract\\_variable\\_matrix\(\)](#)

**Examples**

```
x <- example_draws(example = "multi_normal")

mu <- extract_variable_array(x, variable = "mu")
str(mu)

mu1 <- extract_variable_array(x, variable = "mu[1]")
str(mu1)

Sigma <- extract_variable_array(x, variable = "Sigma")
str(Sigma)
```

---

`extract_variable_matrix`

*Extract matrix of a single variable*

---

**Description**

Extract an iterations x chains matrix of draws of a single variable. This is primarily used for convergence diagnostic functions such as [rhat\(\)](#).

**Usage**

```
extract_variable_matrix(x, variable, ...)

## Default S3 method:
extract_variable_matrix(x, variable, ...)

## S3 method for class 'draws'
extract_variable_matrix(x, variable, ...)

## S3 method for class 'draws_df'
extract_variable_matrix(x, variable, ...)

## S3 method for class 'draws_list'
extract_variable_matrix(x, variable, ...)

## S3 method for class 'draws_rvars'
extract_variable_matrix(x, variable, ...)
```



**Arguments**

x	(draws) A draws object or another R object for which the method is defined.
variable	(string) The name of the variable to extract. Must include indices for array variables (e.g. "x[1]", "y[1,2]"). To extract all dimensions from variables with indices, use <a href="#">extract_variable_array()</a> .
...	Arguments passed to individual methods (if applicable).

**Value**

A matrix with dimension iterations x chains.

**See Also**

Other variable extraction methods: [extract\\_variable\(\)](#), [extract\\_variable\\_array\(\)](#)

**Examples**

```
x <- example_draws()
mu <- extract_variable_matrix(x, variable = "mu")
dim(mu)
rhat(mu)
```

---

for_each_draw	<i>Loop over draws</i>
---------------	------------------------

---

**Description**

Executes an expression once for every draw in a draws object. Used primarily for its side effects and returns the input x invisibly.

**Usage**

```
for_each_draw(x, expr)
```

**Arguments**

x	(draws) A draws object or another R object for which the method is defined.
expr	(expression) A bare expression that can contain references to variables in x by name. This expression will be executed once per draw of x, where references to variables in x resolve to the value of that variable in that draw. The expression supports <a href="#">quasiquoteation</a> .

## Details

If `x` is not in the `draws_rvars` format, it is first converted to that format. This allows the variables in `x` to include their dimensions (i.e, to act as R vectors and arrays) when being referred to in `expr`.

Within `expr`, use `.draw` to refer to the draw index, which will be a value between 1 and `ndraws(x)`. `expr` is executed in the calling environment of `for_each_draw()`, so it can use variables in that environment (however, due to the use of data masking, to modify variables in that environment, one must use `<<-`.)

## Value

As `for_each_draw()` is used primarily for its side effects (the expression executed for each draw of `x`), it returns the input `x` invisibly.

## Examples

```
eight_schools <- as_draws_rvars(example_draws())

# 1. A simple example --- looping over draws and printing each draw
# NOTE: You probably don't want to do this in practice! This example is
# just intended to show what for_each_draw() is doing. If you just want to
# print the draws of an rvar, it is probably better to use draws_of()
for_each_draw(eight_schools, {
  print(mu)
})

# 2. A more complex example --- building a parallel coordinates plot
# First, construct the plot bounds
plot(1, type = "n",
     xlim = c(1, length(eight_schools$theta)),
     ylim = range(range(eight_schools$theta)),
     xlab = "school", ylab = "theta"
)

# Then, use for_each_draw() to make a parallel coordinates plot of all draws
# of eight_schools$theta. Use resample_draws(eight_schools, n = ...)
# in place of eight_schools if a smaller sample is desired for the plot.
for_each_draw(eight_schools, {
  lines(seq_along(theta), theta, col = rgb(1, 0, 0, 0.05))
})

# Finally, add means and 90% intervals
lines(seq_along(eight_schools$theta), mean(eight_schools$theta))
with(summarise_draws(eight_schools$theta),
     segments(seq_along(eight_schools$theta), y0 = q5, y1 = q95)
)
```

---

is_rvar	<i>Is x a random variable?</i>
---------	--------------------------------

---

**Description**

Test if x is an [rvar](#).

**Usage**

```
is_rvar(x)
```

**Arguments**

x (any object) An object to test.

**Value**

TRUE if x is an [rvar](#), FALSE otherwise.

**See Also**

[as\\_rvar\(\)](#) to convert objects to rvars.

---

is_rvar_factor	<i>Is x a factor random variable?</i>
----------------	---------------------------------------

---

**Description**

Test if x is an [rvar\\_factor](#) or [rvar\\_ordered](#).

**Usage**

```
is_rvar_factor(x)
```

```
is_rvar_ordered(x)
```

**Arguments**

x (any object) An object to test.

**Value**

TRUE if x is an [rvar\\_factor](#) or [rvar\\_ordered](#), FALSE otherwise.

**See Also**

[as\\_rvar\\_factor\(\)](#) and [as\\_rvar\\_ordered\(\)](#) to convert objects to rvar\_factors and rvar\_ordereds.

---

match	<i>Value Matching</i>
-------	-----------------------

---

**Description**

Generic version of `base::match()`. For base vectors, returns a vector of the positions of (first) matches of its first argument in its second. For *rvars*, returns an *rvar* of the matches.

**Usage**

```
match(x, table, ...)

## Default S3 method:
match(x, ...)

## S3 method for class 'rvar'
match(x, ...)

x %in% table
```

**Arguments**

x	(multiple options) the values to be matched. Can be: <ul style="list-style-type: none"> <li>• A base vector: see <code>base::match()</code></li> <li>• An <i>rvar</i></li> </ul>
table	(vector) the values to be matched against.
...	Arguments passed on to <code>base::match</code>
	<code>nomatch</code> the value to be returned in the case when no match is found. Note that it is coerced to integer.
	<code>incomparables</code> a vector of values that cannot be matched. Any value in x matching a value in this vector is assigned the <code>nomatch</code> value. For historical reasons, FALSE is equivalent to NULL.

**Details**

For more information on how `match` behaves with base vectors, see `base::match()`.

When x is an *rvar*, the draws of x are matched against table using `base::match()`, and the result is returned as an *rvar*.

The implementation of `%in%` here is identical to `base::%in%`, except it uses the generic version of `match()` so that non-base vectors (such as *rvars*) are supported.

**Value**

When x is a base vector, a vector of the same length as x.

When x is an *rvar*, an *rvar* the same shape as x.

**Examples**

```
x <- rvar(c("a","b","b","c","d"))
x %in% c("b","d")

# for additional examples, see base::match()
```

---

mcse_mean	<i>Monte Carlo standard error for the mean</i>
-----------	--

---

**Description**

Compute the Monte Carlo standard error for the mean (expectation) of a single variable.

**Usage**

```
mcse_mean(x, ...)

## Default S3 method:
mcse_mean(x, ...)

## S3 method for class 'rvar'
mcse_mean(x, ...)
```

**Arguments**

**x** (multiple options) One of:

- A matrix of draws for a single variable (iterations x chains). See [extract\\_variable\\_matrix\(\)](#).
- An [rvar](#).

**...** Arguments passed to individual methods (if applicable).

**Value**

If the input is an array, returns a single numeric value. If any of the draws is non-finite, that is, NA, NaN, Inf, or -Inf, the returned output will be (numeric) NA. Also, if all draws within any of the chains of a variable are the same (constant), the returned output will be (numeric) NA as well. The reason for the latter is that, for constant draws, we cannot distinguish between variables that are supposed to be constant (e.g., a diagonal element of a correlation matrix is always 1) or variables that just happened to be constant because of a failure of convergence or other problems in the sampling process.

If the input is an [rvar](#), returns an array of the same dimensions as the [rvar](#), where each element is equal to the value that would be returned by passing the draws array for that element of the [rvar](#) to this function.

**References**

Andrew Gelman, John B. Carlin, Hal S. Stern, David B. Dunson, Aki Vehtari and Donald B. Rubin (2013). *Bayesian Data Analysis, Third Edition*. Chapman and Hall/CRC.

**See Also**

Other diagnostics: [ess\\_basic\(\)](#), [ess\\_bulk\(\)](#), [ess\\_quantile\(\)](#), [ess\\_sd\(\)](#), [ess\\_tail\(\)](#), [mcse\\_quantile\(\)](#), [mcse\\_sd\(\)](#), [pareto\\_diags\(\)](#), [pareto\\_khat\(\)](#), [rhat\(\)](#), [rhat\\_basic\(\)](#), [rhat\\_nested\(\)](#), [rstar\(\)](#)

**Examples**

```
mu <- extract_variable_matrix(example_draws(), "mu")
mcse_mean(mu)
```

```
d <- as_draws_rvars(example_draws("multi_normal"))
mcse_mean(d$Sigma)
```

---

 mcse\_quantile

*Monte Carlo standard error for quantiles*


---

**Description**

Compute Monte Carlo standard errors for quantile estimates of a single variable.

**Usage**

```
mcse_quantile(x, probs = c(0.05, 0.95), ...)

## Default S3 method:
mcse_quantile(x, probs = c(0.05, 0.95), names = TRUE, ...)

## S3 method for class 'rvar'
mcse_quantile(x, probs = c(0.05, 0.95), names = TRUE, ...)

mcse_median(x, ...)
```

**Arguments**

<code>x</code>	(multiple options) One of: <ul style="list-style-type: none"> <li>• A matrix of draws for a single variable (iterations x chains). See <a href="#">extract_variable_matrix()</a>.</li> <li>• An <a href="#">rvar</a>.</li> </ul>
<code>probs</code>	(numeric vector) Probabilities in $[0, 1]$ .
<code>...</code>	Arguments passed to individual methods (if applicable).
<code>names</code>	(logical) Should the result have a names attribute? The default is TRUE, but use FALSE for improved speed if there are many values in probs.

**Value**

If the input is an array, returns a numeric vector with one element per quantile. If any of the draws is non-finite, that is, NA, NaN, Inf, or -Inf, the returned output will be a vector of (numeric) NA values. Also, if all draws of a variable are the same (constant), the returned output will be a vector of (numeric) NA values as well. The reason for the latter is that, for constant draws, we cannot distinguish between variables that are supposed to be constant (e.g., a diagonal element of a correlation matrix is always 1) or variables that just happened to be constant because of a failure of convergence or other problems in the sampling process.

If the input is an `rvar` and `length(probs) == 1`, returns an array of the same dimensions as the `rvar`, where each element is equal to the value that would be returned by passing the draws array for that element of the `rvar` to this function. If `length(probs) > 1`, the first dimension of the result indexes the input probabilities; i.e. the result has dimension `c(length(probs), dim(x))`.

**References**

Aki Vehtari, Andrew Gelman, Daniel Simpson, Bob Carpenter, and Paul-Christian Bürkner (2021). Rank-normalization, folding, and localization: An improved R-hat for assessing convergence of MCMC (with discussion). *Bayesian Analysis*. 16(2), 667–718. doi:10.1214/20-BA1221

**See Also**

Other diagnostics: `ess_basic()`, `ess_bulk()`, `ess_quantile()`, `ess_sd()`, `ess_tail()`, `mcse_mean()`, `mcse_sd()`, `pareto_diags()`, `pareto_khat()`, `rhat()`, `rhat_basic()`, `rhat_nested()`, `rstar()`

**Examples**

```
mu <- extract_variable_matrix(example_draws(), "mu")
mcse_quantile(mu, probs = c(0.1, 0.9))

d <- as_draws_rvars(example_draws("multi_normal"))
mcse_quantile(d$mu)
```

---

mcse\_sd

*Monte Carlo standard error for the standard deviation*


---

**Description**

Compute the Monte Carlo standard error for the standard deviation (SD) of a single variable without assuming normality using moments of moments and first order Taylor series approximation (Kenney and Keeping, 1951, p. 141).

**Usage**

```
mcse_sd(x, ...)

## Default S3 method:
mcse_sd(x, ...)

## S3 method for class 'rvar'
mcse_sd(x, ...)
```

**Arguments**

`x` (multiple options) One of:

- A matrix of draws for a single variable (iterations x chains). See `extract_variable_matrix()`.
- An `rvar`.

`...` Arguments passed to individual methods (if applicable).

**Value**

If the input is an array, returns a single numeric value. If any of the draws is non-finite, that is, NA, NaN, Inf, or -Inf, the returned output will be (numeric) NA. Also, if all draws within any of the chains of a variable are the same (constant), the returned output will be (numeric) NA as well. The reason for the latter is that, for constant draws, we cannot distinguish between variables that are supposed to be constant (e.g., a diagonal element of a correlation matrix is always 1) or variables that just happened to be constant because of a failure of convergence or other problems in the sampling process.

If the input is an `rvar`, returns an array of the same dimensions as the `rvar`, where each element is equal to the value that would be returned by passing the draws array for that element of the `rvar` to this function.

**References**

Aki Vehtari, Andrew Gelman, Daniel Simpson, Bob Carpenter, and Paul-Christian Bürkner (2021). Rank-normalization, folding, and localization: An improved R-hat for assessing convergence of MCMC (with discussion). *Bayesian Analysis*. 16(2), 667–718. doi:10.1214/20-BA1221

J. F. Kenney & E. S. Keeping (1951). *Mathematics of Statistics, Vol. II*.

**See Also**

Other diagnostics: `ess_basic()`, `ess_bulk()`, `ess_quantile()`, `ess_sd()`, `ess_tail()`, `mcse_mean()`, `mcse_quantile()`, `pareto_diags()`, `pareto_khat()`, `rhat()`, `rhat_basic()`, `rhat_nested()`, `rstar()`

**Examples**

```
mu <- extract_variable_matrix(example_draws(), "mu")
mcse_sd(mu)

d <- as_draws_rvars(example_draws("multi_normal"))
```



```
mcse_sd(d$Sigma)
```

---

merge_chains	<i>Merge chains of draws objects</i>
--------------	--------------------------------------

---

### Description

Merge chains of [draws](#) objects into a single chain. Some operations will trigger an automatic merging of chains, for example, because chains do not match between two objects involved in a binary operation. By default, no warning will be issued when this happens but you can activate one via `options(posterior.warn_on_merge_chains = TRUE)`.

### Usage

```
merge_chains(x, ...)  
  
## S3 method for class 'draws_matrix'  
merge_chains(x, ...)  
  
## S3 method for class 'draws_array'  
merge_chains(x, ...)  
  
## S3 method for class 'draws_df'  
merge_chains(x, ...)  
  
## S3 method for class 'draws_list'  
merge_chains(x, ...)  
  
## S3 method for class 'rvar'  
merge_chains(x, ...)  
  
## S3 method for class 'draws_rvars'  
merge_chains(x, ...)
```

### Arguments

x	(draws) A draws object or another R object for which the method is defined.
...	Arguments passed to individual methods (if applicable).

### Value

A draws object of the same class as x.

