

# Package ‘loo’

October 13, 2022

**Type** Package

**Title** Efficient Leave-One-Out Cross-Validation and WAIC for Bayesian Models

**Version** 2.5.1

**Date** 2022-03-23

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**URL** <https://mc-stan.org/loo/>, <https://discourse.mc-stan.org>

**BugReports** <https://github.com/stan-dev/loo/issues>

**Description** Efficient approximate leave-one-out cross-validation (LOO) for Bayesian models fit using Markov chain Monte Carlo, as described in Vehtari, Gelman, and Gabry (2017) <[doi:10.1007/s11222-016-9696-4](https://doi.org/10.1007/s11222-016-9696-4)>.

The approximation uses Pareto smoothed importance sampling (PSIS), a new procedure for regularizing importance weights.

As a byproduct of the calculations, we also obtain approximate standard errors for estimated predictive errors and for the comparison of predictive errors between models. The package also provides methods for using stacking and other model weighting techniques to average Bayesian predictive distributions.

**License** GPL (>= 3)

**LazyData** TRUE

**Depends** R (>= 3.1.2)

**Imports** checkmate, matrixStats (>= 0.52), parallel, stats

**Suggests** bayesplot (>= 1.7.0), brms (>= 2.10.0), ggplot2, graphics, knitr, rmarkdown, rstan, rstanarm (>= 2.19.0), rstantools, spdep, testthat (>= 2.1.0)

**VignetteBuilder** knitr

**Encoding** UTF-8

**SystemRequirements** pandoc (>= 1.12.3), pandoc-citeproc

**RoxygenNote** 7.1.2

**NeedsCompilation** no

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**Repository** CRAN

**Date/Publication** 2022-03-24 10:30:02 UTC

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## Description

*Stan Development Team*

This package implements the methods described in Vehtari, Gelman, and Gabry (2017), Vehtari, Simpson, Gelman, Yao, and Gabry (2019), and Yao et al. (2018). To get started see the **loo** package [vignettes](#), the `loo()` function for efficient approximate leave-one-out cross-validation (LOO-CV), the `psis()` function for the Pareto smoothed importance sampling (PSIS) algorithm, or `loo_model_weights()` for an implementation of Bayesian stacking of predictive distributions from multiple models.

## Details

Leave-one-out cross-validation (LOO-CV) and the widely applicable information criterion (WAIC) are methods for estimating pointwise out-of-sample prediction accuracy from a fitted Bayesian model using the log-likelihood evaluated at the posterior simulations of the parameter values. LOO-CV and WAIC have various advantages over simpler estimates of predictive error such as AIC and DIC but are less used in practice because they involve additional computational steps. This package implements the fast and stable computations for approximate LOO-CV laid out in Vehtari, Gelman, and Gabry (2017). From existing posterior simulation draws, we compute LOO-CV using Pareto smoothed importance sampling (PSIS; Vehtari, Simpson, Gelman, Yao, and Gabry, 2019), a new procedure for stabilizing and diagnosing importance weights. As a byproduct of our calculations, we also obtain approximate standard errors for estimated predictive errors and for comparing of predictive errors between two models.

We recommend PSIS-LOO-CV instead of WAIC, because PSIS provides useful diagnostics and effective sample size and Monte Carlo standard error estimates.

## References

- Vehtari, A., Gelman, A., and Gabry, J. (2017). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*, 27(5), 1413–1432. doi:10.1007/s11222-016-9696-4 ([journal version](#), [preprint arXiv:1507.04544](#)).
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- Stan Development Team (2018). RStan: the R interface to Stan, Version 2.17.3. <https://mc-stan.org>.
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- Zhang, J., and Stephens, M. A. (2009). A new and efficient estimation method for the generalized Pareto distribution. *Technometrics* **51**, 316-325.

---

ap\_psis

*Pareto smoothed importance sampling (PSIS) using approximate posteriors*


---

## Description

Pareto smoothed importance sampling (PSIS) using approximate posteriors

## Usage

```
ap_psis(log_ratios, log_p, log_g, ...)

## S3 method for class 'array'
ap_psis(log_ratios, log_p, log_g, ..., cores = getOption("mc.cores", 1))

## S3 method for class 'matrix'
ap_psis(log_ratios, log_p, log_g, ..., cores = getOption("mc.cores", 1))

## Default S3 method:
ap_psis(log_ratios, log_p, log_g, ...)
```

**Arguments**

<code>log_ratios</code>	The log-likelihood ratios (ie <code>-log_lik</code> s)
<code>log_p</code>	The log-posterior (target) evaluated at $S$ samples from the proposal distribution ( $g$ ). A vector of length $S$ .
<code>log_g</code>	The log-density (proposal) evaluated at $S$ samples from the proposal distribution ( $g$ ). A vector of length $S$ .
<code>...</code>	Currently not in use.
<code>cores</code>	The number of cores to use for parallelization. This defaults to the option <code>mc.cores</code> which can be set for an entire R session by <code>options(mc.cores = NUMBER)</code> . The old option <code>loo.cores</code> is now deprecated but will be given precedence over <code>mc.cores</code> until <code>loo.cores</code> is removed in a future release. <b>As of version 2.0.0 the default is now 1 core if <code>mc.cores</code> is not set</b> , but we recommend using as many (or close to as many) cores as possible. <ul style="list-style-type: none"> <li>Note for Windows 10 users: it is <b>strongly recommended</b> to avoid using the <code>.Rprofile</code> file to set <code>mc.cores</code> (using the <code>cores</code> argument or setting <code>mc.cores</code> interactively or in a script is fine).</li> </ul>

**Methods (by class)**

- `array`: An  $I$  by  $C$  by  $N$  array, where  $I$  is the number of MCMC iterations per chain,  $C$  is the number of chains, and  $N$  is the number of data points.
- `matrix`: An  $S$  by  $N$  matrix, where  $S$  is the size of the posterior sample (with all chains merged) and  $N$  is the number of data points.
- `default`: A vector of length  $S$  (posterior sample size).

---

<code>compare</code>	<i>Model comparison (deprecated, old version)</i>
----------------------	---

---

**Description**

**This function is deprecated.** Please use the new `loo_compare()` function instead.

**Usage**

```
compare(..., x = list())
```

**Arguments**

<code>...</code>	At least two objects returned by <code>loo()</code> (or <code>waic()</code> ).
<code>x</code>	A list of at least two objects returned by <code>loo()</code> (or <code>waic()</code> ). This argument can be used as an alternative to specifying the objects in <code>...</code>

## Details

When comparing two fitted models, we can estimate the difference in their expected predictive accuracy by the difference in `elpd_loo` or `elpd_waic` (or multiplied by `-2`, if desired, to be on the deviance scale).

*When that difference, `elpd_diff`, is positive then the expected predictive accuracy for the second model is higher. A negative `elpd_diff` favors the first model.*

When using `compare()` with more than two models, the values in the `elpd_diff` and `se_diff` columns of the returned matrix are computed by making pairwise comparisons between each model and the model with the best ELPD (i.e., the model in the first row). Although the `elpd_diff` column is equal to the difference in `elpd_loo`, do not expect the `se_diff` column to be equal to the the difference in `se_elpd_loo`.

To compute the standard error of the difference in ELPD we use a paired estimate to take advantage of the fact that the same set of  $N$  data points was used to fit both models. These calculations should be most useful when  $N$  is large, because then non-normality of the distribution is not such an issue when estimating the uncertainty in these sums. These standard errors, for all their flaws, should give a better sense of uncertainty than what is obtained using the current standard approach of comparing differences of deviances to a Chi-squared distribution, a practice derived for Gaussian linear models or asymptotically, and which only applies to nested models in any case.

## Value

A vector or matrix with class `'compare.loo'` that has its own print method. If exactly two objects are provided in `...` or `x`, then the difference in expected predictive accuracy and the standard error of the difference are returned. If more than two objects are provided then a matrix of summary information is returned (see **Details**).

## References

Vehtari, A., Gelman, A., and Gabry, J. (2017). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*. 27(5), 1413–1432. doi:10.1007/s11222-016-9696-4 ([journal version](#), [preprint arXiv:1507.04544](#)).

Vehtari, A., Simpson, D., Gelman, A., Yao, Y., and Gabry, J. (2019). Pareto smoothed importance sampling. [preprint arXiv:1507.02646](#)

## Examples

```
## Not run:
loo1 <- loo(log_lik1)
loo2 <- loo(log_lik2)
print(compare(loo1, loo2), digits = 3)
print(compare(x = list(loo1, loo2)))

waic1 <- waic(log_lik1)
waic2 <- waic(log_lik2)
compare(waic1, waic2)

## End(Not run)
```

---

`elpd`*Generic (expected) log-predictive density*

---

## Description

The `elpd()` methods for arrays and matrices can compute the expected log pointwise predictive density for a new dataset or the log pointwise predictive density of the observed data (an overestimate of the `elpd`).

## Usage

```
elpd(x, ...)  
  
## S3 method for class 'array'  
elpd(x, ...)  
  
## S3 method for class 'matrix'  
elpd(x, ...)
```

## Arguments

`x` A log-likelihood array or matrix. The **Methods (by class)** section, below, has detailed descriptions of how to specify the inputs for each method.

`...` Currently ignored.

## Details

The `elpd()` function is an S3 generic and methods are provided for 3-D pointwise log-likelihood arrays and matrices.

## Methods (by class)

- `array`: An  $I$  by  $C$  by  $N$  array, where  $I$  is the number of MCMC iterations per chain,  $C$  is the number of chains, and  $N$  is the number of data points.
- `matrix`: An  $S$  by  $N$  matrix, where  $S$  is the size of the posterior sample (with all chains merged) and  $N$  is the number of data points.

## See Also

The vignette *Holdout validation and K-fold cross-validation of Stan programs with the loo package* for demonstrations of using the `elpd()` methods.

## Examples

```
# Calculate the lpd of the observed data  
LLarr <- example_loglik_array()  
elpd(LLarr)
```

---

example\_loglik\_array *Objects to use in examples and tests*

---

### Description

Example pointwise log-likelihood objects to use in demonstrations and tests. See the **Value** and **Examples** sections below.

### Usage

```
example_loglik_array()
```

```
example_loglik_matrix()
```

### Value

example\_loglik\_array() returns a 500 (draws) x 2 (chains) x 32 (observations) pointwise log-likelihood array.

example\_loglik\_matrix() returns the same pointwise log-likelihood values as example\_loglik\_array() but reshaped into a 1000 (draws\*chains) x 32 (observations) matrix.

### Examples

```
LLarr <- example_loglik_array()
(dim_arr <- dim(LLarr))
LLmat <- example_loglik_matrix()
(dim_mat <- dim(LLmat))

all.equal(dim_mat[1], dim_arr[1] * dim_arr[2])
all.equal(dim_mat[2], dim_arr[3])

all.equal(LLarr[, 1, ], LLmat[1:500, ])
all.equal(LLarr[, 2, ], LLmat[501:1000, ])
```

---

extract\_log\_lik *Extract pointwise log-likelihood from a Stan model*

---

### Description

Convenience function for extracting the pointwise log-likelihood matrix or array from a stanfit object from the **rstan** package. Note: recent versions of **rstan** now include a loo() method for stanfit objects that handles this internally.

### Usage

```
extract_log_lik(stanfit, parameter_name = "log_lik", merge_chains = TRUE)
```



**Arguments**

stanfit	A stanfit object ( <b>rstan</b> package).
parameter_name	A character string naming the parameter (or generated quantity) in the Stan model corresponding to the log-likelihood.
merge_chains	If TRUE (the default), all Markov chains are merged together (i.e., stacked) and a matrix is returned. If FALSE they are kept separate and an array is returned.

**Details**

Stan does not automatically compute and store the log-likelihood. It is up to the user to incorporate it into the Stan program if it is to be extracted after fitting the model. In a Stan model, the pointwise log likelihood can be coded as a vector in the transformed parameters block (and then summed up in the model block) or it can be coded entirely in the generated quantities block. We recommend using the generated quantities block so that the computations are carried out only once per iteration rather than once per HMC leapfrog step.

For example, the following is the generated quantities block for computing and saving the log-likelihood for a linear regression model with  $N$  data points, outcome  $y$ , predictor matrix  $X$ , coefficients  $\beta$ , and standard deviation  $\sigma$ :

```
vector[N] log_lik;
for (n in 1:N) log_lik[n] = normal_lpdf(y[n] | X[n, ] * beta, sigma);
```

**Value**

If merge\_chains=TRUE, an  $S$  by  $N$  matrix of (post-warmup) extracted draws, where  $S$  is the size of the posterior sample and  $N$  is the number of data points. If merge\_chains=FALSE, an  $I$  by  $C$  by  $N$  array, where  $I \times C = S$ .

**References**

- Stan Development Team (2017). The Stan C++ Library, Version 2.16.0. <https://mc-stan.org/>
- Stan Development Team (2017). RStan: the R interface to Stan, Version 2.16.1. <https://mc-stan.org/>

---

E\_loo

---

*Compute weighted expectations*


---

**Description**

The E\_loo() function computes weighted expectations (means, variances, quantiles) using the importance weights obtained from the [PSIS](#) smoothing procedure. The expectations estimated by the E\_loo() function assume that the PSIS approximation is working well. **A small Pareto k estimate is necessary, but not sufficient, for E\_loo() to give reliable estimates.** Additional diagnostic checks for gauging the reliability of the estimates are in development and will be added in a future release.

**Usage**

```
E_loo(x, psis_object, ...)

## Default S3 method:
E_loo(
  x,
  psis_object,
  ...,
  type = c("mean", "variance", "quantile"),
  probs = NULL,
  log_ratios = NULL
)

## S3 method for class 'matrix'
E_loo(
  x,
  psis_object,
  ...,
  type = c("mean", "variance", "quantile"),
  probs = NULL,
  log_ratios = NULL
)
```

**Arguments**

<code>x</code>	A numeric vector or matrix.
<code>psis_object</code>	An object returned by <code>psis()</code> .
<code>...</code>	Arguments passed to individual methods.
<code>type</code>	The type of expectation to compute. The options are "mean", "variance", and "quantile".
<code>probs</code>	For computing quantiles, a vector of probabilities.
<code>log_ratios</code>	Optionally, a vector or matrix (the same dimensions as <code>x</code> ) of raw (not smoothed) log ratios. If working with log-likelihood values, the log ratios are the <b>negative</b> of those values. If <code>log_ratios</code> is specified we are able to compute <a href="#">Pareto k</a> diagnostics specific to <code>E_loo()</code> .

**Value**

A named list with the following components:

`value` The result of the computation.

For the matrix method, `value` is a vector with `ncol(x)` elements, with one exception: when `type="quantile"` and multiple values are specified in `probs` the `value` component of the returned object is a `length(probs) by ncol(x)` matrix.

For the default/vector method the `value` component is scalar, with one exception: when `type` is "quantile" and multiple values are specified in `probs` the `value` component is a vector with `length(probs)` elements.

pareto\_k Function-specific diagnostic.

If `log_ratios` is not specified when calling `E_loo()`, `pareto_k` will be `NULL`. Otherwise, for the matrix method it will be a vector of length `ncol(x)` containing estimates of the shape parameter  $k$  of the generalized Pareto distribution. For the default/vector method, the estimate is a scalar.

## Examples

```
if (requireNamespace("rstanarm", quietly = TRUE)) {
  # Use rstanarm package to quickly fit a model and get both a log-likelihood
  # matrix and draws from the posterior predictive distribution
  library("rstanarm")

  # data from help("lm")
  ctl <- c(4.17,5.58,5.18,6.11,4.50,4.61,5.17,4.53,5.33,5.14)
  trt <- c(4.81,4.17,4.41,3.59,5.87,3.83,6.03,4.89,4.32,4.69)
  d <- data.frame(
    weight = c(ctl, trt),
    group = gl(2, 10, 20, labels = c("Ctl","Trt"))
  )
  fit <- stan_glm(weight ~ group, data = d, refresh = 0)
  yrep <- posterior_predict(fit)
  dim(yrep)

  log_ratios <- -1 * log_lik(fit)
  dim(log_ratios)

  r_eff <- relative_eff(exp(-log_ratios), chain_id = rep(1:4, each = 1000))
  psis_object <- psis(log_ratios, r_eff = r_eff, cores = 2)

  E_loo(yrep, psis_object, type = "mean")
  E_loo(yrep, psis_object, type = "var")
  E_loo(yrep, psis_object, type = "quantile", probs = 0.5) # median
  E_loo(yrep, psis_object, type = "quantile", probs = c(0.1, 0.9))

  # To get Pareto k diagnostic with E_loo we also need to provide the negative
  # log-likelihood values using the log_ratios argument.
  E_loo(yrep, psis_object, type = "mean", log_ratios = log_ratios)
}
```

## Description

Given a sample  $x$ , Estimate the parameters  $k$  and  $\sigma$  of the generalized Pareto distribution (GPD), assuming the location parameter is 0. By default the fit uses a prior for  $k$ , which will stabilize esti-

mates for very small sample sizes (and low effective sample sizes in the case of MCMC samples). The weakly informative prior is a Gaussian prior centered at 0.5.

### Usage

```
gpdfit(x, wip = TRUE, min_grid_pts = 30, sort_x = TRUE)
```

### Arguments

<code>x</code>	A numeric vector. The sample from which to estimate the parameters.
<code>wip</code>	Logical indicating whether to adjust $k$ based on a weakly informative Gaussian prior centered on 0.5. Defaults to TRUE.
<code>min_grid_pts</code>	The minimum number of grid points used in the fitting algorithm. The actual number used is <code>min_grid_pts + floor(sqrt(length(x)))</code> .
<code>sort_x</code>	If TRUE (the default), the first step in the fitting algorithm is to sort the elements of <code>x</code> . If <code>x</code> is already sorted in ascending order then <code>sort_x</code> can be set to FALSE to skip the initial sorting step.

### Details

Here the parameter  $k$  is the negative of  $k$  in Zhang & Stephens (2009).

### Value

A named list with components `k` and `sigma`.

### References

Zhang, J., and Stephens, M. A. (2009). A new and efficient estimation method for the generalized Pareto distribution. *Technometrics* **51**, 316-325.

### See Also

[psis\(\)](#), [pareto-k-diagnostic](#)

---

kfold-generic

*Generic function for K-fold cross-validation for developers*

---

### Description

For developers of Bayesian modeling packages, **loo** includes a generic function `kfold()` so that methods may be defined for K-fold CV without name conflicts between packages. See, for example, the `kfold()` methods in the **rstanarm** and **brms** packages.

The **Value** section below describes the objects that `kfold()` methods should return in order to be compatible with `loo_compare()` and the **loo** package print methods.

**Usage**

```
kfold(x, ...)
```

```
is.kfold(x)
```

**Arguments**

`x`                    A fitted model object.

`...`                 Arguments to pass to specific methods.

**Value**

For developers defining a `kfold()` method for a class "foo", the `kfold.foo()` function should return a list with class `c("kfold", "loo")` with at least the following named elements:

- "estimates": A 1x2 matrix containing the ELPD estimate and its standard error. The matrix must have row name "elpd\_kfold" and column names "Estimate" and "SE".
- "pointwise": A Nx1 matrix with column name "elpd\_kfold" containing the pointwise contributions for each data point.

It is important for the object to have at least these classes and components so that it is compatible with other functions like `loo_compare()` and `print()` methods.

---

kfold-helpers

*Helper functions for K-fold cross-validation*


---

**Description**

These functions can be used to generate indexes for use with K-fold cross-validation. See the **Details** section for explanations.

**Usage**

```
kfold_split_random(K = 10, N = NULL)
```

```
kfold_split_stratified(K = 10, x = NULL)
```

```
kfold_split_grouped(K = 10, x = NULL)
```

**Arguments**

`K`                    The number of folds to use.

`N`                    The number of observations in the data.

`x`                    A discrete variable of length N with at least K levels (unique values). Will be coerced to a [factor](#).

**Details**

`kfold_split_random()` splits the data into  $K$  groups of equal size (or roughly equal size).

For a categorical variable  $x$  `kfold_split_stratified()` splits the observations into  $K$  groups ensuring that relative category frequencies are approximately preserved.

For a grouping variable  $x$ , `kfold_split_grouped()` places all observations in  $x$  from the same group/level together in the same fold. The selection of which groups/levels go into which fold (relevant when there are more groups than folds) is randomized.

**Value**

An integer vector of length  $N$  where each element is an index in  $1:K$ .

**Examples**

```
ids <- kfold_split_random(K = 5, N = 20)
print(ids)
table(ids)

x <- sample(c(0, 1), size = 200, replace = TRUE, prob = c(0.05, 0.95))
table(x)
ids <- kfold_split_stratified(K = 5, x = x)
print(ids)
table(ids, x)

grp <- gl(n = 50, k = 15, labels = state.name)
length(grp)
head(table(grp))

ids_10 <- kfold_split_grouped(K = 10, x = grp)
(tab_10 <- table(grp, ids_10))
colSums(tab_10)

ids_9 <- kfold_split_grouped(K = 9, x = grp)
(tab_9 <- table(grp, ids_9))
colSums(tab_9)
```

---

 loo

---

*Efficient approximate leave-one-out cross-validation (LOO)*


---

**Description**

The `loo()` methods for arrays, matrices, and functions compute PSIS-LOO CV, efficient approximate leave-one-out (LOO) cross-validation for Bayesian models using Pareto smoothed importance sampling (PSIS). This is an implementation of the methods described in Vehtari, Gelman, and Gabry (2017) and Vehtari, Simpson, Gelman, Yao, and Gabry (2019).

The `loo_i()` function enables testing log-likelihood functions for use with the `loo.function()` method.

**Usage**

```
loo(x, ...)  
  
## S3 method for class 'array'  
loo(  
  x,  
  ...,  
  r_eff = NULL,  
  save_psis = FALSE,  
  cores = getOption("mc.cores", 1),  
  is_method = c("psis", "tis", "sis")  
)  
  
## S3 method for class 'matrix'  
loo(  
  x,  
  ...,  
  r_eff = NULL,  
  save_psis = FALSE,  
  cores = getOption("mc.cores", 1),  
  is_method = c("psis", "tis", "sis")  
)  
  
## S3 method for class ``function``  
loo(  
  x,  
  ...,  
  data = NULL,  
  draws = NULL,  
  r_eff = NULL,  
  save_psis = FALSE,  
  cores = getOption("mc.cores", 1),  
  is_method = c("psis", "tis", "sis")  
)  
  
loo_i(  
  i,  
  llfun,  
  ...,  
  data = NULL,  
  draws = NULL,  
  r_eff = NULL,  
  is_method = "psis"  
)  
  
is.loo(x)  
  
is.psis_loo(x)
```

## Arguments

<code>x</code>	A log-likelihood array, matrix, or function. The <b>Methods (by class)</b> section, below, has detailed descriptions of how to specify the inputs for each method.
<code>r_eff</code>	Vector of relative effective sample size estimates for the likelihood ( $\exp(\log\_lik)$ ) of each observation. This is related to the relative efficiency of estimating the normalizing term in self-normalizing importance sampling when using posterior draws obtained with MCMC. If MCMC draws are used and <code>r_eff</code> is not provided then the reported PSIS effective sample sizes and Monte Carlo error estimates will be over-optimistic. If the posterior draws are independent then <code>r_eff=1</code> and can be omitted. The warning message thrown when <code>r_eff</code> is not specified can be disabled by setting <code>r_eff</code> to NA. See the <a href="#">relative_eff()</a> helper functions for computing <code>r_eff</code> .
<code>save_psis</code>	Should the "psis" object created internally by <code>loo()</code> be saved in the returned object? The <code>loo()</code> function calls <code>psis()</code> internally but by default discards the (potentially large) "psis" object after using it to compute the LOO-CV summaries. Setting <code>save_psis=TRUE</code> will add a <code>psis_object</code> component to the list returned by <code>loo</code> . Currently this is only needed if you plan to use the <a href="#">E_loo()</a> function to compute weighted expectations after running <code>loo</code> .
<code>cores</code>	The number of cores to use for parallelization. This defaults to the option <code>mc.cores</code> which can be set for an entire R session by <code>options(mc.cores = NUMBER)</code> . The old option <code>loo.cores</code> is now deprecated but will be given precedence over <code>mc.cores</code> until <code>loo.cores</code> is removed in a future release. <b>As of version 2.0.0 the default is now 1 core if <code>mc.cores</code> is not set</b> , but we recommend using as many (or close to as many) cores as possible. <ul style="list-style-type: none"> <li>• Note for Windows 10 users: it is <b>strongly recommended</b> to avoid using the <code>.Rprofile</code> file to set <code>mc.cores</code> (using the <code>cores</code> argument or setting <code>mc.cores</code> interactively or in a script is fine).</li> </ul>
<code>is_method</code>	The importance sampling method to use. The following methods are implemented: <ul style="list-style-type: none"> <li>• <b>"psis"</b>: Pareto-Smoothed Importance Sampling (PSIS). Default method.</li> <li>• <b>"tis"</b>: Truncated Importance Sampling (TIS) with truncation at <math>\sqrt{S}</math>, where <math>S</math> is the number of posterior draws.</li> <li>• <b>"sis"</b>: Standard Importance Sampling (SIS).</li> </ul>
<code>data, draws, ...</code>	For the <code>loo.function()</code> method and the <code>loo_i()</code> function, these are the data, posterior draws, and other arguments to pass to the log-likelihood function. See the <b>Methods (by class)</b> section below for details on how to specify these arguments.
<code>i</code>	For <code>loo_i()</code> , an integer in $1:N$ .
<code>llfun</code>	For <code>loo_i()</code> , the same as <code>x</code> for the <code>loo.function()</code> method. A log-likelihood function as described in the <b>Methods (by class)</b> section.

## Details

The `loo()` function is an S3 generic and methods are provided for 3-D pointwise log-likelihood arrays, pointwise log-likelihood matrices, and log-likelihood functions. The array and matrix meth-



ods are the most convenient, but for models fit to very large datasets the `loo.function()` method is more memory efficient and may be preferable.

## Value

The `loo()` methods return a named list with class `c("psis_loo", "loo")` and components:

**estimates** A matrix with two columns (Estimate, SE) and three rows (`elpd_loo`, `p_loo`, `looic`). This contains point estimates and standard errors of the expected log pointwise predictive density (`elpd_loo`), the effective number of parameters (`p_loo`) and the LOO information criterion `looic` (which is just  $-2 * \text{elpd\_loo}$ , i.e., converted to deviance scale).

**pointwise** A matrix with five columns (and number of rows equal to the number of observations) containing the pointwise contributions of the measures (`elpd_loo`, `mcse_elpd_loo`, `p_loo`, `looic`, `influence_pareto_k`). In addition to the three measures in `estimates`, we also report pointwise values of the Monte Carlo standard error of `elpd_loo` (`mcse_elpd_loo`), and statistics describing the influence of each observation on the posterior distribution (`influence_pareto_k`). These are the estimates of the shape parameter  $k$  of the generalized Pareto fit to the importance ratios for each leave-one-out distribution (see the [pareto-k-diagnostic](#) page for details).

**diagnostics** A named list containing two vectors:

- `pareto_k`: Importance sampling reliability diagnostics. By default, these are equal to the `influence_pareto_k` in `pointwise`. Some algorithms can improve importance sampling reliability and modify these diagnostics. See the [pareto-k-diagnostic](#) page for details.
- `n_eff`: PSIS effective sample size estimates.

**psis\_object** This component will be `NULL` unless the `save_psis` argument is set to `TRUE` when calling `loo()`. In that case `psis_object` will be the object of class "psis" that is created when the `loo()` function calls `psis()` internally to do the PSIS procedure.