## Examples

```
x <- example_draws()

# draws_array with 4 chains, 100 iters each
str(x)

# draws_array with 1 chain of 400 iterations
str(merge_chains(x))
```

---

modal_category	<i>Modal category</i>
----------------	-----------------------

---

## Description

Modal category of a vector.

## Usage

```
modal_category(x)

## Default S3 method:
modal_category(x)

## S3 method for class 'rvar'
modal_category(x)
```

## Arguments

**x** (multiple options) A vector to be interpreted as draws from a categorical distribution, such as:

- A [factor](#)
- A [numeric](#) (should be [integer](#) or integer-like)
- An [rvar](#), [rvar\\_factor](#), or [rvar\\_ordered](#)

## Details

Finds the modal category (i.e., most frequent value) in *x*. In the case of ties, returns the first tie.

## Value

If *x* is a [factor](#) or [numeric](#), returns a length-1 vector containing the modal value.

If *x* is an [rvar](#), returns an array of the same shape as *x*, where each cell is the modal value of the draws in the corresponding cell of *x*.

**Examples**

```
x <- factor(c("a","b","b","c","d"))
modal_category(x)

# in the case of ties, the first tie is returned
y <- factor(c("a","c","c","d","d"))
modal_category(y)

# both together, as an rvar
xy <- c(rvar(x), rvar(y))
xy
modal_category(xy)
```

---

mutate_variables	<i>Mutate variables in draws objects</i>
------------------	--

---

**Description**

Mutate variables in a [draws](#) object.

**Usage**

```
mutate_variables(.x, ...)

## S3 method for class 'draws_matrix'
mutate_variables(.x, ...)

## S3 method for class 'draws_array'
mutate_variables(.x, ...)

## S3 method for class 'draws_df'
mutate_variables(.x, ...)

## S3 method for class 'draws_list'
mutate_variables(.x, ...)

## S3 method for class 'draws_rvars'
mutate_variables(.x, ...)
```

**Arguments**

<code>.x</code>	(draws) A <a href="#">draws</a> object.
<code>...</code>	Name-value pairs of expressions, each with either length 1 or the same length as in the entire input (i.e., number of iterations or draws). The name of each argument will be the name of a new variable, and the value will be its corresponding value. Use a NULL value in <code>mutate_variables</code> to drop a variable. New variables overwrite existing variables of the same name.

**Details**

In order to mutate variables in `draws_matrix` and `draws_array` objects, they are transformed to `draws_df` objects first and then transformed back after mutation. As those transformations are quite expensive for larger number of draws, we recommend using `mutate_variables` on `draws_df` and `draws_list` objects if speed is an issue.

In `draws_rvars` objects, the output of each expression in `...` is coerced to an `rvar` object if it is not already one using `as_rvar()`.

**Value**

Returns a `draws` object of the same format as `.x`, with variables mutated according to the expressions provided in `....`

**See Also**

[variables](#), [rename\\_variables](#)

**Examples**

```
x <- as_draws_df(example_draws())
x <- subset(x, variable = c("mu", "tau"))

mutate_variables(x, tau2 = tau^2)
mutate_variables(x, scale = 1.96 * tau, lower = mu - scale)
```

---

order\_draws

*Order draws objects*

---

**Description**

Order `draws` objects according to iteration and chain number. By default, draws objects are ordered but subsetting or extracting parts of them may leave them in an unordered state.

**Usage**

```
order_draws(x, ...)
```

## S3 method for class 'draws\_matrix'

```
order_draws(x, ...)
```

## S3 method for class 'draws\_array'

```
order_draws(x, ...)
```

## S3 method for class 'draws\_df'

```
order_draws(x, ...)
```

```
## S3 method for class 'draws_list'
order_draws(x, ...)

## S3 method for class 'draws_rvars'
order_draws(x, ...)

## S3 method for class 'rvar'
order_draws(x, ...)
```

### Arguments

`x` (draws) A draws object or another R object for which the method is defined.  
`...` Arguments passed to individual methods (if applicable).

### Value

A draws object of the same class as `x`.

### See Also

[repair\\_draws\(\)](#)

### Examples

```
x <- as_draws_array(example_draws())
dimnames(x[10:5, 4:3, ])
dimnames(order_draws(x[10:5, 4:3, ]))
```

---

pareto\_diags

*Pareto smoothing diagnostics*

---

### Description

Compute diagnostics for Pareto smoothing the tail draws of `x` by replacing tail draws by order statistics of a generalized Pareto distribution fit to the tail(s).

### Usage

```
pareto_diags(x, ...)

## Default S3 method:
pareto_diags(
  x,
  tail = c("both", "right", "left"),
  r_eff = NULL,
  ndraws_tail = NULL,
  verbose = FALSE,
```

```

    are_log_weights = FALSE,
    ...
)

## S3 method for class 'rvar'
pareto_diags(x, ...)

pareto_khat_threshold(x, ...)

## Default S3 method:
pareto_khat_threshold(x, ...)

## S3 method for class 'rvar'
pareto_khat_threshold(x, ...)

pareto_min_ss(x, ...)

## Default S3 method:
pareto_min_ss(x, ...)

## S3 method for class 'rvar'
pareto_min_ss(x, ...)

pareto_convergence_rate(x, ...)

## Default S3 method:
pareto_convergence_rate(x, ...)

## S3 method for class 'rvar'
pareto_convergence_rate(x, ...)

```

## Arguments

<code>x</code>	(multiple options) One of: <ul style="list-style-type: none"> <li>• A matrix of draws for a single variable (iterations x chains). See <a href="#">extract_variable_matrix()</a>.</li> <li>• An <code>rvar</code>.</li> </ul>
<code>...</code>	Arguments passed to individual methods (if applicable).
<code>tail</code>	(string) The tail to diagnose/smooth: <ul style="list-style-type: none"> <li>• "right": diagnose/smooth only the right (upper) tail</li> <li>• "left": diagnose/smooth only the left (lower) tail</li> <li>• "both": diagnose/smooth both tails and return the maximum k-hat value</li> </ul> The default is "both".
<code>r_eff</code>	(numeric) relative effective sample size estimate. If <code>r_eff</code> is NULL, it will be calculated assuming the draws are from MCMC. Default is NULL.
<code>ndraws_tail</code>	(numeric) number of draws for the tail. If <code>ndraws_tail</code> is not specified, it will be calculated as $\text{ceiling}(3 * \sqrt{\text{length}(x) / r\_eff})$ if $\text{length}(x) > 225$ and $\text{length}(x) / 5$ otherwise (see Appendix H in Vehtari et al. (2024)).

- `verbose` (logical) Should diagnostic messages be printed? If TRUE, messages related to Pareto diagnostics will be printed. Default is FALSE.
- `are_log_weights` (logical) Are the draws log weights? Default is FALSE. If TRUE computation will take into account that the draws are log weights, and only right tail will be smoothed.

## Details

When the fitted Generalized Pareto Distribution is used to smooth the tail values and these smoothed values are used to compute expectations, the following diagnostics can give further information about the reliability of these estimates.

- `min_ss`: Minimum sample size for reliable Pareto smoothed estimate. If the actual sample size is greater than `min_ss`, then Pareto smoothed estimates can be considered reliable. If the actual sample size is lower than `min_ss`, increasing the sample size might result in more reliable estimates. For further details, see Section 3.2.3, Equation 11 in Vehtari et al. (2024).
- `khat_threshold`: Threshold below which  $\hat{k}$  values result in reliable Pareto smoothed estimates. The threshold is lower for smaller effective sample sizes. If  $\hat{k}$  is larger than the threshold, increasing the total sample size may improve reliability of estimates. For further details, see Section 3.2.4, Equation 13 in Vehtari et al. (2024).
- `convergence_rate`: Relative convergence rate compared to the central limit theorem. Applicable only if the actual sample size is sufficiently large (greater than `min_ss`). The convergence rate tells the rate at which the variance of an estimate reduces when the sample size is increased, compared to the central limit theorem convergence rate. See Appendix B in Vehtari et al. (2024).

## Value

List of Pareto smoothing diagnostics:

- `khat`: estimated Pareto  $k$  shape parameter,
- `min_ss`: minimum sample size for reliable Pareto smoothed estimate,
- `khat_threshold`:  $khat$ -threshold for reliable Pareto smoothed estimate,
- `convergence_rate`: Pareto smoothed estimate RMSE convergence rate.

## References

Aki Vehtari, Daniel Simpson, Andrew Gelman, Yuling Yao and Jonah Gabry (2024). Pareto Smoothed Importance Sampling. *Journal of Machine Learning Research*, 25(72):1-58. [PDF](#)

## See Also

[pareto\\_khat](#), [pareto\\_min\\_ss](#), [pareto\\_khat\\_threshold](#), and [pareto\\_convergence\\_rate](#) for individual diagnostics; and [pareto\\_smooth](#) for Pareto smoothing draws.

Other diagnostics: [ess\\_basic\(\)](#), [ess\\_bulk\(\)](#), [ess\\_quantile\(\)](#), [ess\\_sd\(\)](#), [ess\\_tail\(\)](#), [mcse\\_mean\(\)](#), [mcse\\_quantile\(\)](#), [mcse\\_sd\(\)](#), [pareto\\_khat\(\)](#), [rhat\(\)](#), [rhat\\_basic\(\)](#), [rhat\\_nested\(\)](#), [rstar\(\)](#)

**Examples**

```
mu <- extract_variable_matrix(example_draws(), "mu")
pareto_diags(mu)

d <- as_draws_rvars(example_draws("multi_normal"))
pareto_diags(d$Sigma)
```

---

pareto\_khat

*Pareto khat diagnostic*


---

**Description**

Estimate Pareto k value by fitting a Generalized Pareto Distribution to one or two tails of  $x$ . This can be used to estimate the number of fractional moments that is useful for convergence diagnostics. For further details see Vehtari et al. (2024).

**Usage**

```
pareto_khat(x, ...)

## Default S3 method:
pareto_khat(
  x,
  tail = c("both", "right", "left"),
  r_eff = NULL,
  ndraws_tail = NULL,
  verbose = FALSE,
  are_log_weights = FALSE,
  ...
)

## S3 method for class 'rvar'
pareto_khat(x, ...)
```

**Arguments**

**x** (multiple options) One of:

- A matrix of draws for a single variable (iterations x chains). See [extract\\_variable\\_matrix\(\)](#).
- An [rvar](#).

**...** Arguments passed to individual methods (if applicable).

**tail** (string) The tail to diagnose/smooth:

- "right": diagnose/smooth only the right (upper) tail
- "left": diagnose/smooth only the left (lower) tail
- "both": diagnose/smooth both tails and return the maximum k-hat value

The default is "both".



<code>r_eff</code>	(numeric) relative effective sample size estimate. If <code>r_eff</code> is <code>NULL</code> , it will be calculated assuming the draws are from MCMC. Default is <code>NULL</code> .
<code>ndraws_tail</code>	(numeric) number of draws for the tail. If <code>ndraws_tail</code> is not specified, it will be calculated as $\text{ceiling}(3 * \sqrt{\text{length}(x) / r\_eff})$ if $\text{length}(x) > 225$ and $\text{length}(x) / 5$ otherwise (see Appendix H in Vehtari et al. (2024)).
<code>verbose</code>	(logical) Should diagnostic messages be printed? If <code>TRUE</code> , messages related to Pareto diagnostics will be printed. Default is <code>FALSE</code> .
<code>are_log_weights</code>	(logical) Are the draws log weights? Default is <code>FALSE</code> . If <code>TRUE</code> computation will take into account that the draws are log weights, and only right tail will be smoothed.

### Value

If the input is an array, returns a single numeric value. If any of the draws is non-finite, that is, `NA`, `NaN`, `Inf`, or `-Inf`, the returned output will be (numeric) `NA`. Also, if all draws within any of the chains of a variable are the same (constant), the returned output will be (numeric) `NA` as well. The reason for the latter is that, for constant draws, we cannot distinguish between variables that are supposed to be constant (e.g., a diagonal element of a correlation matrix is always 1) or variables that just happened to be constant because of a failure of convergence or other problems in the sampling process.

If the input is an `rvar`, returns an array of the same dimensions as the `rvar`, where each element is equal to the value that would be returned by passing the draws array for that element of the `rvar` to this function.

### References

Aki Vehtari, Daniel Simpson, Andrew Gelman, Yuling Yao and Jonah Gabry (2024). Pareto Smoothed Importance Sampling. *Journal of Machine Learning Research*, 25(72):1-58. [PDF](#)

### See Also

[pareto\\_diags](#) for additional related diagnostics, and [pareto\\_smooth](#) for Pareto smoothed draws.

Other diagnostics: [ess\\_basic\(\)](#), [ess\\_bulk\(\)](#), [ess\\_quantile\(\)](#), [ess\\_sd\(\)](#), [ess\\_tail\(\)](#), [mcse\\_mean\(\)](#), [mcse\\_quantile\(\)](#), [mcse\\_sd\(\)](#), [pareto\\_diags\(\)](#), [rhat\(\)](#), [rhat\\_basic\(\)](#), [rhat\\_nested\(\)](#), [rstar\(\)](#)

### Examples

```
mu <- extract_variable_matrix(example_draws(), "mu")
pareto_khat(mu)

d <- as_draws_rvars(example_draws("multi_normal"))
pareto_khat(d$Sigma)
```

---

pareto_smooth	<i>Pareto smoothing</i>
---------------	-------------------------

---

### Description

Smooth the tail draws of  $x$  by replacing tail draws by order statistics of a generalized Pareto distribution fit to the tail(s). For further details see Vehtari et al. (2024).

### Usage

```
pareto_smooth(x, ...)

## S3 method for class 'rvar'
pareto_smooth(x, return_k = FALSE, extra_diags = FALSE, ...)

## Default S3 method:
pareto_smooth(
  x,
  tail = c("both", "right", "left"),
  r_eff = NULL,
  ndraws_tail = NULL,
  return_k = FALSE,
  extra_diags = FALSE,
  verbose = TRUE,
  are_log_weights = FALSE,
  ...
)
```

### Arguments

$x$	(multiple options) One of: <ul style="list-style-type: none"> <li>• A matrix of draws for a single variable (iterations x chains). See <a href="#">extract_variable_matrix()</a>.</li> <li>• An <a href="#">rvar</a>.</li> </ul>
...	Arguments passed to individual methods (if applicable).
return_k	(logical) Should the Pareto khat be included in output? If TRUE, output will be a list containing smoothed draws and diagnostics, otherwise it will be a numeric of the smoothed draws. Default is FALSE.
extra_diags	(logical) Should extra Pareto khat diagnostics be included in output? If TRUE, min_ss, khat_threshold and convergence_rate for the estimated k value will be returned. Default is FALSE.
tail	(string) The tail to diagnose/smooth: <ul style="list-style-type: none"> <li>• "right": diagnose/smooth only the right (upper) tail</li> <li>• "left": diagnose/smooth only the left (lower) tail</li> <li>• "both": diagnose/smooth both tails and return the maximum k-hat value</li> </ul>

	The default is "both".
r_eff	(numeric) relative effective sample size estimate. If r_eff is NULL, it will be calculated assuming the draws are from MCMC. Default is NULL.
ndraws_tail	(numeric) number of draws for the tail. If ndraws_tail is not specified, it will be calculated as $\text{ceiling}(3 * \sqrt{\text{length}(x) / r\_eff})$ if $\text{length}(x) > 225$ and $\text{length}(x) / 5$ otherwise (see Appendix H in Vehtari et al. (2024)).
verbose	(logical) Should diagnostic messages be printed? If TRUE, messages related to Pareto diagnostics will be printed. Default is FALSE.
are_log_weights	(logical) Are the draws log weights? Default is FALSE. If TRUE computation will take into account that the draws are log weights, and only right tail will be smoothed.