The `loo_i()` function returns a named list with components `pointwise` and `diagnostics`. These components have the same structure as the `pointwise` and `diagnostics` components of the object returned by `loo()` except they contain results for only a single observation.

## Methods (by class)

- `array`: An  $I$  by  $C$  by  $N$  array, where  $I$  is the number of MCMC iterations per chain,  $C$  is the number of chains, and  $N$  is the number of data points.
- `matrix`: An  $S$  by  $N$  matrix, where  $S$  is the size of the posterior sample (with all chains merged) and  $N$  is the number of data points.
- `function`: A function `f()` that takes arguments `data_i` and draws and returns a vector containing the log-likelihood for a single observation  $i$  evaluated at each posterior draw. The function should be written such that, for each observation  $i$  in  $1:N$ , evaluating

```
f(data_i = data[i,, drop=FALSE], draws = draws)
```

results in a vector of length  $S$  (size of posterior sample). The log-likelihood function can also have additional arguments but `data_i` and `draws` are required.

If using the function method then the arguments `data` and `draws` must also be specified in the call to `loo()`:

- `data`: A data frame or matrix containing the data (e.g. observed outcome and predictors) needed to compute the pointwise log-likelihood. For each observation  $i$ , the  $i$ th row of data will be passed to the `data_i` argument of the log-likelihood function.
- `draws`: An object containing the posterior draws for any parameters needed to compute the pointwise log-likelihood. Unlike `data`, which is indexed by observation, for each observation the entire object `draws` will be passed to the `draws` argument of the log-likelihood function.
- The `...` can be used if your log-likelihood function takes additional arguments. These arguments are used like the `draws` argument in that they are recycled for each observation.

### Defining `loo()` methods in a package

Package developers can define `loo()` methods for fitted models objects. See the example `loo.stanfit()` method in the **Examples** section below for an example of defining a method that calls `loo.array()`. The `loo.stanreg()` method in the **rstanarm** package is an example of defining a method that calls `loo.function()`.

### References

Vehtari, A., Gelman, A., and Gabry, J. (2017). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*. 27(5), 1413–1432. doi:10.1007/s11222-016-9696-4 ([journal version](#), [preprint arXiv:1507.04544](#)).

Vehtari, A., Simpson, D., Gelman, A., Yao, Y., and Gabry, J. (2019). Pareto smoothed importance sampling. [preprint arXiv:1507.02646](#)

### See Also

- The **loo** package [vignettes](#) for demonstrations.
- The [FAQ page](#) on the **loo** website for answers to frequently asked questions.
- [psis\(\)](#) for the underlying Pareto Smoothed Importance Sampling (PSIS) procedure used in the LOO-CV approximation.
- [pareto-k-diagnostic](#) for convenience functions for looking at diagnostics.
- [loo\\_compare\(\)](#) for model comparison.

### Examples

```
### Array and matrix methods (using example objects included with loo package)
# Array method
LLarr <- example_loglik_array()
rel_n_eff <- relative_eff(exp(LLarr))
loo(LLarr, r_eff = rel_n_eff, cores = 2)

# Matrix method
LLmat <- example_loglik_matrix()
rel_n_eff <- relative_eff(exp(LLmat), chain_id = rep(1:2, each = 500))
loo(LLmat, r_eff = rel_n_eff, cores = 2)

### Using log-likelihood function instead of array or matrix
```

```

set.seed(124)

# Simulate data and draw from posterior
N <- 50; K <- 10; S <- 100; a0 <- 3; b0 <- 2
p <- rbeta(1, a0, b0)
y <- rbinom(N, size = K, prob = p)
a <- a0 + sum(y); b <- b0 + N * K - sum(y)
fake_posterior <- as.matrix(rbeta(S, a, b))
dim(fake_posterior) # S x 1
fake_data <- data.frame(y,K)
dim(fake_data) # N x 2

llfun <- function(data_i, draws) {
  # each time called internally within loo the arguments will be equal to:
  # data_i: ith row of fake_data (fake_data[i,, drop=FALSE])
  # draws: entire fake_posterior matrix
  dbinom(data_i$y, size = data_i$K, prob = draws, log = TRUE)
}

# Use the loo_i function to check that llfun works on a single observation
# before running on all obs. For example, using the 3rd obs in the data:
loo_3 <- loo_i(i = 3, llfun = llfun, data = fake_data, draws = fake_posterior, r_eff = NA)
print(loo_3$pointwise[, "elpd_loo"])

# Use loo.function method (setting r_eff=NA since this posterior not obtained via MCMC)
loo_with_fn <- loo(llfun, draws = fake_posterior, data = fake_data, r_eff = NA)

# If we look at the elpd_loo contribution from the 3rd obs it should be the
# same as what we got above with the loo_i function and i=3:
print(loo_with_fn$pointwise[3, "elpd_loo"])
print(loo_3$pointwise[, "elpd_loo"])

# Check that the loo.matrix method gives same answer as loo.function method
log_lik_matrix <- sapply(1:N, function(i) {
  llfun(data_i = fake_data[i,, drop=FALSE], draws = fake_posterior)
})
loo_with_mat <- loo(log_lik_matrix, r_eff = NA)
all.equal(loo_with_mat$estimates, loo_with_fn$estimates) # should be TRUE!

## Not run:
### For package developers: defining loo methods

# An example of a possible loo method for 'stanfit' objects (rstan package).
# A similar method is included in the rstan package.
# In order for users to be able to call loo(stanfit) instead of
# loo.stanfit(stanfit) the NAMESPACE needs to be handled appropriately
# (roxygen2 and devtools packages are good for that).
#
loo.stanfit <-
  function(x,
    pars = "log_lik",
    ...,

```

```

      save_psis = FALSE,
      cores = getOption("mc.cores", 1)) {
stopifnot(length(pars) == 1L)
LLarray <- loo::extract_log_lik(stanfit = x,
                             parameter_name = pars,
                             merge_chains = FALSE)
r_eff <- loo::relative_eff(x = exp(LLarray), cores = cores)
loo::loo.array(LLarray,
              r_eff = r_eff,
              cores = cores,
              save_psis = save_psis)
}

## End(Not run)

```

---

 loo-datasets

*Datasets for loo examples and vignettes*


---

## Description

Small datasets for use in **loo** examples and vignettes. The Kline and milk datasets are also included in the **rethinking** package (McElreath, 2016a), but we include them here as **rethinking** is not on CRAN.

## Details

Currently the data sets included are:

- Kline: Small dataset from Kline and Boyd (2010) on tool complexity and demography in Oceanic islands societies. This data is discussed in detail in McElreath (2016a,2016b). ([Link to variable descriptions](#))
- milk: Small dataset from Hinde and Milligan (2011) on primate milk composition. This data is discussed in detail in McElreath (2016a,2016b). ([Link to variable descriptions](#))

## References

Hinde and Milligan. 2011. *Evolutionary Anthropology* 20:9-23.

Kline, M.A. and R. Boyd. 2010. *Proc R Soc B* 277:2559-2564.

McElreath, R. (2016a). *rethinking*: Statistical Rethinking book package. R package version 1.59.

McElreath, R. (2016b). *Statistical rethinking: A Bayesian course with examples in R and Stan*. Chapman & Hall/CRC.

## Examples

```

str(Kline)
str(milk)

```

---

 loo-glossary

*LOO package glossary*


---

## Description

The pages provides definitions to key terms. Also see the [FAQ page](#) on the **loo** website for answers to frequently asked questions.

Note: VGG2017 refers to Vehtari, Gelman, and Gabry (2017). See **References**, below.

## ELPD and `elpd_loo`

The ELPD is the theoretical expected log pointwise predictive density for a new dataset (Eq 1 in VGG2017), which can be estimated, e.g., using cross-validation. `elpd_loo` is the Bayesian LOO estimate of the expected log pointwise predictive density (Eq 4 in VGG2017) and is a sum of  $N$  individual pointwise log predictive densities. Probability densities can be smaller or larger than 1, and thus log predictive densities can be negative or positive. For simplicity the ELPD acronym is used also for expected log pointwise predictive probabilities for discrete models. Probabilities are always equal or less than 1, and thus log predictive probabilities are 0 or negative.

## Standard error of `elpd_loo`

As `elpd_loo` is defined as the sum of  $N$  independent components (Eq 4 in VGG2017), we can compute the standard error by using the standard deviation of the  $N$  components and multiplying by  $\sqrt{N}$  (Eq 23 in VGG2017). This standard error is a coarse description of our uncertainty about the predictive performance for unknown future data. When  $N$  is small or there is severe model misspecification, the current SE estimate is overoptimistic and the actual SE can even be twice as large. Even for moderate  $N$ , when the SE estimate is an accurate estimate for the scale, it ignores the skewness. When making model comparisons, the SE of the component-wise (pairwise) differences should be used instead (see the `se_diff` section below and Eq 24 in VGG2017).

## Monte Carlo SE of `elpd_loo`

The Monte Carlo standard error is the estimate for the computational accuracy of MCMC and importance sampling used to compute `elpd_loo`. Usually this is negligible compared to the standard describing the uncertainty due to finite number of observations (Eq 23 in VGG2017).

## `p_loo` (effective number of parameters)

`p_loo` is the difference between `elpd_loo` and the non-cross-validated log posterior predictive density. It describes how much more difficult it is to predict future data than the observed data. Asymptotically under certain regularity conditions, `p_loo` can be interpreted as the *effective number of parameters*. In well behaving cases  $p_{\text{loo}} < N$  and  $p_{\text{loo}} < p$ , where  $p$  is the total number of parameters in the model.  $p_{\text{loo}} > N$  or  $p_{\text{loo}} > p$  indicates that the model has very weak predictive capability and may indicate a severe model misspecification. See below for more on interpreting `p_loo` when there are warnings about high Pareto  $k$  diagnostic values.

### Pareto k estimates

The Pareto k estimate is a diagnostic for Pareto smoothed importance sampling (PSIS), which is used to compute components of  $\text{elpd}_{\text{loo}}$ . In importance-sampling LOO (the full posterior distribution is used as the proposal distribution). The Pareto k diagnostic estimates how far an individual leave-one-out distribution is from the full distribution. If leaving out an observation changes the posterior too much then importance sampling is not able to give reliable estimate. If  $k < 0.5$ , then the corresponding component of  $\text{elpd}_{\text{loo}}$  is estimated with high accuracy. If  $0.5 < k < 0.7$  the accuracy is lower, but still ok. If  $k > 0.7$ , then importance sampling is not able to provide useful estimate for that component/observation. Pareto k is also useful as a measure of influence of an observation. Highly influential observations have high k values. Very high k values often indicate model misspecification, outliers or mistakes in data processing. See Section 6 of Gabry et al. (2019) for an example.

**Interpreting  $p_{\text{loo}}$  when Pareto k is large:** If  $k > 0.7$  then we can also look at the  $p_{\text{loo}}$  estimate for some additional information about the problem:

- If  $p_{\text{loo}} \ll p$  (the total number of parameters in the model), then the model is likely to be misspecified. Posterior predictive checks (PPCs) are then likely to also detect the problem. Try using an overdispersed model, or add more structural information (nonlinearity, mixture model, etc.).
- If  $p_{\text{loo}} < p$  and the number of parameters  $p$  is relatively large compared to the number of observations (e.g.,  $p > N/5$ ), it is likely that the model is so flexible or the population prior so weak that it's difficult to predict the left out observation (even for the true model). This happens, for example, in the simulated 8 schools (in VGG2017), random effect models with a few observations per random effect, and Gaussian processes and spatial models with short correlation lengths.
- If  $p_{\text{loo}} > p$ , then the model is likely to be badly misspecified. If the number of parameters  $p \ll N$ , then PPCs are also likely to detect the problem. See the case study at <https://avehtari.github.io/modelselection/roaches.html> for an example. If  $p$  is relatively large compared to the number of observations, say  $p > N/5$  (more accurately we should count number of observations influencing each parameter as in hierarchical models some groups may have few observations and other groups many), it is possible that PPCs won't detect the problem.

### elpd\_diff

$\text{elpd}_{\text{diff}}$  is the difference in  $\text{elpd}_{\text{loo}}$  for two models. If more than two models are compared, the difference is computed relative to the model with highest  $\text{elpd}_{\text{loo}}$ .

### se\_diff

The standard error of component-wise differences of  $\text{elpd}_{\text{loo}}$  (Eq 24 in VGG2017) between two models. This SE is *smaller* than the SE for individual models due to correlation (i.e., if some observations are easier and some more difficult to predict for all models).

### References

Vehtari, A., Gelman, A., and Gabry, J. (2017). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*, 27(5), 1413–1432. doi:10.1007/s11222-016-9696-4 (journal version, preprint arXiv:1507.04544).

Vehtari, A., Simpson, D., Gelman, A., Yao, Y., and Gabry, J. (2019). Pareto smoothed importance sampling. [preprint arXiv:1507.02646](#)

Gabry, J. , Simpson, D. , Vehtari, A. , Betancourt, M. and Gelman, A. (2019), Visualization in Bayesian workflow. *J. R. Stat. Soc. A*, 182: 389-402. doi:10.1111/rssa.12378 ([journal version](#), [preprint arXiv:1709.01449](#), [code on GitHub](#))

loo\_approximate\_posterior

*Efficient approximate leave-one-out cross-validation (LOO) for posterior approximations*

## Description

Efficient approximate leave-one-out cross-validation (LOO) for posterior approximations

## Usage

```
loo_approximate_posterior(x, log_p, log_g, ...)
```

```
## S3 method for class 'array'
loo_approximate_posterior(
  x,
  log_p,
  log_g,
  ...,
  save_psis = FALSE,
  cores = getOption("mc.cores", 1)
)
```

```
## S3 method for class 'matrix'
loo_approximate_posterior(
  x,
  log_p,
  log_g,
  ...,
  save_psis = FALSE,
  cores = getOption("mc.cores", 1)
)
```

```
## S3 method for class '`function`'
loo_approximate_posterior(
  x,
  ...,
  data = NULL,
  draws = NULL,
  log_p = NULL,
  log_g = NULL,
)
```

```

save_psis = FALSE,
cores = getOption("mc.cores", 1)
)

```

## Arguments

x	A log-likelihood array, matrix, or function. The <b>Methods (by class)</b> section, below, has detailed descriptions of how to specify the inputs for each method.
log_p	The log-posterior (target) evaluated at S samples from the proposal distribution (g). A vector of length S.
log_g	The log-density (proposal) evaluated at S samples from the proposal distribution (g). A vector of length S.
save_psis	Should the "psis" object created internally by loo_approximate_posterior() be saved in the returned object? See <a href="#">loo()</a> for details.
cores	The number of cores to use for parallelization. This defaults to the option mc.cores which can be set for an entire R session by options(mc.cores = NUMBER). The old option loo.cores is now deprecated but will be given precedence over mc.cores until loo.cores is removed in a future release. <b>As of version 2.0.0 the default is now 1 core if mc.cores is not set</b> , but we recommend using as many (or close to as many) cores as possible. <ul style="list-style-type: none"> <li>Note for Windows 10 users: it is <b>strongly recommended</b> to avoid using the .Rprofile file to set mc.cores (using the cores argument or setting mc.cores interactively or in a script is fine).</li> </ul>
data, draws, ...	For the loo_approximate_posterior.function() method, these are the data, posterior draws, and other arguments to pass to the log-likelihood function. See the <b>Methods (by class)</b> section below for details on how to specify these arguments.

## Details

The loo\_approximate\_posterior() function is an S3 generic and methods are provided for 3-D pointwise log-likelihood arrays, pointwise log-likelihood matrices, and log-likelihood functions. The implementation works for posterior approximations where it is possible to compute the log density for the posterior approximation.

## Value

The loo\_approximate\_posterior() methods return a named list with class c("psis\_loo\_ap", "psis\_loo", "loo"). It has the same structure as the objects returned by [loo\(\)](#) but with the additional slot:

**posterior\_approximation** A list with two vectors, log\_p and log\_g of the same length containing the posterior density and the approximation density for the individual draws.



**Methods (by class)**

- **array:** An  $I$  by  $C$  by  $N$  array, where  $I$  is the number of MCMC iterations per chain,  $C$  is the number of chains, and  $N$  is the number of data points.
- **matrix:** An  $S$  by  $N$  matrix, where  $S$  is the size of the posterior sample (with all chains merged) and  $N$  is the number of data points.
- **function:** A function  $f()$  that takes arguments `data_i` and `draws` and returns a vector containing the log-likelihood for a single observation  $i$  evaluated at each posterior draw. The function should be written such that, for each observation  $i$  in  $1:N$ , evaluating

```
f(data_i = data[i,, drop=FALSE], draws = draws)
```

results in a vector of length  $S$  (size of posterior sample). The log-likelihood function can also have additional arguments but `data_i` and `draws` are required.

If using the function method then the arguments `data` and `draws` must also be specified in the call to `loo()`:

- `data:` A data frame or matrix containing the data (e.g. observed outcome and predictors) needed to compute the pointwise log-likelihood. For each observation  $i$ , the  $i$ th row of `data` will be passed to the `data_i` argument of the log-likelihood function.
- `draws:` An object containing the posterior draws for any parameters needed to compute the pointwise log-likelihood. Unlike `data`, which is indexed by observation, for each observation the entire object `draws` will be passed to the `draws` argument of the log-likelihood function.
- The `...` can be used if your log-likelihood function takes additional arguments. These arguments are used like the `draws` argument in that they are recycled for each observation.

**References**

Magnusson, M., Riis Andersen, M., Jonasson, J. and Vehtari, A. (2019). Leave-One-Out Cross-Validation for Large Data. In *International Conference on Machine Learning*

Magnusson, M., Riis Andersen, M., Jonasson, J. and Vehtari, A. (2020). Leave-One-Out Cross-Validation for Model Comparison in Large Data. In *International Conference on Artificial Intelligence and Statistics (AISTATS)*

**See Also**

[loo\(\)](#), [psis\(\)](#), [loo\\_compare\(\)](#)

---

loo\_compare

*Model comparison*

---

**Description**

Compare fitted models based on [ELPD](#).

By default the `print` method shows only the most important information. Use `print(..., simplify=FALSE)` to print a more detailed summary.

**Usage**

```
loo_compare(x, ...)

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

## S3 method for class 'compare.loo'
print(x, ..., digits = 1, simplify = TRUE)

## S3 method for class 'compare.loo_ss'
print(x, ..., digits = 1, simplify = TRUE)
```

**Arguments**

x	An object of class "loo" or a list of such objects. If a list is used then the list names will be used as the model names in the output. See <b>Examples</b> .
...	Additional objects of class "loo", if not passed in as a single list.
digits	For the print method only, the number of digits to use when printing.
simplify	For the print method only, should only the essential columns of the summary matrix be printed? The entire matrix is always returned, but by default only the most important columns are printed.

**Details**

When comparing two fitted models, we can estimate the difference in their expected predictive accuracy by the difference in `elpd_loo` or `elpd_waic` (or multiplied by  $-2$ , if desired, to be on the deviance scale).

When using `loo_compare()`, the returned matrix will have one row per model and several columns of estimates. The values in the `elpd_diff` and `se_diff` columns of the returned matrix are computed by making pairwise comparisons between each model and the model with the largest ELPD (the model in the first row). For this reason the `elpd_diff` column will always have the value  $0$  in the first row (i.e., the difference between the preferred model and itself) and negative values in subsequent rows for the remaining models.

To compute the standard error of the difference in **ELPD** — which should not be expected to equal the difference of the standard errors — we use a paired estimate to take advantage of the fact that the same set of  $N$  data points was used to fit both models. These calculations should be most useful when  $N$  is large, because then non-normality of the distribution is not such an issue when estimating the uncertainty in these sums. These standard errors, for all their flaws, should give a better sense of uncertainty than what is obtained using the current standard approach of comparing differences of deviances to a Chi-squared distribution, a practice derived for Gaussian linear models or asymptotically, and which only applies to nested models in any case.

**Value**

A matrix with class "compare.loo" that has its own print method. See the **Details** section.

## References

- Vehtari, A., Gelman, A., and Gabry, J. (2017). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*. 27(5), 1413–1432. doi:10.1007/s11222-016-9696-4 ([journal version](#), [preprint arXiv:1507.04544](#)).
- Vehtari, A., Simpson, D., Gelman, A., Yao, Y., and Gabry, J. (2019). Pareto smoothed importance sampling. [preprint arXiv:1507.02646](#)

## See Also

- The [FAQ page](#) on the **loo** website for answers to frequently asked questions.

## Examples

```
# very artificial example, just for demonstration!
LL <- example_loglik_array()
loo1 <- loo(LL, r_eff = NA) # should be worst model when compared
loo2 <- loo(LL + 1, r_eff = NA) # should be second best model when compared
loo3 <- loo(LL + 2, r_eff = NA) # should be best model when compared

comp <- loo_compare(loo1, loo2, loo3)
print(comp, digits = 2)

# show more details with simplify=FALSE
# (will be the same for all models in this artificial example)
print(comp, simplify = FALSE, digits = 3)

# can use a list of objects with custom names
# will use apple, banana, and cherry, as the names in the output
loo_compare(list("apple" = loo1, "banana" = loo2, "cherry" = loo3))

## Not run:
# works for waic (and kfold) too
loo_compare(waic(LL), waic(LL - 10))

## End(Not run)
```

---

 loo\_model\_weights

*Model averaging/weighting via stacking or pseudo-BMA weighting*


---

## Description

Model averaging via stacking of predictive distributions, pseudo-BMA weighting or pseudo-BMA+ weighting with the Bayesian bootstrap. See Yao et al. (2018), Vehtari, Gelman, and Gabry (2017), and Vehtari, Simpson, Gelman, Yao, and Gabry (2019) for background.

**Usage**

```
loo_model_weights(x, ...)

## Default S3 method:
loo_model_weights(
  x,
  ...,
  method = c("stacking", "pseudobma"),
  optim_method = "BFGS",
  optim_control = list(),
  BB = TRUE,
  BB_n = 1000,
  alpha = 1,
  r_eff_list = NULL,
  cores = getOption("mc.cores", 1)
)

stacking_weights(lp_d_point, optim_method = "BFGS", optim_control = list())

pseudobma_weights(lp_d_point, BB = TRUE, BB_n = 1000, alpha = 1)
```

**Arguments**

x	A list of pointwise log-likelihood matrices or "psis_loo" objects (objects returned by <code>loo()</code> ), one for each model. Each matrix/object should have dimensions $S$ by $N$ , where $S$ is the size of the posterior sample (with all chains merged) and $N$ is the number of data points. If <code>x</code> is a list of log-likelihood matrices then <code>loo()</code> is called internally on each matrix. Currently the <code>loo_model_weights()</code> function is not implemented to be used with results from K-fold CV, but you can still obtain weights using K-fold CV results by calling the <code>stacking_weights()</code> function directly.
...	Unused, except for the generic to pass arguments to individual methods.
method	Either "stacking" (the default) or "pseudobma", indicating which method to use for obtaining the weights. "stacking" refers to stacking of predictive distributions and "pseudobma" refers to pseudo-BMA+ weighting (or plain pseudo-BMA weighting if argument <code>BB</code> is FALSE).
optim_method	If <code>method="stacking"</code> , a string passed to the <code>method</code> argument of <code>stats::constrOptim()</code> to specify the optimization algorithm. The default is <code>optim_method="BFGS"</code> , but other options are available (see <code>stats::optim()</code> ).
optim_control	If <code>method="stacking"</code> , a list of control parameters for optimization passed to the <code>control</code> argument of <code>stats::constrOptim()</code> .
BB	Logical used when <code>method="pseudobma"</code> . If TRUE (the default), the Bayesian bootstrap will be used to adjust the pseudo-BMA weighting, which is called pseudo-BMA+ weighting. It helps regularize the weight away from 0 and 1, so as to reduce the variance.
BB_n	For pseudo-BMA+ weighting only, the number of samples to use for the Bayesian bootstrap. The default is <code>BB_n=1000</code> .

alpha	Positive scalar shape parameter in the Dirichlet distribution used for the Bayesian bootstrap. The default is <code>alpha=1</code> , which corresponds to a uniform distribution on the simplex space.
r_eff_list	Optionally, a list of relative effective sample size estimates for the likelihood ( <code>exp(log_lik)</code> ) of each observation in each model. See <code>psis()</code> and <code>relative_eff()</code> helper function for computing <code>r_eff</code> . If <code>x</code> is a list of "psis_loo" objects then <code>r_eff_list</code> is ignored.
cores	The number of cores to use for parallelization. This defaults to the option <code>mc.cores</code> which can be set for an entire R session by <code>options(mc.cores = NUMBER)</code> . The old option <code>loo.cores</code> is now deprecated but will be given precedence over <code>mc.cores</code> until <code>loo.cores</code> is removed in a future release. <b>As of version 2.0.0 the default is now 1 core if <code>mc.cores</code> is not set</b> , but we recommend using as many (or close to as many) cores as possible. <ul style="list-style-type: none"> <li>Note for Windows 10 users: it is <b>strongly recommended</b> to avoid using the <code>.Rprofile</code> file to set <code>mc.cores</code> (using the <code>cores</code> argument or setting <code>mc.cores</code> interactively or in a script is fine).</li> </ul>
lpd_point	If calling <code>stacking_weights()</code> or <code>pseudobma_weights()</code> directly, a matrix of pointwise leave-one-out (or K-fold) log likelihoods evaluated for different models. It should be a $N$ by $K$ matrix where $N$ is sample size and $K$ is the number of models. Each column corresponds to one model. These values can be calculated approximately using <code>loo()</code> or by running exact leave-one-out or K-fold cross-validation.

## Details

`loo_model_weights()` is a wrapper around the `stacking_weights()` and `pseudobma_weights()` functions that implements stacking, pseudo-BMA, and pseudo-BMA+ weighting for combining multiple predictive distributions. We can use approximate or exact leave-one-out cross-validation (LOO-CV) or K-fold CV to estimate the expected log predictive density (ELPD).

The stacking method (`method="stacking"`), which is the default for `loo_model_weights()`, combines all models by maximizing the leave-one-out predictive density of the combination distribution. That is, it finds the optimal linear combining weights for maximizing the leave-one-out log score.

The pseudo-BMA method (`method="pseudobma"`) finds the relative weights proportional to the ELPD of each model. However, when `method="pseudobma"`, the default is to also use the Bayesian bootstrap (`BB=TRUE`), which corresponds to the pseudo-BMA+ method. The Bayesian bootstrap takes into account the uncertainty of finite data points and regularizes the weights away from the extremes of 0 and 1.

In general, we recommend stacking for averaging predictive distributions, while pseudo-BMA+ can serve as a computationally easier alternative.

## Value

A numeric vector containing one weight for each model.

## References

- Vehtari, A., Gelman, A., and Gabry, J. (2017). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*. 27(5), 1413–1432. doi:10.1007/s11222-016-9696-4 ([journal version](#), [preprint arXiv:1507.04544](#)).
- Vehtari, A., Simpson, D., Gelman, A., Yao, Y., and Gabry, J. (2019). Pareto smoothed importance sampling. [preprint arXiv:1507.02646](#)
- Yao, Y., Vehtari, A., Simpson, D., and Gelman, A. (2018) Using stacking to average Bayesian predictive distributions. *Bayesian Analysis*, advance publication, doi:10.1214/17-BA1091. ([online](#)).

## See Also

- The **loo** package [vignettes](#), particularly [Bayesian Stacking and Pseudo-BMA weights using the loo package](#).
- `loo()` for details on leave-one-out ELPD estimation.
- `constrOptim()` for the choice of optimization methods and control-parameters.
- `relative_eff()` for computing `r_eff`.