### Value

Either a vector  $x$  of smoothed values or a named list containing the vector  $x$  and a named list diagnostics containing numeric values:

- khat: estimated Pareto  $k$  shape parameter, and optionally
- min\_ss: minimum sample size for reliable Pareto smoothed estimate
- khat\_threshold: sample size specific khat threshold for reliable Pareto smoothed estimates
- convergence\_rate: Relative convergence rate for Pareto smoothed estimates

If any of the draws is non-finite, that is, NA, NaN, Inf, or -Inf, Pareto smoothing will not be performed, and the original draws will be returned and diagnostics will be NA (numeric).

### References

Aki Vehtari, Daniel Simpson, Andrew Gelman, Yuling Yao and Jonah Gabry (2024). Pareto Smoothed Importance Sampling. *Journal of Machine Learning Research*, 25(72):1-58. [PDF](#)

### See Also

[pareto\\_khat](#) for only calculating khat, and [pareto\\_diags](#) for additional diagnostics.

### Examples

```
mu <- extract_variable_matrix(example_draws(), "mu")
pareto_smooth(mu)

d <- as_draws_rvars(example_draws("multi_normal"))
pareto_smooth(d$Sigma)
```

---

```
print.draws_array      Print draws_array objects
```

---

### Description

Pretty printing for [draws\\_array](#) objects.

### Usage

```
## S3 method for class 'draws_array'
print(
  x,
  digits = 2,
  max_iterations = getOption("posterior.max_iterations", 5),
  max_chains = getOption("posterior.max_chains", 8),
  max_variables = getOption("posterior.max_variables", 4),
  reserved = FALSE,
  ...
)
```

### Arguments

<code>x</code>	(draws) A draws object or another R object for which the method is defined.
<code>digits</code>	(nonnegative integer) The minimum number of significant digits to print. If NULL, defaults to <code>getOption("posterior.digits", 2)</code> .
<code>max_iterations</code>	(positive integer) The maximum number of iterations to print. Can be controlled globally via the <code>"posterior.max_iterations"</code> <a href="#">option</a> .
<code>max_chains</code>	(positive integer) The maximum number of chains to print. Can be controlled globally via the <code>"posterior.max_chains"</code> <a href="#">option</a> .
<code>max_variables</code>	(positive integer) The maximum number of variables to print. Can be controlled globally via the <code>"posterior.max_variables"</code> <a href="#">option</a> .
<code>reserved</code>	(logical) Should reserved variables be included in the output? Defaults to FALSE. See <a href="#">reserved_variables</a> for an overview of currently reserved variable names.
<code>...</code>	Further arguments passed to the underlying <code>print()</code> methods.

### Value

A draws object of the same class as `x`.

### Examples

```
x <- as_draws_array(example_draws())
print(x)
```

---

print.draws_df	<i>Print draws_df objects</i>
----------------	-------------------------------

---

## Description

Pretty printing for [draws\\_df](#) objects.

## Usage

```
## S3 method for class 'draws_df'
print(
  x,
  digits = 2,
  max_draws = getOption("posterior.max_draws", 10),
  max_variables = getOption("posterior.max_variables", 8),
  reserved = FALSE,
  ...
)
```

## Arguments

x	(draws) A draws object or another R object for which the method is defined.
digits	(nonnegative integer) The minimum number of significant digits to print. If NULL, defaults to <code>getOption("posterior.digits", 2)</code> .
max_draws	(positive integer) The maximum number of draws to print. Can be controlled globally via the <code>"posterior.max_draws"</code> <a href="#">option</a> .
max_variables	(positive integer) The maximum number of variables to print. Can be controlled globally via the <code>"posterior.max_variables"</code> <a href="#">option</a> .
reserved	(logical) Should reserved variables be included in the output? Defaults to FALSE. See <a href="#">reserved_variables</a> for an overview of currently reserved variable names.
...	Further arguments passed to the underlying <code>print()</code> methods.

## Value

A draws object of the same class as x.

## Examples

```
x <- as_draws_df(example_draws())
print(x)
```

---

```
print.draws_list      Print draws_list objects
```

---

## Description

Pretty printing for [draws\\_list](#) objects.

## Usage

```
## S3 method for class 'draws_list'
print(
  x,
  digits = 2,
  max_iterations = getOption("posterior.max_iterations", 10),
  max_chains = getOption("posterior.max_chains", 2),
  max_variables = getOption("posterior.max_variables", 4),
  reserved = FALSE,
  ...
)
```

## Arguments

<code>x</code>	(draws) A draws object or another R object for which the method is defined.
<code>digits</code>	(nonnegative integer) The minimum number of significant digits to print. If NULL, defaults to <code>getOption("posterior.digits", 2)</code> .
<code>max_iterations</code>	(positive integer) The maximum number of iterations to print. Can be controlled globally via the <code>"posterior.max_iterations"</code> <a href="#">option</a> .
<code>max_chains</code>	(positive integer) The maximum number of chains to print. Can be controlled globally via the <code>"posterior.max_chains"</code> <a href="#">option</a> .
<code>max_variables</code>	(positive integer) The maximum number of variables to print. Can be controlled globally via the <code>"posterior.max_variables"</code> <a href="#">option</a> .
<code>reserved</code>	(logical) Should reserved variables be included in the output? Defaults to FALSE. See <a href="#">reserved_variables</a> for an overview of currently reserved variable names.
<code>...</code>	Further arguments passed to the underlying <code>print()</code> methods.

## Value

A draws object of the same class as `x`.

## Examples

```
x <- as_draws_list(example_draws())
print(x)
```

---

print.draws\_matrix     *Print draws\_matrix objects*

---

## Description

Pretty printing for `draws_matrix` objects.

## Usage

```
## S3 method for class 'draws_matrix'
print(
  x,
  digits = 2,
  max_draws = getOption("posterior.max_draws", 10),
  max_variables = getOption("posterior.max_variables", 8),
  reserved = FALSE,
  ...
)
```

## Arguments

<code>x</code>	(draws) A draws object or another R object for which the method is defined.
<code>digits</code>	(nonnegative integer) The minimum number of significant digits to print. If NULL, defaults to <code>getOption("posterior.digits", 2)</code> .
<code>max_draws</code>	(positive integer) The maximum number of draws to print. Can be controlled globally via the <code>"posterior.max_draws"</code> <a href="#">option</a> .
<code>max_variables</code>	(positive integer) The maximum number of variables to print. Can be controlled globally via the <code>"posterior.max_variables"</code> <a href="#">option</a> .
<code>reserved</code>	(logical) Should reserved variables be included in the output? Defaults to FALSE. See <a href="#">reserved_variables</a> for an overview of currently reserved variable names.
<code>...</code>	Further arguments passed to the underlying <code>print()</code> methods.

## Value

A draws object of the same class as `x`.

## Examples

```
x <- as_draws_matrix(example_draws())
print(x)
```

---

```
print.draws_rvars      Print draws_rvars objects
```

---

### Description

Pretty printing for `draws_rvars` objects.

### Usage

```
## S3 method for class 'draws_rvars'
print(
  x,
  digits = 2,
  max_variables = getOption("posterior.max_variables", 8),
  summary = getOption("posterior.rvar_summary", "mean_sd"),
  reserved = FALSE,
  ...
)
```

### Arguments

<code>x</code>	(draws) A draws object or another R object for which the method is defined.
<code>digits</code>	(nonnegative integer) The minimum number of significant digits to print. If NULL, defaults to <code>getOption("posterior.digits", 2)</code> .
<code>max_variables</code>	(positive integer) The maximum number of variables to print. Can be controlled globally via the <code>"posterior.max_variables"</code> <a href="#">option</a> .
<code>summary</code>	(string) The style of summary to display: <ul style="list-style-type: none"> <li>• <code>"mean_sd"</code> displays mean <math>\pm</math> sd</li> <li>• <code>"median_mad"</code> displays median <math>\pm</math> mad</li> <li>• <code>"mode_entropy"</code> displays mode &lt;entropy&gt;, and is used automatically for <a href="#">rvar_factors</a>. It shows normalized entropy, which ranges from 0 (all probability in one category) to 1 (uniform). See <a href="#">entropy()</a>.</li> <li>• <code>"mode_dissent"</code> displays mode &lt;dissent&gt;, and is used automatically for <a href="#">rvar_ordereds</a>. It shows Tastle and Wierman's (2007) <i>dissent</i> measure, which ranges from 0 (all probability in one category) through 0.5 (uniform) to 1 (bimodal: all probability split equally between the first and last category). See <a href="#">dissent()</a>.</li> <li>• NULL uses <code>getOption("posterior.rvar_summary")</code> (default <code>"mean_sd"</code>)</li> </ul>
<code>reserved</code>	(logical) Should reserved variables be included in the output? Defaults to FALSE. See <a href="#">reserved_variables</a> for an overview of currently reserved variable names.
<code>...</code>	Further arguments passed to the underlying <code>print()</code> methods.

### Value

A draws object of the same class as `x`.



**Examples**

```
x <- as_draws_rvars(example_draws())
print(x)
```

---

```
print.draws_summary Print summaries of draws objects
```

---

**Description**

Print output from `summarise_draws()`.

**Usage**

```
## S3 method for class 'draws_summary'
print(x, ..., num_args = NULL)
```

**Arguments**

x	(draws_summary) A "draws_summary" object as output by <code>summarise_draws()</code> .
...	Additional arguments passed to <code>tibble::print.tbl_df()</code>
num_args	(named list) Optional arguments passed to <code>num()</code> for pretty printing of summaries. If NULL (the default), uses the arguments stored in the "num_args" attribute of x, as set by the <code>.num_args</code> argument of <code>summarise_draws()</code> , which itself can be controlled globally via the posterior <code>.num_args</code> option.

**Value**

An invisible version of the input object.

**Examples**

```
x <- example_draws("eight_schools")

# adjust how summaries are printed when calling summarise_draws()...
summarise_draws(x, .num_args = list(sigfig = 2, notation = "dec"))

# ... or when printing
s <- summarise_draws(x)
print(s, num_args = list(sigfig = 2, notation = "dec"))
print(s, num_args = list(digits = 3))
```

---

print.rvar                      *Print or format a random variable*

---

## Description

Printing and formatting methods for `rvars`.

## Usage

```
## S3 method for class 'rvar'
print(
  x,
  ...,
  summary = NULL,
  digits = NULL,
  color = TRUE,
  width = getOption("width")
)

## S3 method for class 'rvar'
format(x, ..., summary = NULL, digits = NULL, color = FALSE)

## S3 method for class 'rvar'
str(
  object,
  ...,
  summary = NULL,
  vec.len = NULL,
  indent.str = paste(rep.int(" ", max(0, nest.lev + 1)), collapse = ".."),
  nest.lev = 0,
  give.attr = TRUE
)
```

## Arguments

<code>x, object</code>	( <code>rvar</code> ) The <code>rvar</code> to print.
<code>...</code>	Further arguments passed to the underlying <code>print()</code> methods.
<code>summary</code>	(string) The style of summary to display: <ul style="list-style-type: none"> <li>• <code>"mean_sd"</code> displays mean <math>\pm</math> sd</li> <li>• <code>"median_mad"</code> displays median <math>\pm</math> mad</li> <li>• <code>"mode_entropy"</code> displays mode <math>\langle</math>entropy<math>\rangle</math>, and is used automatically for <code>rvar_factors</code>. It shows normalized entropy, which ranges from 0 (all probability in one category) to 1 (uniform). See <code>entropy()</code>.</li> <li>• <code>"mode_dissent"</code> displays mode <math>\langle</math>dissent<math>\rangle</math>, and is used automatically for <code>rvar_ordereds</code>. It shows Tastle and Wierman's (2007) <i>dissention</i> measure, which ranges from 0 (all probability in one category) through 0.5 (uniform)</li> </ul>

	to 1 (bimodal: all probability split equally between the first and last category). See <code>dissent()</code> .
	• NULL uses <code>getOption("posterior.rvar.summary")</code> (default "mean_sd")
<code>digits</code>	(nonnegative integer) The minimum number of significant digits to print. If NULL, defaults to <code>getOption("posterior.digits", 2)</code> .
<code>color</code>	(logical) Whether or not to use color when formatting the output. If TRUE, the <code>pillar::style_num()</code> functions may be used to produce strings containing control sequences to produce colored output on the terminal.
<code>width</code>	The maximum width used to print out lists of factor levels for <code>rvar_factors</code> . See <code>format()</code> .
<code>vec.len</code>	(nonnegative integer) How many 'first few' elements are displayed of each vector. If NULL, defaults to <code>getOption("str")\$vec.len</code> , which defaults to 4.
<code>indent.str</code>	(string) The indentation string to use.
<code>nest.lev</code>	(nonnegative integer) Current nesting level in the recursive calls to <code>str()</code> .
<code>give.attr</code>	(logical) If TRUE (default), show attributes as sub structures.

## Details

`print()` and `str()` print out `rvar` objects by summarizing each element in the random variable with either its  $\text{mean} \pm \text{sd}$  or  $\text{median} \pm \text{mad}$ , depending on the value of `summary`. Both functions use the `format()` implementation for `rvar` objects under the hood, which returns a character vector in the  $\text{mean} \pm \text{sd}$  or  $\text{median} \pm \text{mad}$  form.

## Value

For `print()`, an invisible version of the input object.

For `str()`, nothing; i.e. `invisible(NULL)`.

For `format()`, a character vector of the same dimensions as `x` where each entry is of the form " $\text{mean} \pm \text{sd}$ " or " $\text{median} \pm \text{mad}$ ", depending on the value of `summary`.

## References

William J. Tastle, Mark J. Wierman (2007). Consensus and dissent: A measure of ordinal dispersion. *International Journal of Approximate Reasoning*. 45(3), 531–545. doi:10.1016/j.ijar.2006.06.024.