## Examples

```
## Not run:
### Demonstrating usage after fitting models with RStan
library(rstan)

# generate fake data from N(0,1).
N <- 100
y <- rnorm(N, 0, 1)

# Suppose we have three models: N(-1, sigma), N(0.5, sigma) and N(0.6,sigma).
stan_code <- "
  data {
    int N;
    vector[N] y;
    real mu_fixed;
  }
  parameters {
    real<lower=0> sigma;
  }
  model {
    sigma ~ exponential(1);
    y ~ normal(mu_fixed, sigma);
  }
  generated quantities {
    vector[N] log_lik;
    for (n in 1:N) log_lik[n] = normal_lpdf(y[n] | mu_fixed, sigma);
  }"

mod <- stan_model(model_code = stan_code)
fit1 <- sampling(mod, data=list(N=N, y=y, mu_fixed=-1))
fit2 <- sampling(mod, data=list(N=N, y=y, mu_fixed=0.5))
```

```
fit3 <- sampling(mod, data=list(N=N, y=y, mu_fixed=0.6))
model_list <- list(fit1, fit2, fit3)
log_lik_list <- lapply(model_list, extract_log_lik)

# optional but recommended
r_eff_list <- lapply(model_list, function(x) {
  ll_array <- extract_log_lik(x, merge_chains = FALSE)
  relative_eff(exp(ll_array))
})

# stacking method:
wts1 <- loo_model_weights(
  log_lik_list,
  method = "stacking",
  r_eff_list = r_eff_list,
  optim_control = list(reltol=1e-10)
)
print(wts1)

# can also pass a list of psis_loo objects to avoid recomputing loo
loo_list <- lapply(1:length(log_lik_list), function(j) {
  loo(log_lik_list[[j]], r_eff = r_eff_list[[j]])
})

wts2 <- loo_model_weights(
  loo_list,
  method = "stacking",
  optim_control = list(reltol=1e-10)
)
all.equal(wts1, wts2)

# pseudo-BMA+ method:
set.seed(1414)
loo_model_weights(loo_list, method = "pseudobma")

# pseudo-BMA method (set BB = FALSE):
loo_model_weights(loo_list, method = "pseudobma", BB = FALSE)

# calling stacking_weights or pseudobma_weights directly
lpd1 <- loo(log_lik_list[[1]], r_eff = r_eff_list[[1]])$pointwise[,1]
lpd2 <- loo(log_lik_list[[2]], r_eff = r_eff_list[[2]])$pointwise[,1]
lpd3 <- loo(log_lik_list[[3]], r_eff = r_eff_list[[3]])$pointwise[,1]
stacking_weights(cbind(lpd1, lpd2, lpd3))
pseudobma_weights(cbind(lpd1, lpd2, lpd3))
pseudobma_weights(cbind(lpd1, lpd2, lpd3), BB = FALSE)

## End(Not run)
```

---

loo\_moment\_match      *Moment matching for efficient approximate leave-one-out cross-validation (LOO)*

---

### Description

Moment matching algorithm for updating a loo object when Pareto k estimates are large.

### Usage

```
loo_moment_match(x, ...)

## Default S3 method:
loo_moment_match(
  x,
  loo,
  post_draws,
  log_lik_i,
  unconstrain_pars,
  log_prob_upars,
  log_lik_i_upars,
  max_iters = 30L,
  k_threshold = 0.7,
  split = TRUE,
  cov = TRUE,
  cores = getOption("mc.cores", 1),
  ...
)
```

### Arguments

x	A fitted model object.
...	Further arguments passed to the custom functions documented above.
loo	A loo object to be modified.
post_draws	A function that takes x as the first argument and returns a matrix of posterior draws of the model parameters.
log_lik_i	A function that takes x and i and returns a matrix (one column per chain) or a vector (all chains stacked) of log-likelihood draws of the i-th observation based on the model x. If the draws are obtained using MCMC, the matrix with MCMC chains separated is preferred.
unconstrain_pars	A function that takes arguments x, and pars and returns posterior draws on the unconstrained space based on the posterior draws on the constrained space passed via pars.
log_prob_upars	A function that takes arguments x and upars and returns a matrix of log-posterior density values of the unconstrained posterior draws passed via upars.



log_lik_i_upars	A function that takes arguments <code>x</code> , <code>upars</code> , and <code>i</code> and returns a vector of log-likelihood draws of the <code>i</code> th observation based on the unconstrained posterior draws passed via <code>upars</code> .
max_iters	Maximum number of moment matching iterations. Usually this does not need to be modified. If the maximum number of iterations is reached, there will be a warning, and increasing <code>max_iters</code> may improve accuracy.
k_threshold	Threshold value for Pareto <code>k</code> values above which the moment matching algorithm is used. The default value is 0.5.
split	Logical; Indicate whether to do the split transformation or not at the end of moment matching for each LOO fold.
cov	Logical; Indicate whether to match the covariance matrix of the samples or not. If FALSE, only the mean and marginal variances are matched.
cores	The number of cores to use for parallelization. This defaults to the option <code>mc.cores</code> which can be set for an entire R session by <code>options(mc.cores = NUMBER)</code> . The old option <code>loo.cores</code> is now deprecated but will be given precedence over <code>mc.cores</code> until <code>loo.cores</code> is removed in a future release. <b>As of version 2.0.0 the default is now 1 core if <code>mc.cores</code> is not set</b> , but we recommend using as many (or close to as many) cores as possible. <ul style="list-style-type: none"> <li>Note for Windows 10 users: it is <b>strongly recommended</b> to avoid using the <code>.Rprofile</code> file to set <code>mc.cores</code> (using the <code>cores</code> argument or setting <code>mc.cores</code> interactively or in a script is fine).</li> </ul>

## Details

The `loo_moment_match()` function is an S3 generic and we provide a default method that takes as arguments user-specified functions `post_draws`, `log_lik_i`, `unconstrain_pars`, `log_prob_upars`, and `log_lik_i_upars`. All of these functions should take `...` as an argument in addition to those specified for each function.

## Value

The `loo_moment_match()` methods return an updated `loo` object. The structure of the updated `loo` object is similar, but the method also stores the original Pareto `k` diagnostic values in the `diagnostics` field.

## Methods (by class)

- `default`: A default method that takes as arguments a user-specified model object `x`, a `loo` object and user-specified functions `post_draws`, `log_lik_i`, `unconstrain_pars`, `log_prob_upars`, and `log_lik_i_upars`.

## References

Paananen, T., Piironen, J., Buerkner, P.-C., Vehtari, A. (2021). Implicitly adaptive importance sampling. *Statistics and Computing*, 31, 16. doi:10.1007/s11222-020-09982-2. arXiv preprint arXiv:1906.08850.

**See Also**

[loo\(\)](#), [loo\\_moment\\_match\\_split\(\)](#)

**Examples**

```
# See the vignette for loo_moment_match()
```

---

```
loo_moment_match_split
```

*Split moment matching for efficient approximate leave-one-out cross-validation (LOO)*

---

**Description**

A function that computes the split moment matching importance sampling loo. Takes in the moment matching total transformation, transforms only half of the draws, and computes a single elpd using multiple importance sampling.

**Usage**

```
loo_moment_match_split(
  x,
  upars,
  cov,
  total_shift,
  total_scaling,
  total_mapping,
  i,
  log_prob_upars,
  log_lik_i_upars,
  r_eff_i,
  cores,
  is_method,
  ...
)
```

**Arguments**

x	A fitted model object.
upars	A matrix containing the model parameters in unconstrained space where they can have any real value.
cov	Logical; Indicate whether to match the covariance matrix of the samples or not. If FALSE, only the mean and marginal variances are matched.
total_shift	A vector representing the total shift made by the moment matching algorithm.
total_scaling	A vector representing the total scaling of marginal variance made by the moment matching algorithm.

total_mapping	A vector representing the total covariance transformation made by the moment matching algorithm.
i	Observation index.
log_prob_upars	A function that takes arguments <code>x</code> and <code>upars</code> and returns a matrix of log-posterior density values of the unconstrained posterior draws passed via <code>upars</code> .
log_lik_i_upars	A function that takes arguments <code>x</code> , <code>upars</code> , and <code>i</code> and returns a vector of log-likelihood draws of the <code>i</code> th observation based on the unconstrained posterior draws passed via <code>upars</code> .
r_eff_i	MCMC relative effective sample size of the <code>i</code> 'th log likelihood draws.
cores	The number of cores to use for parallelization. This defaults to the option <code>mc.cores</code> which can be set for an entire R session by <code>options(mc.cores = NUMBER)</code> . The old option <code>loo.cores</code> is now deprecated but will be given precedence over <code>mc.cores</code> until <code>loo.cores</code> is removed in a future release. <b>As of version 2.0.0 the default is now 1 core if <code>mc.cores</code> is not set</b> , but we recommend using as many (or close to as many) cores as possible. <ul style="list-style-type: none"> <li>• Note for Windows 10 users: it is <b>strongly recommended</b> to avoid using the <code>.Rprofile</code> file to set <code>mc.cores</code> (using the <code>cores</code> argument or setting <code>mc.cores</code> interactively or in a script is fine).</li> </ul>
is_method	The importance sampling method to use. The following methods are implemented: <ul style="list-style-type: none"> <li>• <code>"psis"</code>: Pareto-Smoothed Importance Sampling (PSIS). Default method.</li> <li>• <code>"tis"</code>: Truncated Importance Sampling (TIS) with truncation at <code>sqrt(S)</code>, where <code>S</code> is the number of posterior draws.</li> <li>• <code>"sis"</code>: Standard Importance Sampling (SIS).</li> </ul>
...	Further arguments passed to the custom functions documented above.

### Value

A list containing the updated log-importance weights and log-likelihood values. Also returns the updated MCMC effective sample size and the integrand-specific log-importance weights.

### References

Paananen, T., Pironen, J., Buerkner, P.-C., Vehtari, A. (2021). Implicitly adaptive importance sampling. *Statistics and Computing*, 31, 16. doi:10.1007/s11222-020-09982-2. arXiv preprint arXiv:1906.08850.

### See Also

[loo\(\)](#), [loo\\_moment\\_match\(\)](#)

---

loo_subsample	<i>Efficient approximate leave-one-out cross-validation (LOO) using subsampling</i>
---------------	---

---

### Description

Efficient approximate leave-one-out cross-validation (LOO) using subsampling

### Usage

```
loo_subsample(x, ...)

## S3 method for class ``function``
loo_subsample(
  x,
  ...,
  data = NULL,
  draws = NULL,
  observations = 400,
  log_p = NULL,
  log_g = NULL,
  r_eff = NULL,
  save_psis = FALSE,
  cores = getOption("mc.cores", 1),
  loo_approximation = "plpd",
  loo_approximation_draws = NULL,
  estimator = "diff_srs",
  llgrad = NULL,
  llhess = NULL
)
```

### Arguments

x	A function. The <b>Methods (by class)</b> section, below, has detailed descriptions of how to specify the inputs.
data, draws, ...	For <code>loo_subsample.function()</code> , these are the data, posterior draws, and other arguments to pass to the log-likelihood function. Note that for some <code>loo_approximations</code> , the draws will be replaced by the posteriors summary statistics to compute loo approximations. See argument <code>loo_approximation</code> for details.
observations	The subsample observations to use. The argument can take four (4) types of arguments: <ul style="list-style-type: none"> <li>• NULL to use all observations. The algorithm then just uses standard <code>loo()</code> or <code>loo_approximate_posterior()</code>.</li> <li>• A single integer to specify the number of observations to be subsampled.</li> </ul>

- A vector of integers to provide the indices used to subset the data. *These observations need to be subsampled with the same scheme as given by the estimator argument.*
  - A `psis_loo_ss` object to use the same observations that were used in a previous call to `loo_subsample()`.
- `log_p, log_g` Should be supplied only if approximate posterior draws are used. The default (NULL) indicates draws are from "true" posterior (i.e. using MCMC). If not NULL then they should be specified as described in `loo_approximate_posterior()`.
- `r_eff` Vector of relative effective sample size estimates for the likelihood ( $\exp(\log\_lik)$ ) of each observation. This is related to the relative efficiency of estimating the normalizing term in self-normalizing importance sampling when using posterior draws obtained with MCMC. If MCMC draws are used and `r_eff` is not provided then the reported PSIS effective sample sizes and Monte Carlo error estimates will be over-optimistic. If the posterior draws are independent then `r_eff`=1 and can be omitted. The warning message thrown when `r_eff` is not specified can be disabled by setting `r_eff` to NA. See the `relative_eff()` helper functions for computing `r_eff`.
- `save_psis` Should the "psis" object created internally by `loo_subsample()` be saved in the returned object? See `loo()` for details.
- `cores` The number of cores to use for parallelization. This defaults to the option `mc.cores` which can be set for an entire R session by `options(mc.cores = NUMBER)`. The old option `loo.cores` is now deprecated but will be given precedence over `mc.cores` until `loo.cores` is removed in a future release. **As of version 2.0.0 the default is now 1 core if `mc.cores` is not set**, but we recommend using as many (or close to as many) cores as possible.
- Note for Windows 10 users: it is **strongly recommended** to avoid using the `.Rprofile` file to set `mc.cores` (using the `cores` argument or setting `mc.cores` interactively or in a script is fine).
- `loo_approximation` What type of approximation of the `loo_i`'s should be used? The default is "p1pd" (the log predictive density using the posterior expectation). There are six different methods implemented to approximate `loo_i`'s (see the references for more details):
- "p1pd": uses the lpd based on point estimates (i.e.,  $p(y_i|\hat{\theta})$ ).
  - "lpd": uses the lpds (i.e.,  $p(y_i|y)$ ).
  - "tis": uses truncated importance sampling to approximate PSIS-LOO.
  - "waic": uses waic (i.e.,  $p(y_i|y) - p_{waic}$ ).
  - "waic\_grad\_marginal": uses waic approximation using first order delta method and posterior marginal variances to approximate  $p_{waic}$  (ie.  $p(y_i|\hat{\theta})$ -`p_waic_grad_marginal`). Requires gradient of likelihood function.
  - "waic\_grad": uses waic approximation using first order delta method and posterior covariance to approximate  $p_{waic}$  (ie.  $p(y_i|\hat{\theta})$ -`p_waic_grad`). Requires gradient of likelihood function.
  - "waic\_hess": uses waic approximation using second order delta method and posterior covariance to approximate  $p_{waic}$  (ie.  $p(y_i|\hat{\theta})$ -`p_waic_grad`). Requires gradient and Hessian of likelihood function.