## Examples

```
set.seed(5678)
x = rbind(
  cbind(rvar(rnorm(1000, 1)), rvar(rnorm(1000, 2))),
  cbind(rvar(rnorm(1000, 3)), rvar(rnorm(1000, 4)))
)

print(x)
print(x, summary = "median_mad")

str(x)
```

format(x)

---

ps\_convergence\_rate     *Pareto convergence rate*

---

### Description

Given number of draws and scalar or array of k's, compute the relative convergence rate of PSIS estimate RMSE. See Appendix B of Vehtari et al. (2024). This function is exported to be usable by other packages. For user-facing diagnostic functions, see [pareto\\_convergence\\_rate](#) and [pareto\\_diags](#).

### Usage

```
ps_convergence_rate(k, ndraws, ...)
```

### Arguments

k	pareto-k values
ndraws	number of draws
...	unused

### Value

convergence rate

### See Also

Other helper-functions: [ps\\_khat\\_threshold\(\)](#), [ps\\_min\\_ss\(\)](#), [ps\\_tail\\_length\(\)](#)

---

ps\_khat\_threshold     *Pareto k-hat threshold*

---

### Description

Given number of draws, computes khat threshold for reliable Pareto smoothed estimate (to have small probability of large error). See section 3.2.4, equation (13) of Vehtari et al. (2024). This function is exported to be usable by other packages. For user-facing diagnostic functions, see [pareto\\_khat\\_threshold](#) and [pareto\\_diags](#).

### Usage

```
ps_khat_threshold(ndraws, ...)
```

**Arguments**

ndraws	number of draws
...	unused

**Value**

threshold

**See Also**

Other helper-functions: [ps\\_convergence\\_rate\(\)](#), [ps\\_min\\_ss\(\)](#), [ps\\_tail\\_length\(\)](#)

---

ps_min_ss	<i>Pareto-smoothing minimum sample-size</i>
-----------	---

---

**Description**

Given Pareto-k computes the minimum sample size for reliable Pareto smoothed estimate (to have small probability of large error). See section 3.2.3 in Vehtari et al. (2024). This function is exported to be usable by other packages. For user-facing diagnostic functions, see [pareto\\_min\\_ss](#) and [pareto\\_diags](#).

**Usage**

```
ps_min_ss(k, ...)
```

**Arguments**

k	pareto k value
...	unused

**Value**

minimum sample size

**See Also**

Other helper-functions: [ps\\_convergence\\_rate\(\)](#), [ps\\_khat\\_threshold\(\)](#), [ps\\_tail\\_length\(\)](#)

---

ps_tail_length	<i>Pareto tail length</i>
----------------	---------------------------

---

### Description

Calculate the tail length from number of draws and relative efficiency `r_eff`. See Appendix H in Vehtari et al. (2024). This function is used internally and is exported to be available for other packages.

### Usage

```
ps_tail_length(ndraws, r_eff, ...)
```

### Arguments

<code>ndraws</code>	number of draws
<code>r_eff</code>	relative efficiency
<code>...</code>	unused

### Value

tail length

### See Also

Other helper-functions: [ps\\_convergence\\_rate\(\)](#), [ps\\_khat\\_threshold\(\)](#), [ps\\_min\\_ss\(\)](#)

---

quantile2	<i>Compute Quantiles</i>
-----------	--------------------------

---

### Description

Compute quantiles of a sample and return them in a format consistent with other summary functions in the **posterior** package.

### Usage

```
quantile2(x, probs = c(0.05, 0.95), na.rm = FALSE, ...)
```

```
## Default S3 method:
```

```
quantile2(x, probs = c(0.05, 0.95), na.rm = FALSE, names = TRUE, ...)
```

```
## S3 method for class 'rvar'
```

```
quantile2(x, probs = c(0.05, 0.95), na.rm = FALSE, names = TRUE, ...)
```

**Arguments**

x	(multiple options) One of: <ul style="list-style-type: none"> <li>• A matrix of draws for a single variable (iterations x chains). See <code>extract_variable_matrix()</code>.</li> <li>• An <code>rvar</code>.</li> </ul>
probs	(numeric vector) Probabilities in $[0, 1]$ .
na.rm	(logical) Should NA and NaN values be removed from x prior to computing quantiles? The default is FALSE.
...	Arguments passed to individual methods (if applicable) and then on to <code>stats::quantile()</code> .
names	(logical) Should the result have a names attribute? The default is TRUE, but use FALSE for improved speed if there are many values in probs.

**Value**

A numeric vector of length `length(probs)`. If `names = TRUE`, it has a `names` attribute with names like "q5", "q95", etc, based on the values of probs.

**Examples**

```
mu <- extract_variable_matrix(example_draws(), "mu")
quantile2(mu)
```

rdo

*Execute expressions of random variables***Description**

Execute (nearly) arbitrary R expressions that may include `rvars`, producing a new `rvar`.

**Usage**

```
rdo(expr, dim = NULL, ndraws = NULL)
```

**Arguments**

expr	(expression) A bare expression that can (optionally) contain <code>rvars</code> . The expression supports <code>quasiquote</code> .
dim	(integer vector) One or more integers giving the maximal indices in each dimension to override the dimensions of the <code>rvar</code> to be created (see <code>dim()</code> ). If NULL (the default), <code>dim</code> is determined by the input. <b>NOTE:</b> This argument controls the dimensions of the <code>rvar</code> , not the underlying array, so you cannot change the number of draws using this argument.
ndraws	(positive integer) The number of draws used to construct new random variables if no <code>rvars</code> are supplied in <code>expr</code> . If NULL, <code>getOption("posterior.rvar.ndraws")</code> is used (default 4000). If <code>expr</code> contains <code>rvars</code> , the number of draws in the provided <code>rvars</code> is used instead of the value of this argument.

## Details

This function evaluates `expr` possibly multiple times, once for each draw of the `rvars` it contains, then returns a new `rvar` representing the output of those expressions. To identify `rvars`, `rdo()` searches the calling environment for any variables named in `expr` for which `is_rvar()` evaluates to `TRUE`. If `expr` contains no `rvars`, then it will be executed `ndraws` times and an `rvar` with that many draws returned.

`rdo()` is not necessarily *fast* (in fact in some cases it may be very slow), but it has the advantage of allowing a nearly arbitrary R expression to be executed against `rvars` simply by wrapping it with `rdo( ... )`. This makes it especially useful as a prototyping tool. If you create code with `rdo()` and it is unacceptably slow for your application, consider rewriting it using math operations directly on `rvars` (which should be fast), using `rvar_rng()`, and/or using operations directly on the arrays that back the `rvars` (via `draws_of()`).

## Value

An `rvar`.

## See Also

Other rfun: `rfun()`, `rvar_rng()`

## Examples

```
mu <- rdo(rnorm(10, mean = 1:10, sd = 1))
sigma <- rdo(rgamma(1, shape = 1, rate = 1))
x <- rdo(rnorm(10, mu, sigma))
x
```

---

rename\_variables

*Rename variables in draws objects*

---

## Description

Rename variables in a `draws` object.

## Usage

```
rename_variables(.x, ...)
```

```
## S3 method for class 'draws'
rename_variables(.x, ...)
```



**Arguments**

`.x` (draws) A [draws](#) object.

`...` One or more expressions, separated by commas, indicating the variables to rename. The variable names can be unquoted (`new_name = old_name`) or quoted (`"new_name" = "old_name"`). For non-scalar variables, all elements can be renamed together (`"new_name" = "old_name"`) or they can be renamed individually (`"new_name[1]" = "old_name[1]"`).

**Value**

Returns a [draws](#) object of the same format as `.x`, with variables renamed according to the expressions provided in `...`

**See Also**

[variables](#), [variables<-](#), [mutate\\_variables](#)

**Examples**

```
x <- as_draws_df(example_draws())
variables(x)

x <- rename_variables(x, mean = mu, sigma = tau)
variables(x)

x <- rename_variables(x, b = `theta[1]`) # or b = "theta[1]"
variables(x)

# rename all elements of 'theta' at once
x <- rename_variables(x, alpha = theta)
variables(x)
```

---

 repair\_draws

*Repair indices of draws objects*


---

**Description**

Repair indices of draws objects so that iterations, chains, and draws are continuously and consistently numbered.

**Usage**

```
repair_draws(x, order = TRUE, ...)
```

## S3 method for class 'draws\_matrix'

```
repair_draws(x, order = TRUE, ...)
```

```
## S3 method for class 'draws_array'
repair_draws(x, order = TRUE, ...)

## S3 method for class 'draws_df'
repair_draws(x, order = TRUE, ...)

## S3 method for class 'draws_list'
repair_draws(x, order = TRUE, ...)

## S3 method for class 'draws_rvars'
repair_draws(x, order = TRUE, ...)

## S3 method for class 'rvar'
repair_draws(x, order = TRUE, ...)
```

### Arguments

x	(draws) A draws object or another R object for which the method is defined.
order	(logical) Should draws be ordered (via <a href="#">order_draws()</a> ) before repairing indices? Defaults to TRUE.
...	Arguments passed to individual methods (if applicable).

### Value

A draws object of the same class as x.

### See Also

[order\\_draws\(\)](#)

### Examples

```
x <- as_draws_array(example_draws())
(x <- x[10:5, 3:4, ])
repair_draws(x)
```

---

resample\_draws

*Resample draws objects*

---

### Description

Resample [draws](#) objects according to provided weights, for example weights obtained through importance sampling.

**Usage**

```
resample_draws(x, ...)

## S3 method for class 'draws'
resample_draws(x, weights = NULL, method = "stratified", ndraws = NULL, ...)

## S3 method for class 'rvar'
resample_draws(x, ...)
```

**Arguments**

x	(draws) A draws object or another R object for which the method is defined.
...	Arguments passed to individual methods (if applicable).
weights	(numeric vector) A vector of positive weights of length <code>ndraws(x)</code> . The weights will be internally normalized. If <code>weights</code> is not specified, an attempt will be made to extract any weights already stored in the draws object (via <code>weight_draws()</code> ). If no weights are stored in the draws object, equal weight is supplied to each draw. How exactly the weights influence the resampling depends on the method argument.
method	(string) The resampling method to use: <ul style="list-style-type: none"> <li>• "simple": simple random resampling with replacement</li> <li>• "simple_no_replace": simple random resampling without replacement</li> <li>• "stratified": stratified resampling with replacement</li> <li>• "deterministic": deterministic resampling with replacement</li> </ul> <p>Currently, "stratified" is the default as it has comparably low variance and bias with respect to ideal resampling. The latter would sample perfectly proportional to the weights, but this is not possible in practice due to the finite number of draws available. For more details about resampling methods, see Kitagawa (1996).</p>
ndraws	(positive integer) The number of draws to be returned. By default <code>ndraws</code> is set internally to the total number of draws in <code>x</code> if sensible.

**Details**

Upon usage of `resample_draws()`, chains will automatically be merged due to subsetting of individual draws (see `subset_draws` for details). Also, weights stored in the draws object will be removed in the process, as resampling invalidates existing weights.

**Value**

A draws object of the same class as `x`.

**References**

Kitagawa, G., Monte Carlo Filter and Smoother for Non-Gaussian Nonlinear ' State Space Models, *Journal of Computational and Graphical Statistics*, 5(1):1-25, 1996.

**See Also**[resample\\_draws\(\)](#)**Examples**

```
x <- as_draws_df(example_draws())

# random weights for just for demonstration
w <- runif(ndraws(x), 0, 10)

# use default stratified sampling
x_rs <- resample_draws(x, weights = w)
summarise_draws(x_rs, default_summary_measures())

# use simple random sampling
x_rs <- resample_draws(x, weights = w, method = "simple")
summarise_draws(x_rs, default_summary_measures())
```

---

reserved_variables	<i>Reserved variables</i>
--------------------	---------------------------

---

**Description**

Get names of reserved variables from objects in the **posterior** package.

**Usage**

```
reserved_variables(x, ...)
```

## Default S3 method:  
reserved\_variables(x, ...)

## S3 method for class 'draws\_matrix'  
reserved\_variables(x, ...)

## S3 method for class 'draws\_array'  
reserved\_variables(x, ...)

## S3 method for class 'draws\_df'  
reserved\_variables(x, ...)

## S3 method for class 'draws\_list'  
reserved\_variables(x, ...)

## S3 method for class 'draws\_rvars'  
reserved\_variables(x, ...)

## Arguments

- `x` (draws) A draws object or another R object for which the method is defined.  
`...` Arguments passed to individual methods (if applicable).

## Details

`reserved_variables()` returns the names of reserved variables in use by an object.

The following variables names are currently reserved for special use cases in all `draws` formats:

- `.log_weight`: Log weights per draw (see `weight_draws`).

Further, specific for the `draws_df` format, there are three additional reserved variables:

- `.chain`: Chain index per draw
- `.iteration`: Iteration index within each chain
- `.draw`: Draw index across chains

More reserved variables may be added in the future.

## Value

A character vector of reserved variables used in `x`.

## Examples

```
x <- example_draws()
reserved_variables(x)

# if we add weights, the .log_weight reserved variable is used
x <- weight_draws(x, rexp(ndraws(x)))
reserved_variables(x)
```

## Description

Function that create functions that can accept and/or produce `rvars`.

## Usage

```
rfun(.f, rvar_args = NULL, rvar_dots = TRUE, ndraws = NULL)
```

## Arguments

<code>.f</code>	(multiple options) A function to turn into a function that accepts and/or produces random variables: <ul style="list-style-type: none"> <li>• A function</li> <li>• A one-sided formula that can be parsed by <code>rlang::as_function()</code></li> </ul>
<code>rvar_args</code>	(character vector) The names of the arguments of <code>.f</code> that should be allowed to accept <code>rvars</code> as arguments. If <code>NULL</code> (the default), all arguments to <code>.f</code> are turned into arguments that accept <code>rvars</code> , including arguments passed via <code>...</code> (if <code>rvar_dots</code> is <code>TRUE</code> ).
<code>rvar_dots</code>	(logical) Should dots ( <code>...</code> ) arguments also be converted? Only applies if <code>rvar_args</code> is <code>NULL</code> (i.e., all arguments are allowed to be <code>rvars</code> ).
<code>ndraws</code>	(positive integer). The number of draws used to construct new random variables if no <code>rvars</code> are supplied as arguments to the returned function. If <code>NULL</code> , <code>getOption("posterior.rvar.ndraws")</code> is used (default 4000). If any arguments to the returned function contain <code>rvars</code> , the number of draws in the provided <code>rvars</code> is used instead of the value of this argument.

## Details

This function wraps an existing function (`.f`) such that it returns `rvars` containing whatever type of data `.f` would normally return.

The returned function, when called, executes `.f` possibly multiple times, once for each draw of the `rvars` passed to it, then returns a new `rvar` representing the output of those function evaluations. If the arguments contain no `rvars`, then `.f` will be executed `ndraws` times and an `rvar` with that many draws returned.