	As point estimates of $\hat{\theta}$ , the posterior expectations of the parameters are used.
loo_approximation_draws	The number of posterior draws used when integrating over the posterior. This is used if loo_approximation is set to "lpd", "waic", or "tis".
estimator	How should elpd_loo, p_loo and looic be estimated? The default is "diff_srs". <ul style="list-style-type: none"> <li>• "diff_srs": uses the difference estimator with simple random sampling (srs). p_loo is estimated using standard srs.</li> <li>• "hh": uses the Hansen-Hurwitz estimator with sampling proportional to size, where abs of loo_approximation is used as size.</li> <li>• "srs": uses simple random sampling and ordinary estimation.</li> </ul>
llgrad	The gradient of the log-likelihood. This is only used when loo_approximation is "waic_grad", "waic_grad_marginal", or "waic_hess". The default is NULL.
llhess	The hessian of the log-likelihood. This is only used with loo_approximation = "waic_hess". The default is NULL.

### Details

The `loo_subsample()` function is an S3 generic and a methods is currently provided for log-likelihood functions. The implementation works for both MCMC and for posterior approximations where it is possible to compute the log density for the approximation.

### Value

`loo_subsample()` returns a named list with class `c("psis_loo_ss", "psis_loo", "loo")`. This has the same structure as objects returned by `loo()` but with the additional slot:

- `loo_subsampling`: A list with two vectors, `log_p` and `log_g`, of the same length containing the posterior density and the approximation density for the individual draws.

### Methods (by class)

- `function`: A function `f()` that takes arguments `data_i` and `draws` and returns a vector containing the log-likelihood for a single observation `i` evaluated at each posterior draw. The function should be written such that, for each observation `i` in `1:N`, evaluating

```
f(data_i = data[i, , drop=FALSE], draws = draws)
```

results in a vector of length `S` (size of posterior sample). The log-likelihood function can also have additional arguments but `data_i` and `draws` are required.

If using the function method then the arguments `data` and `draws` must also be specified in the call to `loo()`:

- `data`: A data frame or matrix containing the data (e.g. observed outcome and predictors) needed to compute the pointwise log-likelihood. For each observation `i`, the `i`th row of `data` will be passed to the `data_i` argument of the log-likelihood function.
- `draws`: An object containing the posterior draws for any parameters needed to compute the pointwise log-likelihood. Unlike `data`, which is indexed by observation, for each observation the entire object `draws` will be passed to the `draws` argument of the log-likelihood function.

- The ... can be used if your log-likelihood function takes additional arguments. These arguments are used like the draws argument in that they are recycled for each observation.

## References

- Magnusson, M., Riis Andersen, M., Jonasson, J. and Vehtari, A. (2019). Leave-One-Out Cross-Validation for Large Data. In *International Conference on Machine Learning*
- Magnusson, M., Riis Andersen, M., Jonasson, J. and Vehtari, A. (2020). Leave-One-Out Cross-Validation for Model Comparison in Large Data. In *International Conference on Artificial Intelligence and Statistics (AISTATS)*

## See Also

[loo\(\)](#), [psis\(\)](#), [loo\\_compare\(\)](#)

---

nobs.psis_loo_ss	<i>The number of observations in a psis_loo_ss object.</i>
------------------	--

---

## Description

The number of observations in a psis\_loo\_ss object.

## Usage

```
## S3 method for class 'psis_loo_ss'
nobs(object, ...)
```

## Arguments

object	a psis_loo_ss object.
...	Currently unused.

---

obs_idx	<i>Get observation indices used in subsampling</i>
---------	--

---

## Description

Get observation indices used in subsampling

## Usage

```
obs_idx(x, rep = TRUE)
```

**Arguments**

x	A <code>psis_loo_ss</code> object.
rep	If sampling with replacement is used, an observation can have multiple samples and these are then repeated in the returned object if <code>rep=TRUE</code> (e.g., a vector <code>c(1,1,2)</code> indicates that observation 1 has been subsampled two times). If <code>rep=FALSE</code> only the unique indices are returned.

**Value**

An integer vector.

---

pareto-k-diagnostic     *Diagnostics for Pareto smoothed importance sampling (PSIS)*

---

**Description**

Print a diagnostic table summarizing the estimated Pareto shape parameters and PSIS effective sample sizes, find the indexes of observations for which the estimated Pareto shape parameter  $k$  is larger than some threshold value, or plot observation indexes vs. diagnostic estimates. The **Details** section below provides a brief overview of the diagnostics, but we recommend consulting Vehtari, Gelman, and Gabry (2017) and Vehtari, Simpson, Gelman, Yao, and Gabry (2019) for full details.

**Usage**

```
pareto_k_table(x)

pareto_k_ids(x, threshold = 0.5)

pareto_k_values(x)

pareto_k_influence_values(x)

psis_n_eff_values(x)

mcse_loo(x, threshold = 0.7)

## S3 method for class 'psis_loo'
plot(
  x,
  diagnostic = c("k", "n_eff"),
  ...,
  label_points = FALSE,
  main = "PSIS diagnostic plot"
)
```



```
## S3 method for class 'psis'
plot(
  x,
  diagnostic = c("k", "n_eff"),
  ...,
  label_points = FALSE,
  main = "PSIS diagnostic plot"
)
```

### Arguments

<code>x</code>	An object created by <code>loo()</code> or <code>psis()</code> .
<code>threshold</code>	For <code>pareto_k_ids()</code> , <code>threshold</code> is the minimum $k$ value to flag (default is 0.5). For <code>mcse_loo()</code> , if any $k$ estimates are greater than <code>threshold</code> the MCSE estimate is returned as NA (default is 0.7). See <b>Details</b> for the motivation behind these defaults.
<code>diagnostic</code>	For the <code>plot</code> method, which diagnostic should be plotted? The options are "k" for Pareto $k$ estimates (the default) or "n_eff" for PSIS effective sample size estimates.
<code>label_points, ...</code>	For the <code>plot()</code> method, if <code>label_points</code> is TRUE the observation numbers corresponding to any values of $k$ greater than 0.5 will be displayed in the plot. Any arguments specified in <code>...</code> will be passed to <code>graphics::text()</code> and can be used to control the appearance of the labels.
<code>main</code>	For the <code>plot()</code> method, a title for the plot.

### Details

The reliability and approximate convergence rate of the PSIS-based estimates can be assessed using the estimates for the shape parameter  $k$  of the generalized Pareto distribution:

- If  $k < 0.5$  then the distribution of raw importance ratios has finite variance and the central limit theorem holds. However, as  $k$  approaches 0.5 the RMSE of plain importance sampling (IS) increases significantly while PSIS has lower RMSE.
- If  $0.5 \leq k < 1$  then the variance of the raw importance ratios is infinite, but the mean exists. TIS and PSIS estimates have finite variance by accepting some bias. The convergence of the estimate is slower with increasing  $k$ . If  $k$  is between 0.5 and approximately 0.7 then we observe practically useful convergence rates and Monte Carlo error estimates with PSIS (the bias of TIS increases faster than the bias of PSIS). If  $k > 0.7$  we observe impractical convergence rates and unreliable Monte Carlo error estimates.
- If  $k \geq 1$  then neither the variance nor the mean of the raw importance ratios exists. The convergence rate is close to zero and bias can be large with practical sample sizes.

**What if the estimated tail shape parameter  $k$  exceeds 0.5:** Importance sampling is likely to work less well if the marginal posterior  $p(\theta^s|y)$  and LOO posterior  $p(\theta^s|y_{-i})$  are very different, which is more likely to happen with a non-robust model and highly influential observations. If the estimated tail shape parameter  $k$  exceeds 0.5, the user should be warned. (Note: If  $k$  is greater than 0.5 then WAIC is also likely to fail, but WAIC lacks its own diagnostic.) In practice, we

have observed good performance for values of  $k$  up to 0.7. When using PSIS in the context of approximate LOO-CV, we recommend one of the following actions when  $k > 0.7$ :

- With some additional computations, it is possible to transform the MCMC draws from the posterior distribution to obtain more reliable importance sampling estimates. This results in a smaller shape parameter  $k$ . See `loo_moment_match()` for an example of this.
- Sampling directly from  $p(\theta^s | y_{-i})$  for the problematic observations  $i$ , or using  $k$ -fold cross-validation will generally be more stable.
- Using a model that is more robust to anomalous observations will generally make approximate LOO-CV more stable.

**Observation influence statistics:** The estimated shape parameter  $k$  for each observation can be used as a measure of the observation's influence on posterior distribution of the model. These can be obtained with `pareto_k_influence_values()`.

**Effective sample size and error estimates:** In the case that we obtain the samples from the proposal distribution via MCMC the `loo` package also computes estimates for the Monte Carlo error and the effective sample size for importance sampling, which are more accurate for PSIS than for IS and TIS (see Vehtari et al (2019) for details). However, the PSIS effective sample size estimate will be **over-optimistic when the estimate of  $k$  is greater than 0.7**.

## Value

`pareto_k_table()` returns an object of class "pareto\_k\_table", which is a matrix with columns "Count", "Proportion", and "Min. n\_eff", and has its own print method.

`pareto_k_ids()` returns an integer vector indicating which observations have Pareto  $k$  estimates above threshold.

`pareto_k_values()` returns a vector of the estimated Pareto  $k$  parameters. These represent the reliability of sampling.

`pareto_k_influence_values()` returns a vector of the estimated Pareto  $k$  parameters. These represent influence of the observations on the model posterior distribution.

`psis_n_eff_values()` returns a vector of the estimated PSIS effective sample sizes.

`mcse_loo()` returns the Monte Carlo standard error (MCSE) estimate for PSIS-LOO. MCSE will be NA if any Pareto  $k$  values are above threshold.

The `plot()` method is called for its side effect and does not return anything. If `x` is the result of a call to `loo()` or `psis()` then `plot(x, diagnostic)` produces a plot of the estimates of the Pareto shape parameters (`diagnostic = "k"`) or estimates of the PSIS effective sample sizes (`diagnostic = "n_eff"`).

## References

- Vehtari, A., Gelman, A., and Gabry, J. (2017). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*. 27(5), 1413–1432. doi:10.1007/s11222-016-9696-4 ([journal version](#), [preprint arXiv:1507.04544](#)).
- Vehtari, A., Simpson, D., Gelman, A., Yao, Y., and Gabry, J. (2019). Pareto smoothed importance sampling. [preprint arXiv:1507.02646](#)

**See Also**

- [psis\(\)](#) for the implementation of the PSIS algorithm.
- The [FAQ page](#) on the **loo** website for answers to frequently asked questions.

print.loo

*Print methods***Description**

Print methods

**Usage**

```
## S3 method for class 'loo'
print(x, digits = 1, ...)

## S3 method for class 'waic'
print(x, digits = 1, ...)

## S3 method for class 'psis_loo'
print(x, digits = 1, plot_k = FALSE, ...)

## S3 method for class 'importance_sampling_loo'
print(x, digits = 1, plot_k = FALSE, ...)

## S3 method for class 'psis_loo_ap'
print(x, digits = 1, plot_k = FALSE, ...)

## S3 method for class 'psis'
print(x, digits = 1, plot_k = FALSE, ...)

## S3 method for class 'importance_sampling'
print(x, digits = 1, plot_k = FALSE, ...)
```

**Arguments**

x	An object returned by <a href="#">loo()</a> , <a href="#">psis()</a> , or <a href="#">waic()</a> .
digits	An integer passed to <code>base::round()</code> .
...	Arguments passed to <a href="#">plot.psis_loo()</a> if <code>plot_k</code> is TRUE.
plot_k	Logical. If TRUE the estimates of the Pareto shape parameter $k$ are plotted. Ignored if <code>x</code> was generated by <a href="#">waic()</a> . To just plot $k$ without printing use the <a href="#">plot()</a> method for 'loo' objects.

**Value**

x, invisibly.

**See Also**[pareto-k-diagnostic](#)

---

`psis`*Pareto smoothed importance sampling (PSIS)*

---

**Description**

Implementation of Pareto smoothed importance sampling (PSIS), a method for stabilizing importance ratios. The version of PSIS implemented here corresponds to the algorithm presented in Vehtari, Simpson, Gelman, Yao, and Gabry (2019). For PSIS diagnostics see the [pareto-k-diagnostic](#) page.

**Usage**

```
psis(log_ratios, ...)

## S3 method for class 'array'
psis(log_ratios, ..., r_eff = NULL, cores = getOption("mc.cores", 1))

## S3 method for class 'matrix'
psis(log_ratios, ..., r_eff = NULL, cores = getOption("mc.cores", 1))

## Default S3 method:
psis(log_ratios, ..., r_eff = NULL)

is.psis(x)

is.sis(x)

is.tis(x)
```

**Arguments**

<code>log_ratios</code>	An array, matrix, or vector of importance ratios on the log scale (for PSIS-LOO these are <i>negative</i> log-likelihood values). See the <b>Methods (by class)</b> section below for a detailed description of how to specify the inputs for each method.
<code>...</code>	Arguments passed on to the various methods.
<code>r_eff</code>	Vector of relative effective sample size estimates containing one element per observation. The values provided should be the relative effective sample sizes of $1/\exp(\text{log\_ratios})$ (i.e., $1/\text{ratios}$ ). This is related to the relative efficiency of estimating the normalizing term in self-normalizing importance sampling. If <code>r_eff</code> is not provided then the reported PSIS effective sample sizes and Monte Carlo error estimates will be over-optimistic. See the <a href="#">relative_eff()</a> helper function for computing <code>r_eff</code> . If using <code>psis</code> with draws of the <code>log_ratios</code> not obtained from MCMC then the warning message thrown when not specifying <code>r_eff</code> can be disabled by setting <code>r_eff</code> to NA.

cores	The number of cores to use for parallelization. This defaults to the option <code>mc.cores</code> which can be set for an entire R session by <code>options(mc.cores = NUMBER)</code> . The old option <code>loo.cores</code> is now deprecated but will be given precedence over <code>mc.cores</code> until <code>loo.cores</code> is removed in a future release. <b>As of version 2.0.0 the default is now 1 core if <code>mc.cores</code> is not set</b> , but we recommend using as many (or close to as many) cores as possible. <ul style="list-style-type: none"> <li>Note for Windows 10 users: it is <b>strongly recommended</b> to avoid using the <code>.Rprofile</code> file to set <code>mc.cores</code> (using the <code>cores</code> argument or setting <code>mc.cores</code> interactively or in a script is fine).</li> </ul>
x	For <code>is.psis()</code> , an object to check.

### Value

The `psis()` methods return an object of class "psis", which is a named list with the following components:

`log_weights` Vector or matrix of smoothed (and truncated) but *unnormalized* log weights. To get normalized weights use the `weights()` method provided for objects of class "psis".

`diagnostics` A named list containing two vectors:

- `pareto_k`: Estimates of the shape parameter  $k$  of the generalized Pareto distribution. See the [pareto-k-diagnostic](#) page for details.
- `n_eff`: PSIS effective sample size estimates.

Objects of class "psis" also have the following [attributes](#):

`norm_const_log` Vector of precomputed values of `colLogSumExps(log_weights)` that are used internally by the `weights` method to normalize the log weights.

`tail_len` Vector of tail lengths used for fitting the generalized Pareto distribution.

`r_eff` If specified, the user's `r_eff` argument.

`dims` Integer vector of length 2 containing  $S$  (posterior sample size) and  $N$  (number of observations).

`method` Method used for importance sampling, here `psis`.

### Methods (by class)

- `array`: An  $I$  by  $C$  by  $N$  array, where  $I$  is the number of MCMC iterations per chain,  $C$  is the number of chains, and  $N$  is the number of data points.
- `matrix`: An  $S$  by  $N$  matrix, where  $S$  is the size of the posterior sample (with all chains merged) and  $N$  is the number of data points.
- `default`: A vector of length  $S$  (posterior sample size).

### References

Vehtari, A., Gelman, A., and Gabry, J. (2017). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*. 27(5), 1413–1432. doi:10.1007/s11222-016-9696-4 ([journal version](#), [preprint arXiv:1507.04544](#)).

Vehtari, A., Simpson, D., Gelman, A., Yao, Y., and Gabry, J. (2019). Pareto smoothed importance sampling. [preprint arXiv:1507.02646](#)

**See Also**

- [loo\(\)](#) for approximate LOO-CV using PSIS.
- [pareto-k-diagnostic](#) for PSIS diagnostics.
- The **loo** package [vignettes](#) for demonstrations.
- The [FAQ page](#) on the **loo** website for answers to frequently asked questions.

**Examples**

```
log_ratios <- -1 * example_loglik_array()
r_eff <- relative_eff(exp(-log_ratios))
psis_result <- psis(log_ratios, r_eff = r_eff)
str(psis_result)
plot(psis_result)

# extract smoothed weights
lw <- weights(psis_result) # default args are log=TRUE, normalize=TRUE
ulw <- weights(psis_result, normalize=FALSE) # unnormalized log-weights

w <- weights(psis_result, log=FALSE) # normalized weights (not log-weights)
uw <- weights(psis_result, log=FALSE, normalize = FALSE) # unnormalized weights
```

---

psislw

*Pareto smoothed importance sampling (deprecated, old version)*


---

**Description**

As of version 2.0.0 this function is **deprecated**. Please use the [psis\(\)](#) function for the new PSIS algorithm.

**Usage**

```
psislw(
  lw,
  wcp = 0.2,
  wtrunc = 3/4,
  cores = getOption("mc.cores", 1),
  llfun = NULL,
  llargs = NULL,
  ...
)
```

**Arguments**

lw	A matrix or vector of log weights. For computing LOO, $lw = -\log\_lik$ , the <i>negative</i> of an $S$ (simulations) by $N$ (data points) pointwise log-likelihood matrix.
wcp	The proportion of importance weights to use for the generalized Pareto fit. The $100*wcp\%$ from which to estimate the parameters of the generalized Pareto distribution.
wtrunc	For truncating very large weights to $S^{wtrunc}$ . Set to zero for no truncation.
cores	The number of cores to use for parallelization. This defaults to the option <code>mc.cores</code> which can be set for an entire R session by <code>options(mc.cores = NUMBER)</code> , the old option <code>loo.cores</code> is now deprecated but will be given precedence over <code>mc.cores</code> until it is removed. <b>As of version 2.0.0, the default is now 1 core if <code>mc.cores</code> is not set, but we recommend using as many (or close to as many) cores as possible.</b>
llfun, llargs	See <code>loo.function()</code> .
...	Ignored when <code>psislw()</code> is called directly. The ... is only used internally when <code>psislw()</code> is called by the <code>loo()</code> function.

**Value**

A named list with components `lw_smooth` (modified log weights) and `pareto_k` (estimated generalized Pareto shape parameter(s)  $k$ ).

**References**

- Vehtari, A., Gelman, A., and Gabry, J. (2017). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*. 27(5), 1413–1432. doi:10.1007/s11222-016-9696-4 ([journal version](#), [preprint arXiv:1507.04544](#)).
- Vehtari, A., Simpson, D., Gelman, A., Yao, Y., and Gabry, J. (2019). Pareto smoothed importance sampling. [preprint arXiv:1507.02646](#)

**See Also**

[pareto-k-diagnostic](#) for PSIS diagnostics.

---

relative\_eff

*Convenience function for computing relative efficiencies*


---

**Description**

`relative_eff()` computes the the MCMC effective sample size divided by the total sample size.

**Usage**

```

relative_eff(x, ...)

## Default S3 method:
relative_eff(x, chain_id, ...)

## S3 method for class 'matrix'
relative_eff(x, chain_id, ..., cores = getOption("mc.cores", 1))

## S3 method for class 'array'
relative_eff(x, ..., cores = getOption("mc.cores", 1))

## S3 method for class '`function`'
relative_eff(
  x,
  chain_id,
  ...,
  cores = getOption("mc.cores", 1),
  data = NULL,
  draws = NULL
)

## S3 method for class 'importance_sampling'
relative_eff(x, ...)

```

**Arguments**

x	A vector, matrix, 3-D array, or function. See the <b>Methods (by class)</b> section below for details on specifying x, but where "log-likelihood" is mentioned replace it with one of the following depending on the use case: <ul style="list-style-type: none"> <li>• For use with the <code>loo()</code> function, the values in x (or generated by x, if a function) should be <b>likelihood</b> values (i.e., <math>\exp(\log\_lik)</math>), not on the log scale.</li> <li>• For generic use with <code>psis()</code>, the values in x should be the reciprocal of the importance ratios (i.e., <math>\exp(-\log\_ratios)</math>).</li> </ul>
chain_id	A vector of length <code>NROW(x)</code> containing MCMC chain indexes for each each row of x (if a matrix) or each value in x (if a vector). No <code>chain_id</code> is needed if x is a 3-D array. If there are C chains then valid chain indexes are values in 1:C.
cores	The number of cores to use for parallelization.
data, draws, ...	Same as for the <code>loo()</code> function method.

**Value**

A vector of relative effective sample sizes.



**Methods (by class)**

- **default**: A vector of length  $S$  (posterior sample size).
- **matrix**: An  $S$  by  $N$  matrix, where  $S$  is the size of the posterior sample (with all chains merged) and  $N$  is the number of data points.
- **array**: An  $I$  by  $C$  by  $N$  array, where  $I$  is the number of MCMC iterations per chain,  $C$  is the number of chains, and  $N$  is the number of data points.
- **function**: A function  $f()$  that takes arguments `data_i` and `draws` and returns a vector containing the log-likelihood for a single observation  $i$  evaluated at each posterior draw. The function should be written such that, for each observation  $i$  in  $1:N$ , evaluating

```
f(data_i = data[i, , drop=FALSE], draws = draws)
```

results in a vector of length  $S$  (size of posterior sample). The log-likelihood function can also have additional arguments but `data_i` and `draws` are required.

If using the function method then the arguments `data` and `draws` must also be specified in the call to `loo()`:

- **data**: A data frame or matrix containing the data (e.g. observed outcome and predictors) needed to compute the pointwise log-likelihood. For each observation  $i$ , the  $i$ th row of `data` will be passed to the `data_i` argument of the log-likelihood function.
  - **draws**: An object containing the posterior draws for any parameters needed to compute the pointwise log-likelihood. Unlike `data`, which is indexed by observation, for each observation the entire object `draws` will be passed to the `draws` argument of the log-likelihood function.
  - The `...` can be used if your log-likelihood function takes additional arguments. These arguments are used like the `draws` argument in that they are recycled for each observation.
- **importance\_sampling**: If  $x$  is an object of class "psis", `relative_eff()` simply returns the `r_eff` attribute of  $x$ .

**Examples**

```
LLarr <- example_loglik_array()
LLmat <- example_loglik_matrix()
dim(LLarr)
dim(LLmat)

rel_n_eff_1 <- relative_eff(exp(LLarr))
rel_n_eff_2 <- relative_eff(exp(LLmat), chain_id = rep(1:2, each = 500))
all.equal(rel_n_eff_1, rel_n_eff_2)
```

**Description**

Implementation of standard importance sampling (SIS).

**Usage**

```

sis(log_ratios, ...)

## S3 method for class 'array'
sis(log_ratios, ..., r_eff = NULL, cores = getOption("mc.cores", 1))

## S3 method for class 'matrix'
sis(log_ratios, ..., r_eff = NULL, cores = getOption("mc.cores", 1))

## Default S3 method:
sis(log_ratios, ..., r_eff = NULL)

```

**Arguments**

log_ratios	An array, matrix, or vector of importance ratios on the log scale (for Importance sampling LOO, these are <i>negative</i> log-likelihood values). See the <b>Methods (by class)</b> section below for a detailed description of how to specify the inputs for each method.
...	Arguments passed on to the various methods.
r_eff	Vector of relative effective sample size estimates containing one element per observation. The values provided should be the relative effective sample sizes of $1/\exp(\log\_ratios)$ (i.e., $1/ratios$ ). This is related to the relative efficiency of estimating the normalizing term in self-normalizing importance sampling. See the <a href="#">relative_eff()</a> helper function for computing r_eff. If using psis with draws of the log_ratios not obtained from MCMC then the warning message thrown when not specifying r_eff can be disabled by setting r_eff to NA.
cores	The number of cores to use for parallelization. This defaults to the option mc.cores which can be set for an entire R session by options(mc.cores = NUMBER). The old option loo.cores is now deprecated but will be given precedence over mc.cores until loo.cores is removed in a future release. <b>As of version 2.0.0 the default is now 1 core if mc.cores is not set</b> , but we recommend using as many (or close to as many) cores as possible. <ul style="list-style-type: none"> <li>Note for Windows 10 users: it is <b>strongly recommended</b> to avoid using the .Rprofile file to set mc.cores (using the cores argument or setting mc.cores interactively or in a script is fine).</li> </ul>

**Value**

The `sis()` methods return an object of class "sis", which is a named list with the following components:

log_weights	Vector or matrix of smoothed but <i>unnormalized</i> log weights. To get normalized weights use the <a href="#">weights()</a> method provided for objects of class sis.
diagnostics	A named list containing one vector: <ul style="list-style-type: none"> <li>pareto_k: Not used in sis, all set to 0.</li> <li>n_eff: effective sample size estimates.</li> </ul>

Objects of class "sis" also have the following [attributes](#):

`norm_const_log` Vector of precomputed values of `colLogSumExps(log_weights)` that are used internally by the `weights` method to normalize the log weights.

`r_eff` If specified, the user's `r_eff` argument.

`tail_len` Not used for `sis`.

`dims` Integer vector of length 2 containing `S` (posterior sample size) and `N` (number of observations).

`method` Method used for importance sampling, here `sis`.

### Methods (by class)

- `array`: An  $I$  by  $C$  by  $N$  array, where  $I$  is the number of MCMC iterations per chain,  $C$  is the number of chains, and  $N$  is the number of data points.
- `matrix`: An  $S$  by  $N$  matrix, where  $S$  is the size of the posterior sample (with all chains merged) and  $N$  is the number of data points.
- `default`: A vector of length  $S$  (posterior sample size).

### References

Vehtari, A., Gelman, A., and Gabry, J. (2017). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*. 27(5), 1413–1432. doi:10.1007/s11222-016-9696-4 ([journal version](#), [preprint arXiv:1507.04544](#)).

Vehtari, A., Simpson, D., Gelman, A., Yao, Y., and Gabry, J. (2019). Pareto smoothed importance sampling. [preprint arXiv:1507.02646](#)

### See Also

- [psis\(\)](#) for approximate LOO-CV using PSIS.
- [loo\(\)](#) for approximate LOO-CV.
- [pareto-k-diagnostic](#) for PSIS diagnostics.

### Examples

```
log_ratios <- -1 * example_loglik_array()
r_eff <- relative_eff(exp(-log_ratios))
sis_result <- sis(log_ratios, r_eff = r_eff)
str(sis_result)

# extract smoothed weights
lw <- weights(sis_result) # default args are log=TRUE, normalize=TRUE
ulw <- weights(sis_result, normalize=FALSE) # unnormalized log-weights

w <- weights(sis_result, log=FALSE) # normalized weights (not log-weights)
uw <- weights(sis_result, log=FALSE, normalize = FALSE) # unnormalized weights
```

tis

*Truncated importance sampling (TIS)***Description**

Implementation of truncated (self-normalized) importance sampling (TIS), truncated at  $S^{1/2}$  as recommended by Ionides (2008).