Functions created by `rfun()` are not necessarily *fast* (in fact in some cases they may be very slow), but they have the advantage of allowing a nearly arbitrary R functions to be executed against `rvars` simply by wrapping them with `rfun()`. This makes it especially useful as a prototyping tool. If you create code with `rfun()` and it is unacceptably slow for your application, consider rewriting it using math operations directly on `rvars` (which should be fast), using `rvar_rng()`, and/or using operations directly on the arrays that back the `rvars` (via `draws_of()`).

## Value

A function with the same argument specification as `.f`, but which can accept and return `rvars`.

## See Also

Other `rfun`: `rdo()`, `rvar_rng()`

## Examples

```
rvar_norm <- rfun(rnorm)
rvar_gamma <- rfun(rgamma)

mu <- rvar_norm(10, mean = 1:10, sd = 1)
sigma <- rvar_gamma(1, shape = 1, rate = 1)
```

```
x <- rvar_norm(10, mu, sigma)
x
```

---

rhat

*Rhat convergence diagnostic*

---

### Description

Compute the Rhat convergence diagnostic for a single variable as the maximum of rank normalized split-Rhat and rank normalized folded-split-Rhat as proposed in Vehtari et al. (2021).

### Usage

```
rhat(x, ...)
```

## Default S3 method:  
rhat(x, ...)

## S3 method for class 'rvar'  
rhat(x, ...)

### Arguments

`x` (multiple options) One of:

- A matrix of draws for a single variable (iterations x chains). See [extract\\_variable\\_matrix\(\)](#).
- An [rvar](#).

`...` Arguments passed to individual methods (if applicable).

### Value

If the input is an array, returns a single numeric value. If any of the draws is non-finite, that is, NA, NaN, Inf, or -Inf, the returned output will be (numeric) NA. Also, if all draws within any of the chains of a variable are the same (constant), the returned output will be (numeric) NA as well. The reason for the latter is that, for constant draws, we cannot distinguish between variables that are supposed to be constant (e.g., a diagonal element of a correlation matrix is always 1) or variables that just happened to be constant because of a failure of convergence or other problems in the sampling process.

If the input is an [rvar](#), returns an array of the same dimensions as the [rvar](#), where each element is equal to the value that would be returned by passing the draws array for that element of the [rvar](#) to this function.

### References

Aki Vehtari, Andrew Gelman, Daniel Simpson, Bob Carpenter, and Paul-Christian Bürkner (2021). Rank-normalization, folding, and localization: An improved R-hat for assessing convergence of MCMC (with discussion). *Bayesian Analysis*. 16(2), 667–718. doi:10.1214/20-BA1221

**See Also**

Other diagnostics: [ess\\_basic\(\)](#), [ess\\_bulk\(\)](#), [ess\\_quantile\(\)](#), [ess\\_sd\(\)](#), [ess\\_tail\(\)](#), [mcse\\_mean\(\)](#), [mcse\\_quantile\(\)](#), [mcse\\_sd\(\)](#), [pareto\\_diags\(\)](#), [pareto\\_khat\(\)](#), [rhat\\_basic\(\)](#), [rhat\\_nested\(\)](#), [rstar\(\)](#)

**Examples**

```
mu <- extract_variable_matrix(example_draws(), "mu")
rhat(mu)
```

```
d <- as_draws_rvars(example_draws("multi_normal"))
rhat(d$Sigma)
```

---

rhat\_basic

*Basic version of the Rhat convergence diagnostic*


---

**Description**

Compute the basic Rhat convergence diagnostic for a single variable as described in Gelman et al. (2013) with some changes according to Vehtari et al. (2021). For practical applications, we strongly recommend the improved Rhat convergence diagnostic implemented in [rhat\(\)](#).

**Usage**

```
rhat_basic(x, ...)

## Default S3 method:
rhat_basic(x, split = TRUE, ...)

## S3 method for class 'rvar'
rhat_basic(x, split = TRUE, ...)
```

**Arguments**

x	(multiple options) One of: <ul style="list-style-type: none"> <li>A matrix of draws for a single variable (iterations x chains). See <a href="#">extract_variable_matrix()</a>.</li> <li>An <a href="#">rvar</a>.</li> </ul>
...	Arguments passed to individual methods (if applicable).
split	(logical) Should the estimate be computed on split chains? The default is TRUE.



**Value**

If the input is an array, returns a single numeric value. If any of the draws is non-finite, that is, NA, NaN, Inf, or -Inf, the returned output will be (numeric) NA. Also, if all draws within any of the chains of a variable are the same (constant), the returned output will be (numeric) NA as well. The reason for the latter is that, for constant draws, we cannot distinguish between variables that are supposed to be constant (e.g., a diagonal element of a correlation matrix is always 1) or variables that just happened to be constant because of a failure of convergence or other problems in the sampling process.

If the input is an `rvar`, returns an array of the same dimensions as the `rvar`, where each element is equal to the value that would be returned by passing the draws array for that element of the `rvar` to this function.

**References**

Andrew Gelman, John B. Carlin, Hal S. Stern, David B. Dunson, Aki Vehtari and Donald B. Rubin (2013). *Bayesian Data Analysis, Third Edition*. Chapman and Hall/CRC.

Aki Vehtari, Andrew Gelman, Daniel Simpson, Bob Carpenter, and Paul-Christian Bürkner (2021). Rank-normalization, folding, and localization: An improved R-hat for assessing convergence of MCMC (with discussion). *Bayesian Analysis*. 16(2), 667–718. doi:10.1214/20-BA1221

**See Also**

Other diagnostics: `ess_basic()`, `ess_bulk()`, `ess_quantile()`, `ess_sd()`, `ess_tail()`, `mcse_mean()`, `mcse_quantile()`, `mcse_sd()`, `pareto_diags()`, `pareto_khat()`, `rhat()`, `rhat_nested()`, `rstar()`

**Examples**

```
mu <- extract_variable_matrix(example_draws(), "mu")
rhat_basic(mu)

d <- as_draws_rvars(example_draws("multi_normal"))
rhat_basic(d$Sigma)
```

---

rhat\_nested

*Nested Rhat convergence diagnostic*


---

**Description**

Compute the nested Rhat convergence diagnostic for a single variable as proposed in Margossian et al. (2024).

**Usage**

```
rhat_nested(x, ...)

## Default S3 method:
rhat_nested(x, superchain_ids, ...)

## S3 method for class 'rvar'
rhat_nested(x, superchain_ids, ...)
```

**Arguments**

**x** (multiple options) One of:

- A matrix of draws for a single variable (iterations x chains). See [extract\\_variable\\_matrix\(\)](#).
- An [rvar](#).

**...** Arguments passed to individual methods (if applicable).

**superchain\_ids** (numeric) Vector of length nchains specifying which superchain each chain belongs to. There should be equal numbers of chains in each superchain. All chains within the same superchain are assumed to have been initialized at the same point.

**Details**

Nested Rhat is a convergence diagnostic useful when running many short chains. It is calculated on superchains, which are groups of chains that have been initialized at the same point.

Note that there is a slight difference in the calculation of Rhat and nested Rhat, as nested Rhat is lower bounded by 1. This means that nested Rhat with one chain per superchain will not be exactly equal to basic Rhat (see Footnote 3 in Margossian et al. (2024)).

**Value**

If the input is an array, returns a single numeric value. If any of the draws is non-finite, that is, NA, NaN, Inf, or -Inf, the returned output will be (numeric) NA. Also, if all draws within any of the chains of a variable are the same (constant), the returned output will be (numeric) NA as well. The reason for the latter is that, for constant draws, we cannot distinguish between variables that are supposed to be constant (e.g., a diagonal element of a correlation matrix is always 1) or variables that just happened to be constant because of a failure of convergence or other problems in the sampling process.

If the input is an [rvar](#), returns an array of the same dimensions as the [rvar](#), where each element is equal to the value that would be returned by passing the draws array for that element of the [rvar](#) to this function.

**References**

Charles C. Margossian, Matthew D. Hoffman, Pavel Sountsov, Lionel Riou-Durand, Aki Vehtari and Andrew Gelman (2024). Nested R-hat: Assessing the convergence of Markov chain Monte Carlo when running many short chains. *Bayesian Analysis*. doi:10.1214/24-BA1453

**See Also**

Other diagnostics: [ess\\_basic\(\)](#), [ess\\_bulk\(\)](#), [ess\\_quantile\(\)](#), [ess\\_sd\(\)](#), [ess\\_tail\(\)](#), [mcse\\_mean\(\)](#), [mcse\\_quantile\(\)](#), [mcse\\_sd\(\)](#), [pareto\\_diags\(\)](#), [pareto\\_khat\(\)](#), [rhat\(\)](#), [rhat\\_basic\(\)](#), [rstar\(\)](#)

**Examples**

```
mu <- extract_variable_matrix(example_draws(), "mu")
rhat_nested(mu, superchain_ids = c(1, 1, 2, 2))

d <- as_draws_rvars(example_draws("multi_normal"))
rhat_nested(d$Sigma, superchain_ids = c(1, 1, 2, 2))
```

rstar

*Calculate R\* convergence diagnostic***Description**

The `rstar()` function generates a measure of convergence for MCMC draws based on whether it is possible to determine the Markov chain that generated a draw with probability greater than chance. To do so, it fits a machine learning classifier to a training set of MCMC draws and evaluates its predictive accuracy on a testing set: giving the ratio of accuracy to predicting a chain uniformly at random.

**Usage**

```
rstar(
  x,
  split = TRUE,
  uncertainty = FALSE,
  method = "rf",
  hyperparameters = NULL,
  training_proportion = 0.7,
  nsimulations = 1000,
  ...
)
```

**Arguments**

<code>x</code>	(draws) A <a href="#">draws_df</a> object or one coercible to a <code>draws_df</code> object.
<code>split</code>	(logical) Should the estimate be computed on split chains? The default is <code>TRUE</code> .
<code>uncertainty</code>	(logical). Indicates whether to provide a vector of $R^*$ values representing uncertainty in the calculated value (if <code>TRUE</code> ) or a single value (if <code>FALSE</code> ). The default is <code>TRUE</code> .
<code>method</code>	(string) The machine learning classifier to use (must be available in the <b>caret</b> package). The default is <code>"rf"</code> , which calls the random forest classifier.

hyperparameters	(named list) Hyperparameter settings passed to the classifier. The default for the random forest classifier ( <code>method = "rf"</code> ) is <code>list(mtry = floor(sqrt(nvariables(x))))</code> . The default for the gradient-based model ( <code>method = "gbm"</code> ) is <code>list(interaction.depth = 3, n.trees = 50, shrinkage = 0.1, n.minobsinnode = 10)</code> .
training_proportion	(positive real) The proportion (in $(0, 1)$ ) of iterations in used to train the classifier. The default is <code>0.7</code> .
nsimulations	(positive integer) The number of $R^*$ values in the returned vector if uncertainty is <code>TRUE</code> . The default is <code>1000</code> .
...	Other arguments passed to <code>caret::train()</code> .

## Details

The `rstar()` function provides a measure of MCMC convergence based on whether it is possible to determine the chain that generated a particular draw with a probability greater than chance. To do so, it fits a machine learning classifier to a subset of the original MCMC draws (the training set) and evaluates its predictive accuracy on the remaining draws (the testing set). If predictive accuracy exceeds chance (i.e. predicting the chain that generated a draw uniformly at random), the diagnostic measure  $R^*$  will be above 1, indicating that convergence has yet to occur. This statistic is recently developed, and it is currently unclear what is a reasonable threshold for diagnosing convergence.

The statistic,  $R^*$ , is stochastic, meaning that each time the test is run, unless the random seed is fixed, it will generally produce a different result. To minimize the implications of this stochasticity, it is recommended to repeatedly run this function to calculate a distribution of  $R^*$ ; alternatively, an approximation to this distribution can be obtained by setting `uncertainty = TRUE`, although this approximation of uncertainty will generally have a lower mean.

By default, a random forest classifier is used (`method = "rf"`), which tends to perform best for target distributions of around 4 dimensions and above. For lower dimensional targets, gradient boosted models (called via `method = "gbm"`) tend to have a higher classification accuracy. On a given MCMC sample, it is recommended to try both of these classifiers.

## Value

A numeric vector of length 1 (by default) or length `nsimulations` (if `uncertainty = TRUE`).

## References

Ben Lambert, Aki Vehtari (2020)  $R^*$ : A robust MCMC convergence diagnostic with uncertainty using gradient-boosted machines. *arXiv preprint* arXiv:2003.07900.

## See Also

Other diagnostics: [ess\\_basic\(\)](#), [ess\\_bulk\(\)](#), [ess\\_quantile\(\)](#), [ess\\_sd\(\)](#), [ess\\_tail\(\)](#), [mcse\\_mean\(\)](#), [mcse\\_quantile\(\)](#), [mcse\\_sd\(\)](#), [pareto\\_diags\(\)](#), [pareto\\_khat\(\)](#), [rhat\(\)](#), [rhat\\_basic\(\)](#), [rhat\\_nested\(\)](#)

## Examples

```

if (require("caret", quietly = TRUE) && require("randomForest", quietly = TRUE)) {
  x <- example_draws("eight_schools")
  print(rstar(x))
  print(rstar(x, split = FALSE))
  print(rstar(x, method = "gbm"))
  # can pass additional arguments to methods
  print(rstar(x, method = "gbm", verbose = FALSE))

  # with uncertainty, returns a vector of R* values
  hist(rstar(x, uncertainty = TRUE))
  hist(rstar(x, uncertainty = TRUE, nsimulations = 100))

  # can use other classification methods in caret library
  print(rstar(x, method = "knn"))
}

```

---

rvar

*Random variables of arbitrary dimension*


---

## Description

Random variables backed by arrays of arbitrary dimension

## Usage

```

rvar(
  x = double(),
  dim = NULL,
  dimnames = NULL,
  nchains = NULL,
  with_chains = FALSE
)

```

## Arguments

- x (multiple options) The object to convert to an rvar:
- A vector of draws from a distribution.
  - An array where the first dimension represents draws from a distribution. The resulting `rvar` will have dimension `dim(x)[-1]`; that is, everything except the first dimension is used for the shape of the variable, and the first dimension is used to index draws from the distribution (see **Examples**). Optionally, if `with_chains == TRUE`, the first dimension indexes the iteration and the second dimension indexes the chain (see `with_chains`).
  - An rvar.

<code>dim</code>	(integer vector) One or more integers giving the maximal indices in each dimension to override the dimensions of the <code>rvar</code> to be created (see <code>dim()</code> ). If NULL (the default), <code>dim</code> is determined by the input. <b>NOTE:</b> This argument controls the dimensions of the <code>rvar</code> , not the underlying array, so you cannot change the number of draws using this argument.
<code>dimnames</code>	(list) Character vectors giving the names in each dimension to override the names of the dimensions of the <code>rvar</code> to be created (see <code>dimnames()</code> ). If NULL (the default), this is determined by the input. <b>NOTE:</b> This argument controls the names of the dimensions of the <code>rvar</code> , not the underlying array.
<code>nchains</code>	(positive integer) The number of chains. The if NULL (the default), 1 is used unless <code>x</code> is already an <code>rvar</code> , in which case the number of chains it has is used.
<code>with_chains</code>	(logical) Does <code>x</code> include a dimension for chains? If FALSE (the default), chains are not included, the first dimension of the input array should index draws, and the <code>nchains</code> argument can be used to determine the number of chains. If TRUE, the <code>nchains</code> argument is ignored and the second dimension of <code>x</code> is used to index chains. Internally, the array will be converted to a format without the chain index. Ignored when <code>x</code> is already an <code>rvar</code> .

## Details

The "rvar" class internally represents random variables as arrays of arbitrary dimension, where the first dimension is used to index draws from the distribution. Most mathematical operators and functions are supported, including efficient matrix multiplication and vector and array-style indexing. The intent is that an `rvar` works as closely as possible to how a base vector/matrix/array does, with a few differences:

- The default behavior when subsetting is not to drop extra dimensions (i.e. the default drop argument for `[]` is FALSE, not TRUE).
- Rather than base R-style recycling, `rvars` use a limited form of broadcasting: if an operation is being performed on two vectors with different size of the same dimension, the smaller vector will be recycled up to the size of the larger one along that dimension so long as it has size 1.

For functions that expect base numeric arrays and for which `rvars` cannot be used directly as arguments, you can use `rfunc()` or `rdo()` to translate your code into code that executes across draws from one or more random variables and returns a random variable as output. Typically `rdo()` offers the most straightforward translation.

As `rfunc()` and `rdo()` incur some performance cost, you can also operate directly on the underlying array using the `draws_of()` function. To re-use existing random number generator functions to efficiently create `rvars`, use `rvar_rng()`.

## Value

An object of class "rvar" representing a random variable.

## See Also

`as_rvar()` to convert objects to `rvars`. See `rdo()`, `rfunc()`, and `rvar_rng()` for higher-level interfaces for creating `rvars`.

**Examples**

```

set.seed(1234)

# To create a "scalar" `rvar`, pass a one-dimensional array or a vector
# whose length (here `4000`) is the desired number of draws:
x <- rvar(rnorm(4000, mean = 1, sd = 1))
x

# Create random vectors by adding an additional dimension:
n <- 4 # length of output vector
x <- rvar(array(rnorm(4000 * n, mean = rep(1:n, each = 4000), sd = 1), dim = c(4000, n)))
x

# Create a random matrix:
rows <- 4
cols <- 3
x <- rvar(array(rnorm(4000 * rows * cols, mean = 1, sd = 1), dim = c(4000, rows, cols)))
x

# If the input sample comes from multiple chains, we can indicate that using the
# nchains argument (here, 1000 draws each from 4 chains):
x <- rvar(rnorm(4000, mean = 1, sd = 1), nchains = 4)
x

# Or if the input sample has chain information as its second dimension, we can
# use with_chains to create the rvar
x <- rvar(array(rnorm(4000, mean = 1, sd = 1), dim = c(1000, 4)), with_chains = TRUE)
x

```

---

rvar-dist

*Density, CDF, and quantile functions of random variables*


---

**Description**

The probability density function (`density()`), cumulative distribution function (`cdf()`), and quantile function / inverse CDF (`quantile()`) of an [rvar](#).

**Usage**

```

## S3 method for class 'rvar'
density(x, at, ...)

## S3 method for class 'rvar_factor'
density(x, at, ...)

## S3 method for class 'rvar'
cdf(x, q, ...)

```

```
## S3 method for class 'rvar_factor'
cdf(x, q, ...)

## S3 method for class 'rvar_ordered'
cdf(x, q, ...)

## S3 method for class 'rvar'
quantile(x, probs, ...)

## S3 method for class 'rvar_factor'
quantile(x, probs, ...)

## S3 method for class 'rvar_ordered'
quantile(x, probs, ...)
```

### Arguments

x	(rvar) An <a href="#">rvar</a> object.
...	Additional arguments passed onto underlying methods: <ul style="list-style-type: none"> <li>• For <code>density()</code>, these are passed to <code>stats::density()</code>.</li> <li>• For <code>cdf()</code>, these are ignored.</li> <li>• For <code>quantile()</code>, these are passed to <code>stats::quantile()</code>.</li> </ul>
q, at	(numeric vector) One or more quantiles.
probs	(numeric vector) One or more probabilities in $[\emptyset, 1]$ .

### Value

If x is a scalar [rvar](#), returns a vector of the same length as the input (q, at, or probs) containing values from the corresponding function of the given [rvar](#).

If x has length greater than 1, returns an array with dimensions `c(length(y), dim(x))` where y is q, at, or probs, where each `result[i, ...]` is the value of the corresponding function, `f(y[i])`, for the corresponding cell in the input array, `x[...]`.

### Examples

```
set.seed(1234)
x = rvar(rnorm(100))

density(x, seq(-2, 2, length.out = 10))
cdf(x, seq(-2, 2, length.out = 10))
quantile(x, ppoints(10))

x2 = c(rvar(rnorm(100, mean = -0.5)), rvar(rnorm(100, mean = 0.5)))
density(x2, seq(-2, 2, length.out = 10))
cdf(x2, seq(-2, 2, length.out = 10))
quantile(x2, ppoints(10))
```



---

`rvar-matmult`*Matrix multiplication of random variables*

---

## Description

Matrix multiplication of random variables.

## Usage

```
x %**% y
```

```
## S3 method for class 'rvar'  
matrixOps(x, y)
```

## Arguments

`x` (multiple options) The object to be postmultiplied by `y`:

- An `rvar`
- A `numeric` vector or matrix
- A `logical` vector or matrix

If a vector is used, it is treated as a *row* vector.

`y` (multiple options) The object to be premultiplied by `x`:

- An `rvar`
- A `numeric` vector or matrix
- A `logical` vector or matrix

If a vector is used, it is treated as a *column* vector.

## Details

If `x` or `y` are vectors, they are converted into matrices prior to multiplication, with `x` converted to a row vector and `y` to a column vector. Numerics and logicals can be multiplied by `rvars` and are broadcasted across all draws of the `rvar` argument. Tensor multiplication is used to efficiently multiply matrices across draws, so if either `x` or `y` is an `rvar`, `x %**% y` will be much faster than `rdo(x %**% y)`.

In R  $\geq$  4.3, you can also use `%**%` in place of `%**%` for matrix multiplication of `rvars`. In R  $<$  4.3, S3 classes cannot properly override `%**%`, so you must use `%**%` for matrix multiplication of `rvars`.

## Value

An `rvar` representing the matrix product of `x` and `y`.

## Examples

```
# d has mu (mean vector of length 3) and Sigma (3x3 covariance matrix)
d <- as_draws_rvars(example_draws("multi_normal"))
d$Sigma

# trivial example: multiplication by a non-random matrix
d$Sigma %**% diag(1:3)

# Decompose Sigma into R s.t. R'R = Sigma ...
R <- chol(d$Sigma)
# ... and recreate Sigma using matrix multiplication
t(R) %**% R
```

---

rvar-slice

*Random variable slicing*


---

## Description

Operations for slicing [rvars](#) and replacing parts of [rvars](#).

## Usage

```
## S3 method for class 'rvar'
x[[i, ...]]

## S3 replacement method for class 'rvar'
x[[i, ...]] <- value

## S3 method for class 'rvar'
x[..., drop = FALSE]

## S3 replacement method for class 'rvar'
x[i, ...] <- value
```

## Arguments

x	an <a href="#">rvar</a> .
i, ...	indices; see <i>Details</i> .
value	( <a href="#">rvar</a> or coercable to <a href="#">rvar</a> ) Value to insert into x at the location determined by the indices.
drop	(logical) Should singular dimensions be dropped when slicing array <a href="#">rvars</a> ? Unlike base array slicing operations, defaults to FALSE.

## Details

The `rvar` slicing operators (`[` and `[[`) attempt to implement the same semantics as the [base array slicing operators](#). There are some exceptions; most notably, `rvar` slicing defaults to `drop = FALSE` instead of `drop = TRUE`.

### Extracting or replacing single elements with `[[`

The `[[` operator extracts (or replaces) single elements. It always returns (or replaces) a scalar (length-1) `rvar`.

The `x[[i, ...]]` operator can be used as follows:

- `x[[<numeric>]]` for scalar numeric `i`: gives the `i`th element of `x`. If `x` is multidimensional (i.e. `length(dim(x)) > 1`), extra dimensions are ignored when indexing. For example, if `x` is a  $6 \times 2$  `rvar` array, the 7th element, `x[[7]]`, will be the first element of the second column, `x[1,2]`.
- `x[[<numeric rvar>]]` for scalar numeric `rvar` `i`: a generalization of indexing when `i` is a scalar numeric. Within each draw of `x`, selects the element corresponding to the value of `i` within that same draw.
- `x[[<character>]]` for scalar character `i`: gives the element of `x` with name equal to `i`. **Unlike with base arrays**, does not work with multidimensional `rvars`.
- `x[[i_1, i_2, ..., i_n]]` for scalar numeric or character `i_1`, `i_2`, etc. Must provide exactly the same number of indices as dimensions in `x`. Selects the element at the corresponding position in the `rvar` by number and/or dimname (as a string).

### Extracting or replacing multiple elements with `[`

The `[` operator extracts (or replaces) multiple elements. It always returns (or replaces) a possibly-multidimensional `rvar`.

The `x[i, ...]` operator can be used as follows:

- `x[<logical>]` for vector logical `i`: `i` is recycled to the same length as `x`, ignoring multiple dimensions in `x`, then an `rvar` vector is returned containing the elements in `x` where `i` is `TRUE`.
- `x[<logical rvar>]` for scalar logical `rvar` `i`: returns an `rvar` the same shape as `x` containing only those draws where `i` is `TRUE`.
- `x[<numeric>]` for vector numeric `i`: an `rvar` vector is returned containing the `i`th elements of `x`, ignoring dimensions.
- `x[<matrix>]` for numeric matrix `i`, where `ncol(i) == length(dim(x))`: each row of `i` should give the multidimensional index for a single element in `x`. The result is an `rvar` vector of length `nrow(i)` containing elements of `x` selected by each row of `i`.
- `x[i_1, i_2, ..., i_n]` for vector numeric, character, or logical `i_1`, `i_2`, etc. Returns a slice of `x` containing all elements from the dimensions specified in `i_1`, `i_2`, etc. If an argument is left empty, all elements from that dimension are included. Unlike base arrays, trailing dimensions can be omitted entirely and will still be selected; for example, if `x` has three dimensions, both `x[1, , ]` and `x[1, ]` can be used to create a slice that includes all elements from the last two dimensions. Unlike base arrays, `[` defaults to `drop = FALSE`, so results retain the same number of dimensions as `x`.

**Examples**

```

x <- rvar(array(1:24, dim = c(4,2,3)))
dimnames(x) <- list(c("a","b"), c("d","e","f"))
x

## Slicing single elements
# x[<numeric>]
x[[2]]

# x[<numeric rvar>]
# notice the draws of x[1:4]...
draws_of(x[1:4])
x[[rvar(c(1,3,4,4))]]
# ... x[[rvar(c(1,3,4,4))]] creates a mixures of those draws
draws_of(x[[rvar(c(1,3,4,4))]])

# x[[i_1,i_2,...]]
x[[2,"e"]]

## Slicing multiple elements
# x[<logical>]
x[c(TRUE,TRUE,FALSE)]

# x[<logical rvar>]
# select every other draw
x[rvar(c(TRUE,FALSE,TRUE,FALSE))]

# x[<numeric>]
x[1:3]

# x[<matrix>]
x[rbind(
  c(1,2),
  c(1,3),
  c(2,2)
)]

# x[i_1,i_2,...,i_n]
x[1,]
x[1,2:3]
x[,2:3]

```

---

rvar-summaries-over-draws

*Summaries of random variables within array elements, over draws*

---

**Description**

Compute summaries within elements of an `rvar` and over draws of each element, producing an array of the same shape as the input random variable (except in the case of `range()`, see **Details**).

**Usage**

```
E(x, ...)  
  
## S3 method for class 'rvar'  
mean(x, ...)  
  
Pr(x, ...)  
  
## Default S3 method:  
Pr(x, ...)  
  
## S3 method for class 'logical'  
Pr(x, ...)  
  
## S3 method for class 'rvar'  
Pr(x, ...)  
  
## S3 method for class 'rvar'  
median(x, ...)  
  
## S3 method for class 'rvar'  
min(x, ...)  
  
## S3 method for class 'rvar'  
max(x, ...)  
  
## S3 method for class 'rvar'  
sum(x, ...)  
  
## S3 method for class 'rvar'  
prod(x, ...)  
  
## S3 method for class 'rvar'  
all(x, ...)  
  
## S3 method for class 'rvar'  
any(x, ...)  
  
## S3 method for class 'rvar'  
Summary(...)  
  
## S3 method for class 'rvar'  
variance(x, ...)  
  
var(x, ...)  
  
## Default S3 method:  
var(x, ...)
```

```

## S3 method for class 'rvar'
var(x, ...)

sd(x, ...)

## Default S3 method:
sd(x, ...)

## S3 method for class 'rvar'
sd(x, ...)

mad(x, ...)

## Default S3 method:
mad(x, ...)

## S3 method for class 'rvar'
mad(x, ...)

## S3 method for class 'rvar_ordered'
mad(x, ...)

## S3 method for class 'rvar'
range(x, ...)

## S3 method for class 'rvar'
is.finite(x)

## S3 method for class 'rvar'
is.infinite(x)

## S3 method for class 'rvar'
is.nan(x)

## S3 method for class 'rvar'
is.na(x)

```

### Arguments

x	(rvar) An <a href="#">rvar</a> .
...	Further arguments passed to underlying functions (e.g., <code>base::mean()</code> or <code>base::median()</code> ), such as <code>na.rm</code> .

### Details

Summaries include expectations (`E()` or `mean()`), probabilities (`Pr()`), medians (`median()`), spread (`var()`, `variance()`, `sd()`, `mad()`), sums and products (`sum()`, `prod()`), extrema and ranges

(`min()`, `max()`, `range()`), logical summaries (`all()`, `any()`), and special value predicates (`is.finite()`, `is.infinite()`, `is.nan()`, `is.na()`).

Unless otherwise stated, these functions return a numeric array with the same shape (same dimensions) as the input `rvar`, `x`.

`range(x)` returns an array with dimensions `c(2, dim(x))`, where the last dimension contains the minimum and maximum values.

`is.infinite(x)`, `is.nan(x)`, and `is.na(x)` return logical arrays, where each element is TRUE if **any** draws in its corresponding element in `x` match the predicate. Each elements in the result of `is.finite(x)` is TRUE if **all** draws in the corresponding element in `x` are finite.

Both `E()`, `mean()`, and `Pr()` return the means of each element in the input. `Pr()` additionally checks that the provided `rvar` is a logical variable (hence, taking its expectation results in a probability).