**Usage**

```
tis(log_ratios, ...)

## S3 method for class 'array'
tis(log_ratios, ..., r_eff = NULL, cores = getOption("mc.cores", 1))

## S3 method for class 'matrix'
tis(log_ratios, ..., r_eff = NULL, cores = getOption("mc.cores", 1))

## Default S3 method:
tis(log_ratios, ..., r_eff = NULL)
```

**Arguments**

log_ratios	An array, matrix, or vector of importance ratios on the log scale (for Importance sampling LOO, these are <i>negative</i> log-likelihood values). See the <b>Methods (by class)</b> section below for a detailed description of how to specify the inputs for each method.
...	Arguments passed on to the various methods.
r_eff	Vector of relative effective sample size estimates containing one element per observation. The values provided should be the relative effective sample sizes of $1/\exp(\log\_ratios)$ (i.e., $1/ratios$ ). This is related to the relative efficiency of estimating the normalizing term in self-normalizing importance sampling. See the <code>relative_eff()</code> helper function for computing <code>r_eff</code> . If using <code>psis</code> with draws of the <code>log_ratios</code> not obtained from MCMC then the warning message thrown when not specifying <code>r_eff</code> can be disabled by setting <code>r_eff</code> to NA.
cores	The number of cores to use for parallelization. This defaults to the option <code>mc.cores</code> which can be set for an entire R session by <code>options(mc.cores = NUMBER)</code> . The old option <code>loo.cores</code> is now deprecated but will be given precedence over <code>mc.cores</code> until <code>loo.cores</code> is removed in a future release. <b>As of version 2.0.0 the default is now 1 core if <code>mc.cores</code> is not set</b> , but we recommend using as many (or close to as many) cores as possible. <ul style="list-style-type: none"> <li>Note for Windows 10 users: it is <b>strongly recommended</b> to avoid using the <code>.Rprofile</code> file to set <code>mc.cores</code> (using the <code>cores</code> argument or setting <code>mc.cores</code> interactively or in a script is fine).</li> </ul>

**Value**

The `tis()` methods return an object of class "tis", which is a named list with the following components:

`log_weights` Vector or matrix of smoothed (and truncated) but *unnormalized* log weights. To get normalized weights use the `weights()` method provided for objects of class `tis`.

`diagnostics` A named list containing one vector:

- `pareto_k`: Not used in `tis`, all set to 0.
- `n_eff`: Effective sample size estimates.

Objects of class "tis" also have the following **attributes**:

`norm_const_log` Vector of precomputed values of `colLogSumExps(log_weights)` that are used internally by the `weights()` method to normalize the log weights.

`r_eff` If specified, the user's `r_eff` argument.

`tail_len` Not used for `tis`.

`dims` Integer vector of length 2 containing  $S$  (posterior sample size) and  $N$  (number of observations).

`method` Method used for importance sampling, here `tis`.

**Methods (by class)**

- `array`: An  $I$  by  $C$  by  $N$  array, where  $I$  is the number of MCMC iterations per chain,  $C$  is the number of chains, and  $N$  is the number of data points.
- `matrix`: An  $S$  by  $N$  matrix, where  $S$  is the size of the posterior sample (with all chains merged) and  $N$  is the number of data points.
- `default`: A vector of length  $S$  (posterior sample size).

**References**

Ionides, Edward L. (2008). Truncated importance sampling. *Journal of Computational and Graphical Statistics* 17(2): 295–311.

**See Also**

- `psis()` for approximate LOO-CV using PSIS.
- `loo()` for approximate LOO-CV.
- `pareto-k-diagnostic` for PSIS diagnostics.

**Examples**

```
log_ratios <- -1 * example_loglik_array()
r_eff <- relative_eff(exp(-log_ratios))
tis_result <- tis(log_ratios, r_eff = r_eff)
str(tis_result)

# extract smoothed weights
lw <- weights(tis_result) # default args are log=TRUE, normalize=TRUE
```

```

ulw <- weights(tis_result, normalize=FALSE) # unnormalized log-weights

w <- weights(tis_result, log=FALSE) # normalized weights (not log-weights)
uw <- weights(tis_result, log=FALSE, normalize = FALSE) # unnormalized weights

```

---

update.psis\_loo\_ss      *Update psis\_loo\_ss objects*

---

## Description

Update psis\_loo\_ss objects

## Usage

```

## S3 method for class 'psis_loo_ss'
update(
  object,
  ...,
  data = NULL,
  draws = NULL,
  observations = NULL,
  r_eff = NULL,
  cores = getOption("mc.cores", 1),
  loo_approximation = NULL,
  loo_approximation_draws = NULL,
  llgrad = NULL,
  llhess = NULL
)

```

## Arguments

object	A psis_loo_ss object to update.
...	Currently not used.
data	For loo_subsample.function(), these are the data, posterior draws, and other arguments to pass to the log-likelihood function. Note that for some loo_approximations, the draws will be replaced by the posteriors summary statistics to compute loo approximations. See argument loo_approximation for details.
draws	For loo_subsample.function(), these are the data, posterior draws, and other arguments to pass to the log-likelihood function. Note that for some loo_approximations, the draws will be replaced by the posteriors summary statistics to compute loo approximations. See argument loo_approximation for details.
observations	The subsample observations to use. The argument can take four (4) types of arguments: <ul style="list-style-type: none"> <li>• NULL to use all observations. The algorithm then just uses standard loo() or loo_approximate_posterior().</li> </ul>

- A single integer to specify the number of observations to be subsampled.
  - A vector of integers to provide the indices used to subset the data. *These observations need to be subsampled with the same scheme as given by the estimator argument.*
  - A psis\_loo\_ss object to use the same observations that were used in a previous call to loo\_subsample().
- r\_eff** Vector of relative effective sample size estimates for the likelihood ( $\exp(\log\_lik)$ ) of each observation. This is related to the relative efficiency of estimating the normalizing term in self-normalizing importance sampling when using posterior draws obtained with MCMC. If MCMC draws are used and r\_eff is not provided then the reported PSIS effective sample sizes and Monte Carlo error estimates will be over-optimistic. If the posterior draws are independent then r\_eff=1 and can be omitted. The warning message thrown when r\_eff is not specified can be disabled by setting r\_eff to NA. See the [relative\\_eff\(\)](#) helper functions for computing r\_eff.
- cores** The number of cores to use for parallelization. This defaults to the option mc.cores which can be set for an entire R session by options(mc.cores = NUMBER). The old option loo.cores is now deprecated but will be given precedence over mc.cores until loo.cores is removed in a future release. **As of version 2.0.0 the default is now 1 core if mc.cores is not set**, but we recommend using as many (or close to as many) cores as possible.
- Note for Windows 10 users: it is **strongly recommended** to avoid using the .Rprofile file to set mc.cores (using the cores argument or setting mc.cores interactively or in a script is fine).
- loo\_approximation** What type of approximation of the loo\_i's should be used? The default is "plpd" (the log predictive density using the posterior expectation). There are six different methods implemented to approximate loo\_i's (see the references for more details):
- "plpd": uses the lpd based on point estimates (i.e.,  $p(y_i|\hat{\theta})$ ).
  - "lpd": uses the lpds (i.e.,  $p(y_i|y)$ ).
  - "tis": uses truncated importance sampling to approximate PSIS-LOO.
  - "waic": uses waic (i.e.,  $p(y_i|y) - p_{waic}$ ).
  - "waic\_grad\_marginal": uses waic approximation using first order delta method and posterior marginal variances to approximate  $p_{waic}$  (ie.  $p(y_i|\hat{\theta})$ -p\_waic\_grad\_marginal). Requires gradient of likelihood function.
  - "waic\_grad": uses waic approximation using first order delta method and posterior covariance to approximate  $p_{waic}$  (ie.  $p(y_i|\hat{\theta})$ -p\_waic\_grad). Requires gradient of likelihood function.
  - "waic\_hess": uses waic approximation using second order delta method and posterior covariance to approximate  $p_{waic}$  (ie.  $p(y_i|\hat{\theta})$ -p\_waic\_grad). Requires gradient and Hessian of likelihood function.
- As point estimates of  $\hat{\theta}$ , the posterior expectations of the parameters are used.
- loo\_approximation\_draws** The number of posterior draws used when integrating over the posterior. This is used if loo\_approximation is set to "lpd", "waic", or "tis".

llgrad	The gradient of the log-likelihood. This is only used when <code>loo_approximation</code> is "waic_grad", "waic_grad_marginal", or "waic_hess". The default is NULL.
llhess	The hessian of the log-likelihood. This is only used with <code>loo_approximation = "waic_hess"</code> . The default is NULL.

### Details

If `observations` is updated then if a vector of indices or a `psis_loo_ss` object is supplied the updated object will have exactly the observations indicated by the vector or `psis_loo_ss` object. If a single integer is supplied, new observations will be sampled to reach the supplied sample size.

### Value

A `psis_loo_ss` object.

---

waic	<i>Widely applicable information criterion (WAIC)</i>
------	---

---

### Description

The `waic()` methods can be used to compute WAIC from the pointwise log-likelihood. However, we recommend LOO-CV using PSIS (as implemented by the `loo()` function) because PSIS provides useful diagnostics as well as effective sample size and Monte Carlo estimates.

### Usage

```
waic(x, ...)

## S3 method for class 'array'
waic(x, ...)

## S3 method for class 'matrix'
waic(x, ...)

## S3 method for class '`function`'
waic(x, ..., data = NULL, draws = NULL)

is.waic(x)
```

### Arguments

`x` A log-likelihood array, matrix, or function. The **Methods (by class)** section, below, has detailed descriptions of how to specify the inputs for each method.

`draws, data, ...` For the function method only. See the **Methods (by class)** section below for details on these arguments.



**Value**

A named list (of class `c("waic", "loo")`) with components:

`estimates` A matrix with two columns ("Estimate", "SE") and three rows ("elpd\_waic", "p\_waic", "waic"). This contains point estimates and standard errors of the expected log pointwise predictive density (elpd\_waic), the effective number of parameters (p\_waic) and the information criterion waic (which is just  $-2 * \text{elpd\_waic}$ , i.e., converted to deviance scale).

`pointwise` A matrix with three columns (and number of rows equal to the number of observations) containing the pointwise contributions of each of the above measures (elpd\_waic, p\_waic, waic).

**Methods (by class)**

- `array`: An  $I$  by  $C$  by  $N$  array, where  $I$  is the number of MCMC iterations per chain,  $C$  is the number of chains, and  $N$  is the number of data points.
- `matrix`: An  $S$  by  $N$  matrix, where  $S$  is the size of the posterior sample (with all chains merged) and  $N$  is the number of data points.
- `function`: A function `f()` that takes arguments `data_i` and `draws` and returns a vector containing the log-likelihood for a single observation  $i$  evaluated at each posterior draw. The function should be written such that, for each observation  $i$  in  $1:N$ , evaluating

```
f(data_i = data[i,, drop=FALSE], draws = draws)
```

results in a vector of length  $S$  (size of posterior sample). The log-likelihood function can also have additional arguments but `data_i` and `draws` are required.

If using the function method then the arguments `data` and `draws` must also be specified in the call to `loo()`:

- `data`: A data frame or matrix containing the data (e.g. observed outcome and predictors) needed to compute the pointwise log-likelihood. For each observation  $i$ , the  $i$ th row of `data` will be passed to the `data_i` argument of the log-likelihood function.
- `draws`: An object containing the posterior draws for any parameters needed to compute the pointwise log-likelihood. Unlike `data`, which is indexed by observation, for each observation the entire object `draws` will be passed to the `draws` argument of the log-likelihood function.
- The `...` can be used if your log-likelihood function takes additional arguments. These arguments are used like the `draws` argument in that they are recycled for each observation.

**References**

- Watanabe, S. (2010). Asymptotic equivalence of Bayes cross validation and widely application information criterion in singular learning theory. *Journal of Machine Learning Research* **11**, 3571-3594.
- Vehtari, A., Gelman, A., and Gabry, J. (2017). Practical Bayesian model evaluation using leave-one-out cross-validation and WAIC. *Statistics and Computing*. 27(5), 1413–1432. doi:10.1007/s11222-016-9696-4 ([journal version](#), [preprint arXiv:1507.04544](#)).
- Vehtari, A., Simpson, D., Gelman, A., Yao, Y., and Gabry, J. (2019). Pareto smoothed importance sampling. [preprint arXiv:1507.02646](#)

**See Also**

- The **loo** package [vignettes](#) and Vehtari, Gelman, and Gabry (2017) and Vehtari, Simpson, Gelman, Yao, and Gabry (2019) for more details on why we prefer loo() to waic().
- [loo\\_compare\(\)](#) for comparing models on approximate LOO-CV or WAIC.

**Examples**

```
### Array and matrix methods
LLarr <- example_loglik_array()
dim(LLarr)

LLmat <- example_loglik_matrix()
dim(LLmat)

waic_arr <- waic(LLarr)
waic_mat <- waic(LLmat)
identical(waic_arr, waic_mat)

## Not run:
log_lik1 <- extract_log_lik(stanfit1)
log_lik2 <- extract_log_lik(stanfit2)
(waic1 <- waic(log_lik1))
(waic2 <- waic(log_lik2))
print(compare(waic1, waic2), digits = 2)

## End(Not run)
```

---

```
weights.importance_sampling
```

```
Extract importance sampling weights
```

---

**Description**

Extract importance sampling weights

**Usage**

```
## S3 method for class 'importance_sampling'
weights(object, ..., log = TRUE, normalize = TRUE)
```

**Arguments**

object	An object returned by <a href="#">psis()</a> , <a href="#">tis()</a> , or <a href="#">sis()</a> .
...	Ignored.
log	Should the weights be returned on the log scale? Defaults to TRUE.
normalize	Should the weights be normalized? Defaults to TRUE.

**Value**

The `weights()` method returns an object with the same dimensions as the `log_weights` component of object. The `normalize` and `log` arguments control whether the returned weights are normalized and whether or not to return them on the log scale.

**Examples**

```
# See the examples at help("psis")
```

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