For consistency, `E()` and `Pr()` are also defined for base arrays so that they can be used as summary functions in `summarise_draws()`.

## Value

A numeric or logical vector with the same dimensions as the given random variable, where each entry in the vector is the mean, median, or variance of the corresponding entry in `x`.

## See Also

[rvar-summaries-within-draws](#) for summary functions within draws. [rvar-dist](#) for density, CDF, and quantile functions of random variables.

Other `rvar-summaries`: [rvar-summaries-within-draws](#), [rvar\\_is\\_finite\(\)](#)

## Examples

```
set.seed(5678)
x = rvar_rng(rnorm, 4, mean = 1:4, sd = 2)

# These should all be ~= c(1, 2, 3, 4)
E(x)
mean(x)
median(x)

# This ...
Pr(x < 1.5)
# ... should be about the same as this:
pnorm(1.5, mean = 1:4, sd = 2)
```

---

 rvar-summaries-within-draws

*Summaries of random variables over array elements, within draws*


---

### Description

Compute summaries of random variables over array elements and within draws, producing a new random variable of length 1 (except in the case of `rvar_range()`, see **Details**).

### Usage

```
rvar_mean(..., na.rm = FALSE)
rvar_median(..., na.rm = FALSE)
rvar_sum(..., na.rm = FALSE)
rvar_prod(..., na.rm = FALSE)
rvar_min(..., na.rm = FALSE)
rvar_max(..., na.rm = FALSE)
rvar_sd(..., na.rm = FALSE)
rvar_var(..., na.rm = FALSE)
rvar_mad(..., constant = 1.4826, na.rm = FALSE)
rvar_range(..., na.rm = FALSE)
rvar_quantile(..., probs, names = FALSE, na.rm = FALSE)
rvar_all(..., na.rm = FALSE)
rvar_any(..., na.rm = FALSE)
```

### Arguments

<code>...</code>	(rvar) One or more <code>rvars</code> .
<code>na.rm</code>	(logical) Should NAs be removed from the input before summaries are computed? The default is FALSE.
<code>constant</code>	(scalar real) For <code>rvar_mad()</code> , a scale factor for computing the median absolute deviation. See the details of <code>stats::mad()</code> for the justification for the default value.
<code>probs</code>	(numeric vector) For <code>rvar_quantile()</code> , probabilities in $[\emptyset, 1]$ .
<code>names</code>	(logical) For <code>rvar_quantile()</code> , if TRUE, the result has a <code>names</code> attribute.



**Details**

These functions compute statistics within each draw of the random variable. For summaries over draws (such as expectations), see [rvar-summaries-over-draws](#).

Each function defined here corresponds to the base function of the same name without the `rvar_` prefix (e.g., `rvar_mean()` calls `mean()` under the hood, etc).

**Value**

An `rvar` of length 1 (for `range()`, length 2; for `quantile()`, length equal to `length(probs)`) with the same number of draws as the input `rvar(s)` containing the summary statistic computed within each draw of the input `rvar(s)`.

**See Also**

[rvar-summaries-over-draws](#) for summary functions across draws (e.g. expectations). [rvar-dist](#) for density, CDF, and quantile functions of random variables.

Other `rvar-summaries`: [rvar-summaries-over-draws](#), [rvar\\_is\\_finite\(\)](#)

**Examples**

```
set.seed(5678)
x = rvar_rng(rnorm, 4, mean = 1:4, sd = 2)

# These will give similar results to mean(1:4),
# median(1:4), sum(1:4), prod(1:4), etc
rvar_mean(x)
rvar_median(x)
rvar_sum(x)
rvar_prod(x)
rvar_range(x)
rvar_quantile(x, probs = c(0.25, 0.5, 0.75), names = TRUE)
```

---

rvar\_apply

*Random variable resulting from a function applied over margins of an array or random variable*


---

**Description**

Returns an `rvar` obtained by applying a function to margins of an array or `rvar`. Acts like `apply()`, except that the function supplied (`.f`) should return an `rvar`, and the final result is always an `rvar`.

**Usage**

```
rvar_apply(.x, .margin, .f, ...)
```

**Arguments**

<code>.x</code>	An array or an <a href="#">rvar</a> .
<code>.margin</code>	(multiple options) The subscripts which the function will be applied over: <ul style="list-style-type: none"> <li>• An integer vector. E.g., for a matrix 1 indicates rows, 2 indicates columns, <code>c(1, 2)</code> indicates rows and columns.</li> <li>• A character vector of dimension names if <code>.x</code> has named dimensions.</li> </ul>
<code>.f</code>	(function) The function to be applied. The function <code>.f</code> must return an <a href="#">rvar</a> and the dimensions of the result of <code>.f</code> applied to each margin of <code>.x</code> must be able to be broadcasted to a common shape (otherwise the resulting <a href="#">rvar</a> cannot be simplified). See <b>Details</b> .
<code>...</code>	Optional arguments passed to <code>.f</code> .

**Details**

This function acts much like `apply()`, except that the function passed to it (`.f`) must return [rvars](#), and the result is simplified into an [rvar](#). Unlike `apply()`, it also keeps the dimensions of the returned values along each margin, rather than simplifying each margin to a vector, and if the results of `.f` do not all have the same dimensions, it applies the [rvar](#) broadcasting rules to bind results together rather than using vector recycling.

If you wish to apply functions over [rvars](#) where the result is not intended to be simplified into an [rvar](#), you can use the standard `apply()`, `lapply()`, `sapply()`, or `vapply()` functions.

**Value**

An [rvar](#).

If the result of each call to `.f` returns an [rvar](#) of dimension `d` after being broadcast to a common shape, then `rvar_apply()` returns an [rvar](#) of dimension `c(d, dim(.x)[.margin])`. If the last dimension of the result would be 1, it is dropped (other dimensions equal to 1 are retained). If `d` is  $\emptyset$ , the result has length  $\emptyset$  but not necessarily the 'correct' dimension.

**See Also**

[as\\_rvar\(\)](#) to convert objects to [rvars](#). See [rdo\(\)](#), [rfun\(\)](#), and [rvar\\_rng\(\)](#) for higher-level interfaces for creating [rvars](#).

**Examples**

```
set.seed(3456)
x <- rvar_rng(rnorm, 24, mean = 1:24)
dim(x) <- c(2,3,4)

# we can find the distributions of marginal means of the above array
# using rvar_mean along with rvar_apply
rvar_apply(x, 1, rvar_mean)
rvar_apply(x, 2:3, rvar_mean)
```

---

rvar_factor	<i>Factor random variables of arbitrary dimension</i>
-------------	---

---

### Description

Random variables backed by [factor](#)-like arrays of arbitrary dimension.

### Usage

```
rvar_factor(
  x = factor(),
  dim = NULL,
  dimnames = NULL,
  nchains = NULL,
  with_chains = FALSE,
  ...
)

rvar_ordered(
  x = ordered(NULL),
  dim = NULL,
  dimnames = NULL,
  nchains = NULL,
  with_chains = FALSE,
  ...
)
```

### Arguments

x	<p>(multiple options) The object to convert to an rvar:</p> <ul style="list-style-type: none"> <li>• A vector of draws from a distribution.</li> <li>• An array where the first dimension represents draws from a distribution. The resulting <a href="#">rvar</a> will have dimension <code>dim(x)[-1]</code>; that is, everything except the first dimension is used for the shape of the variable, and the first dimension is used to index draws from the distribution (see <b>Examples</b>). Optionally, if <code>with_chains == TRUE</code>, the first dimension indexes the iteration and the second dimension indexes the chain (see <code>with_chains</code>).</li> <li>• An rvar.</li> </ul>
dim	<p>(integer vector) One or more integers giving the maximal indices in each dimension to override the dimensions of the <a href="#">rvar</a> to be created (see <code>dim()</code>). If NULL (the default), <code>dim</code> is determined by the input. <b>NOTE:</b> This argument controls the dimensions of the <a href="#">rvar</a>, not the underlying array, so you cannot change the number of draws using this argument.</p>
dimnames	<p>(list) Character vectors giving the names in each dimension to override the names of the dimensions of the <a href="#">rvar</a> to be created (see <code>dimnames()</code>). If NULL (the default), this is determined by the input. <b>NOTE:</b> This argument controls the names of the dimensions of the <a href="#">rvar</a>, not the underlying array.</p>

nchains	(positive integer) The number of chains. The if NULL (the default), 1 is used unless <code>x</code> is already an <code>rvar</code> , in which case the number of chains it has is used.
with_chains	(logical) Does <code>x</code> include a dimension for chains? If FALSE (the default), chains are not included, the first dimension of the input array should index draws, and the <code>nchains</code> argument can be used to determine the number of chains. If TRUE, the <code>nchains</code> argument is ignored and the second dimension of <code>x</code> is used to index chains. Internally, the array will be converted to a format without the chain index. Ignored when <code>x</code> is already an <code>rvar</code> .
...	Arguments passed on to <code>base::factor</code>
levels	an optional vector of the unique values (as character strings) that <code>x</code> might have taken. The default is the unique set of values taken by <code>as.character(x)</code> , sorted into increasing order of <code>x</code> . Note that this set can be specified as smaller than <code>sort(unique(x))</code> .
labels	<i>either</i> an optional character vector of labels for the levels (in the same order as <code>levels</code> after removing those in <code>exclude</code> ), <i>or</i> a character string of length 1. Duplicated values in <code>labels</code> can be used to map different values of <code>x</code> to the same factor level.
exclude	a vector of values to be excluded when forming the set of levels. This may be factor with the same level set as <code>x</code> or should be a character.
ordered	logical flag to determine if the levels should be regarded as ordered (in the order given).
nmax	an upper bound on the number of levels; see ‘Details’.

## Details

A subtype of `rvar()` that represents a (possibly multidimensional) sample of a `factor` or an `ordered` factor. It is otherwise very similar to the basic `rvar()`: it is backed by a multidimensional array with draws as the first dimension. The primary difference is that the backing array has class `"factor"` (for `rvar_factor()`) or `c("ordered", "factor")` (for `rvar_ordered()`). If you pass a `factor` or `ordered` factor to `rvar()` it will automatically return an object with the classes `"rvar_factor"` or `c("rvar_ordered", "rvar_factor")`.

See `rvar()` for more details on the internals of the random variable datatype.

## Value

An object of class `"rvar_factor"` representing a factor-like random variable.

## See Also

`as_rvar_factor()` to convert objects to `rvar_factors`. See `rdo()`, `rfunc()`, and `rvar_rng()` for higher-level interfaces for creating `rvars`.

## Examples

```
set.seed(1234)

# To create a "scalar" `rvar_factor`, pass a one-dimensional array or a vector
# whose length (here `4000`) is the desired number of draws:
```

```

x <- rvar(sample(c("a","a","a","b","c"), 4000, replace = TRUE))
x

# Create random vectors by adding an additional dimension:
x_array <- array(c(
  sample(c("a","a","a","b","c"), 4000, replace = TRUE),
  sample(c("a","a","b","c","c"), 4000, replace = TRUE),
  sample(c("b","b","b","b","c"), 4000, replace = TRUE),
  sample(c("d","d","b","b","c"), 4000, replace = TRUE)
), dim = c(4000, 4))
rvar_factor(x_array)

# You can also create ordered factors
rvar_ordered(x_array)

# arguments of factor() and ordered() are passed down by the constructor
# e.g. we can reorder levels of an ordered factor:
rvar_ordered(x_array, levels = c("d","c","b","a"))

# Unlike base factors, rvar factors can be matrices or arrays:
rvar_factor(x_array, dim = c(2, 2))

# If the input to rvar_factor() is an array with a "levels" attribute, it
# will use those as the levels of the factor
y_array <- t(array(rbinom(3000, 1, c(0.1, 0.5, 0.9)) + 1, dim = c(3, 1000)))
rvar(y_array)
# with levels
attr(y_array, "levels") = c("a", "b")
rvar_factor(y_array)

```

---

rvar\_ifelse

*Random variable ifelse*


---

## Description

A version of `ifelse()` that returns an `rvar`.

## Usage

```
rvar_ifelse(test, yes, no)
```

## Arguments

<code>test</code>	(logical <code>rvar</code> , or castable to one) logical test determining whether the value in <code>yes</code> or <code>no</code> is assigned in the corresponding position of the result.
<code>yes</code>	( <code>rvar</code> , or castable to one) corresponding values assigned for entries in <code>test</code> that are TRUE.
<code>no</code>	( <code>rvar</code> , or castable to one) corresponding values assigned for entries in <code>test</code> that are FALSE.

**Value**

An `rvar` with the common type of `yes` and `no` (as determined by `vctrs::vec_cast_common()`) and a shape determined by broadcasting `test`, `yes`, and `no` to a common shape (see the section on broadcasting rules in `vignette("rvar")`). For every element of `draws_of(test)`, the corresponding element of `draws_of(yes)` or `draws_of(no)` is placed into the result, depending on whether the element of `test` is `TRUE` or `FALSE`.

**Examples**

```
x <- rvar(1:4)
y <- rvar(5:8)

i <- rvar(c(TRUE, FALSE, TRUE, FALSE))
z <- rvar_ifelse(i, x, y)
z
draws_of(z)
```

---

<code>rvar_is_finite</code>	<i>Special value predicates for random variables</i>
-----------------------------	--

---

**Description**

Compute special value predicates (checking for finite / infinite values, `NaN`, and `NA`) on all draws within a random variable, returning a random variable.

**Usage**

```
rvar_is_finite(x)

rvar_is_infinite(x)

rvar_is_nan(x)

rvar_is_na(x)
```

**Arguments**

`x` (rvar) An `rvar`.

**Details**

These functions return a new `rvar` that is the result of applying `is.finite()`, `is.infinite()`, `is.nan()`, or `is.na()` to every draw in the input random variable.

**Value**

A logical `rvar` of the same length as the input.

**See Also**

[rvar-summaries-over-draws](#) for summary functions across draws, including implementations of `is.finite()`, `is.infinite()`, `is.nan()`, and `is.na()` for `rvars`.

Other `rvar`-summaries: [rvar-summaries-over-draws](#), [rvar-summaries-within-draws](#)

**Examples**

```
x <- rvar(c(1, Inf, -Inf, NaN, NA))
x
```

```
rvar_is_finite(x)
rvar_is_infinite(x)
rvar_is_nan(x)
rvar_is_na(x)
```

---

rvar\_rng

---

*Create random variables from existing random number generators*


---

**Description**

Specialized alternative to `rdo()` or `rfun()` for creating `rvars` from existing random-number generator functions (such as `rnorm()`, `rbinom()`, etc).

**Usage**

```
rvar_rng(.f, n, ..., ndraws = NULL)
```

**Arguments**

<code>.f</code>	(function) A function (or string naming a function) representing a random-number generating function that follows the pattern of base random number generators (like <code>rnorm()</code> , <code>rbinom()</code> , etc). It must: <ul style="list-style-type: none"> <li>• Have a first argument, <code>n</code>, giving the number of draws to take from the distribution</li> <li>• Have vectorized parameter arguments</li> <li>• Return a single vector of length <code>n</code></li> </ul>
<code>n</code>	(positive integer) The length of the output <code>rvar</code> vector ( <b>not</b> the number of draws).
<code>...</code>	Arguments passed to <code>.f</code> . These arguments may include <code>rvars</code> , so long as they are vectors only (no multidimensional <code>rvars</code> are allowed).
<code>ndraws</code>	(positive integer) The number of draws used to construct the returned random variable if no <code>rvars</code> are supplied in <code>...</code> . If <code>NULL</code> , <code>getOption("posterior.rvar.ndraws")</code> is used (default 4000). If <code>...</code> contains <code>rvars</code> , the number of draws in the provided <code>rvars</code> is used instead of the value of this argument.

**Details**

This function unwraps the arrays underlying the input `rvars` in `...` and then passes them to `.f`, relying on the vectorization of `.f` to evaluate it across draws from the input `rvars`. This is why the arguments of `.f` **must** be vectorized. It asks for `n` times the number of draws in the input `rvars` (or `ndraws` if none are given) draws from the random number generator `.f`, then reshapes the output from `.f` into an `rvar` with length `n`.

`rvar_rng()` is a fast alternative to `rdo()` or `rfunc()`, but you **must** ensure that `.f` satisfies the preconditions described above for the result to be correct. Most base random number generators satisfy these conditions. It is advisable to test against `rdo()` or `rfunc()` (which should be correct, but slower) if you are uncertain.

**Value**

A single-dimensional `rvar` of length `n`.

**See Also**

Other `rfunc`: `rdo()`, `rfunc()`

**Examples**

```
mu <- rvar_rng(rnorm, 10, mean = 1:10, sd = 1)
sigma <- rvar_rng(rgamma, 1, shape = 1, rate = 1)
x <- rvar_rng(rnorm, 10, mu, sigma)
x
```

---

split\_chains

*Split Chains*

---

**Description**

Split chains by halving the number of iterations per chain and doubling the number of chains.

**Usage**

```
split_chains(x, ...)
```

**Arguments**

`x` (draws) A draws object or another R object for which the method is defined.  
`...` Arguments passed to individual methods (if applicable).

**Value**

A draws object of the same class as `x`.



## Examples

```
x <- example_draws()
niterations(x)
nchains(x)
```

```
x <- split_chains(x)
niterations(x)
nchains(x)
```

---

subset\_draws

*Subset draws objects*

---

## Description

Subset [draws](#) objects by variables, iterations, chains, and draws indices.

## Usage

```
subset_draws(x, ...)
```

```
## S3 method for class 'draws_matrix'
```

```
subset_draws(
  x,
  variable = NULL,
  iteration = NULL,
  chain = NULL,
  draw = NULL,
  regex = FALSE,
  unique = TRUE,
  exclude = FALSE,
  scalar = FALSE,
  ...
)
```

```
## S3 method for class 'draws_array'
```

```
subset_draws(
  x,
  variable = NULL,
  iteration = NULL,
  chain = NULL,
  draw = NULL,
  regex = FALSE,
  unique = TRUE,
  exclude = FALSE,
  scalar = FALSE,
  ...
)
```

```
)

## S3 method for class 'draws_df'
subset_draws(
  x,
  variable = NULL,
  iteration = NULL,
  chain = NULL,
  draw = NULL,
  regex = FALSE,
  unique = TRUE,
  exclude = FALSE,
  scalar = FALSE,
  ...
)

## S3 method for class 'draws_list'
subset_draws(
  x,
  variable = NULL,
  iteration = NULL,
  chain = NULL,
  draw = NULL,
  regex = FALSE,
  unique = TRUE,
  exclude = FALSE,
  scalar = FALSE,
  ...
)

## S3 method for class 'draws_rvars'
subset_draws(
  x,
  variable = NULL,
  iteration = NULL,
  chain = NULL,
  draw = NULL,
  regex = FALSE,
  unique = TRUE,
  exclude = FALSE,
  scalar = FALSE,
  ...
)

## S3 method for class 'rvar'
subset_draws(x, variable = NULL, ...)

## S3 method for class 'draws'
```

```
subset(x, ...)
```

### Arguments

x	(draws) A draws object or another R object for which the method is defined.
...	Arguments passed to individual methods (if applicable).
variable	(character vector) The variables to select. All elements of non-scalar variables can be selected at once.
iteration	(integer vector) The iteration indices to select.
chain	(integer vector) The chain indices to select.
draw	(integer vector) The draw indices to be select. Subsetting draw indices will lead to an automatic merging of chains via <a href="#">merge_chains</a> .
regex	(logical) Should variable should be treated as a (vector of) regular expressions? Any variable in x matching at least one of the regular expressions will be selected. Defaults to FALSE.
unique	(logical) Should duplicated selection of chains, iterations, or draws be allowed? If TRUE (the default) only unique chains, iterations, and draws are selected regardless of how often they appear in the respective selecting arguments.
exclude	(logical) Should the selected subset be excluded? If FALSE (the default) only the selected subset will be returned. If TRUE everything but the selected subset will be returned.
scalar	(logical) Should only scalar variables be selected? If FALSE (the default), all variables with matching names and <i>arbitrary</i> indices will be selected (see examples).

### Details

To ensure that multiple consecutive subsetting operations work correctly, `subset()` *repairs* the draws object before and after subsetting.

### Value

A draws object of the same class as x.

### Examples

```
x <- example_draws()
subset_draws(x, variable = c("mu", "tau"))
subset_draws(x, chain = 2)
subset_draws(x, iteration = 5:10, chain = 3:4)

# extract the first chain twice
subset_draws(x, chain = c(1, 1), unique = FALSE)

# extract all elements of 'theta'
subset_draws(x, variable = "theta")

# trying to extract only a scalar 'theta' will fail
```

```
# subset_draws(x, variable = "theta", scalar = TRUE)
```

---

thin\_draws

*Thin draws objects*


---

### Description

Thin `draws` objects to reduce their size and autocorrelation in the chains.

### Usage

```
thin_draws(x, thin = NULL, ...)

## S3 method for class 'draws'
thin_draws(x, thin = NULL, ...)

## S3 method for class 'rvar'
thin_draws(x, thin = NULL, ...)
```

### Arguments

<code>x</code>	(draws) A draws object or another R object for which the method is defined.
<code>thin</code>	(positive numeric) The period for selecting draws. Must be between 1 and the number of iterations. If the value is not an integer, the draws will be selected such that the number of draws returned is equal to $\text{round}(\text{ndraws}(x) / \text{thin})$ . Intervals between selected draws will be either $\text{ceiling}(\text{thin})$ or $\text{floor}(\text{thin})$ , such that the average interval will be close to the thin value. If NULL, it will be automatically calculated based on bulk and tail effective sample size as suggested by Säilynoja et al. (2022).
<code>...</code>	Arguments passed to individual methods (if applicable).

### Value

A draws object of the same class as `x`.

### References

Teemu Säilynoja, Paul-Christian Bürkner, and Aki Vehtari (2022). Graphical test for discrete uniformity and its applications in goodness-of-fit evaluation and multiple sample comparison. *Statistics and Computing*. 32, 32. doi:10.1007/s11222-022-10090-6

**Examples**

```
x <- example_draws()
niterations(x)

x <- thin_draws(x, thin = 5)
niterations(x)
```

---

variables

*Get variable names from draws objects*


---

**Description**

Get variable names from [draws](#) objects.

**Usage**

```
variables(x, ...)

## S3 method for class 'draws_matrix'
variables(x, reserved = FALSE, with_indices = TRUE, ...)

## S3 method for class 'draws_array'
variables(x, reserved = FALSE, with_indices = TRUE, ...)

## S3 method for class 'draws_df'
variables(x, reserved = FALSE, with_indices = TRUE, ...)

## S3 method for class 'draws_list'
variables(x, reserved = FALSE, with_indices = TRUE, ...)

## S3 method for class 'draws_rvars'
variables(x, reserved = FALSE, with_indices = FALSE, ...)

nvariables(x, ...)
```

**Arguments**

x	(draws) A draws object or another R object for which the method is defined.
...	Arguments passed to individual methods (if applicable).
reserved	(logical) Should reserved variables be included in the output? Defaults to FALSE. See <a href="#">reserved_variables</a> for an overview of currently reserved variable names.
with_indices	(logical) Should indices be included in variable names? For example, if the object includes variables named "x[1]" and "x[2]", if TRUE, c("x[1]", "x[2]") is returned; if FALSE, only "x" is returned. Defaults to TRUE for all formats except <a href="#">draws_rvars()</a> .

**Details**

variables() returns a vector of all variable names, and nvariables() returns the number of variables.

**Value**

For variables(), a character vector.

For nvariables(), a scalar integer.

**See Also**

[variables<-](#), [rename\\_variables](#), [draws-index](#)

**Examples**

```
x <- example_draws()

variables(x)
nvariables(x)
variables(x) <- letters[1:nvariables(x)]
```

---

variables<-

*Set variable names in draws objects*

---

**Description**

Set variable names for all variables in a [draws](#) object. The set\_variables() form is useful when using pipe operators.

**Usage**

```
variables(x, ...) <- value

## S3 replacement method for class 'draws_matrix'
variables(x, with_indices = TRUE, ...) <- value

## S3 replacement method for class 'draws_array'
variables(x, with_indices = TRUE, ...) <- value

## S3 replacement method for class 'draws_df'
variables(x, with_indices = TRUE, ...) <- value

## S3 replacement method for class 'draws_list'
variables(x, with_indices = TRUE, ...) <- value

## S3 replacement method for class 'draws_rvars'
variables(x, with_indices = FALSE, ...) <- value

set_variables(x, variables, ...)
```

**Arguments**

`x` (draws) A draws object or another R object for which the method is defined.

`...` Arguments passed to individual methods (if applicable).

`value, variables` (character vector) new variable names.

`with_indices` (logical) Should indices be included in variable names? For example, if the object includes variables named "x[1]" and "x[2]", if TRUE, c("x[1]", "x[2]") is returned; if FALSE, only "x" is returned. Defaults to TRUE for all formats except `draws_rvars()`.

**Details**

`variables(x) <- value` allows you to modify the vector of variable names, similar to how `names(x) <- value` works for vectors and lists. For renaming specific variables, `set_variables(x, value)` works equivalently, but is more intuitive when using the pipe operator.

For renaming specific variables, `rename_variables()` may offer a more convenient approach.

**Value**

Returns a `draws` object of the same format as `x`, with variables named as specified.

**See Also**

[variables](#), [rename\\_variables](#), [draws-index](#)

**Examples**

```
x <- example_draws()

variables(x)
nvariables(x)
variables(x) <- letters[1:nvariables(x)]

# or equivalently...
x <- set_variables(x, letters[1:nvariables(x)])
```

---

weights.draws

*Extract Weights from Draws Objects*


---

**Description**

Extract weights from `draws` objects, with one weight per draw. See `weight_draws` for details how to add weights to `draws` objects.

**Usage**

```
## S3 method for class 'draws'
weights(object, log = FALSE, normalize = TRUE, ...)
```

**Arguments**

object	(draws) A <a href="#">draws</a> object.
log	(logical) Should the weights be returned on the log scale? Defaults to FALSE.
normalize	(logical) Should the weights be normalized to sum to 1 on the standard scale? Defaults to TRUE.
...	Arguments passed to individual methods (if applicable).

**Value**

A vector of weights, with one weight per draw.

**See Also**

[weight\\_draws](#), [resample\\_draws](#)

**Examples**

```
x <- example_draws()

# sample some random weights for illustration
wts <- rexp(ndraws(x))
head(wts)

# add weights
x <- weight_draws(x, weights = wts)

# extract weights
head(weights(x)) # defaults to normalized weights
head(weights(x, normalize=FALSE)) # recover original weights
head(weights(x, log=TRUE)) # get normalized log-weights

# add weights which are already on the log scale
log_wts <- log(wts)
head(log_wts)

x <- weight_draws(x, weights = log_wts, log = TRUE)
# extract weights
head(weights(x))
head(weights(x, log=TRUE, normalize = FALSE)) # recover original log_wts

# add weights on log scale and Pareto smooth them
x <- weight_draws(x, weights = log_wts, log = TRUE, pareto_smooth = TRUE)
```



---

weight_draws	<i>Weight draws objects</i>
--------------	-----------------------------

---

### Description

Add weights to [draws](#) objects, with one weight per draw, for use in subsequent weighting operations. For reasons of numerical accuracy, weights are stored in the form of unnormalized log-weights (in a variable called `.log_weight`). See [weights.draws\(\)](#) for details how to extract weights from draws objects.

### Usage

```
weight_draws(x, weights, ...)

## S3 method for class 'draws_matrix'
weight_draws(x, weights, log = FALSE, pareto_smooth = FALSE, ...)

## S3 method for class 'draws_array'
weight_draws(x, weights, log = FALSE, pareto_smooth = FALSE, ...)

## S3 method for class 'draws_df'
weight_draws(x, weights, log = FALSE, pareto_smooth = FALSE, ...)

## S3 method for class 'draws_list'
weight_draws(x, weights, log = FALSE, pareto_smooth = FALSE, ...)

## S3 method for class 'draws_rvars'
weight_draws(x, weights, log = FALSE, pareto_smooth = FALSE, ...)
```

### Arguments

x	(draws) A draws object or another R object for which the method is defined.
weights	(numeric vector) A vector of weights of length <code>ndraws(x)</code> . Weights will be internally stored on the log scale (in a variable called <code>.log_weight</code> ) and will not be normalized, but normalized (non-log) weights can be returned via the <a href="#">weights.draws()</a> method later.
...	Arguments passed to individual methods (if applicable).
log	(logical) Are the weights passed already on the log scale? The default is <code>FALSE</code> , that is, expecting weights to be on the standard (non-log) scale.
pareto_smooth	(logical) Should the weights be Pareto-smoothed? The default is <code>FALSE</code> .

### Value

A draws object of the same class as `x`.

**See Also**

[weights.draws\(\)](#), [resample\\_draws\(\)](#)

**Examples**

```
x <- example_draws()

# sample some random weights for illustration
wts <- rexp(ndraws(x))
head(wts)

# add weights
x <- weight_draws(x, weights = wts)

# extract weights
head(weights(x)) # defaults to normalized weights
head(weights(x, normalize=FALSE)) # recover original weights
head(weights(x, log=TRUE)) # get normalized log-weights

# add weights which are already on the log scale
log_wts <- log(wts)
head(log_wts)

x <- weight_draws(x, weights = log_wts, log = TRUE)
# extract weights
head(weights(x))
head(weights(x, log=TRUE, normalize = FALSE)) # recover original log_wts

# add weights on log scale and Pareto smooth them
x <- weight_draws(x, weights = log_wts, log = TRUE, pareto_smooth = TRUE)
```

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