

# Package ‘baggr’

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**Type** Package

**Title** Bayesian Aggregate Treatment Effects

**Version** 0.6.21

**Maintainer** Witold Wiecek <witold.wiecek@gmail.com>

**Description** Running and comparing meta-analyses of data with hierarchical Bayesian models in Stan, including convenience functions for formatting data, plotting and pooling measures specific to meta-analysis. This implements many models from Meager (2019) <[doi:10.1257/app.20170299](https://doi.org/10.1257/app.20170299)>.

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**Author** Witold Wiecek [cre, aut],  
Rachael Meager [aut],  
Brice Green [ctb] (predict(), loo\_compare, many visuals),  
Trustees of Columbia University [cph] (tools/make\_cc.R)

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baggr-package	<i>baggr - a package for Bayesian meta-analysis</i>
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## Description

This is *baggr* (pronounced as *bagger* or *badger*), a Bayesian meta-analysis package for R that uses **Stan** to fit the models. *Baggr* is intended to be user-friendly and transparent so that it's easier to understand the models you are building and criticise them.

## Details

*Baggr* package provides a suite of models that work with both summary data and full data sets, to synthesise evidence collected from different groups, contexts or time periods. The `baggr` command automatically detects the data type and, by default, fits a partial pooling model (which you may know as **random effects models**) with weakly informative priors by calling **Stan** to carry out Bayesian inference. Modelling of variances or quantiles, standardisation and transformation of data are also possible.

## Getting help

This is only a simple package help file. For documentation of the main function for conducting analyses see `baggr`. For description of models, data types and priors available in the package, try the built-in vignette (`vignette("baggr")`).

## References

Stan Development Team (2020). RStan: the R interface to Stan. R package version 2.21.2. <https://mc-stan.org>

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 baggr

*Bayesian aggregate treatment effects model*


---

## Description

Bayesian inference on parameters of an average treatment effects model that's appropriate to the supplied individual- or group-level data, using Hamiltonian Monte Carlo in Stan. (For overall package help file see [baggr-package](#))

## Usage

```
baggr(
  data,
  model = NULL,
  pooling = c("partial", "none", "full"),
  effect = NULL,
  covariates = c(),
  prior_hypermean = NULL,
  prior_hypersd = NULL,
  prior_hypercor = NULL,
  prior_beta = NULL,
  prior_control = NULL,
  prior_control_sd = NULL,
  prior_sigma = NULL,
  prior = NULL,
  ppd = FALSE,
  pooling_control = c("none", "partial"),
  test_data = NULL,
  quantiles = seq(0.05, 0.95, 0.1),
  outcome = "outcome",
  group = "group",
  treatment = "treatment",
  silent = FALSE,
  warn = TRUE,
  ...
)
```

## Arguments

data	data frame with summary or individual level data to meta-analyse; see Details section for how to format your data
model	if NULL, detected automatically from input data otherwise choose from "rubin", "mutau", "rubin_full", "quantiles" (see Details).
pooling	Type of pooling; choose from "none", "partial" (default) and "full". If you are not familiar with the terms, consult the vignette; "partial" can be understood as random effects and "full" as fixed effects

effect	Label for effect. Will default to "mean" in most cases, "log OR" in logistic model, quantiles in quantiles model etc. These labels are used in various print and plot outputs. Comparable models (e.g. in <a href="#">baggr_compare</a> ) should have same effect.
covariates	Character vector with column names in data. The corresponding columns are used as covariates (fixed effects) in the meta-regression model (in case of aggregate data). In the case of individual level data the model does not differentiate between group-level variables (same values of the covariate for all rows related to a given group) and individual-level covariates.
prior_hypermean	prior distribution for hypermean; you can use "plain text" notation like <code>prior_hypermean=normal(0, 100)</code> or <code>uniform(-10, 10)</code> . See <i>Details:Priors</i> section below for more possible specifications. If unspecified, the priors will be derived automatically based on data (and printed out in the console).
prior_hypersd	prior for hyper-standard deviation, used by Rubin and "mutau" models; same rules apply as for <code>_hypermean</code> ;
prior_hypercor	prior for hypercorrelation matrix, used by the "mutau" model
prior_beta	prior for regression coefficients if <code>covariates</code> are specified; will default to experimental <code>normal(0, 10^2)</code> distribution
prior_control	prior for the mean in the control arm (baseline), currently used in "logit" model only; if <code>pooling_control = "partial"</code> , the prior is hyperprior for all baselines, if "none", then it is an independent prior for all baselines
prior_control_sd	prior for the SD in the control arm (baseline), currently used in "logit" model only; this can only be used if <code>pooling_control = "partial"</code>
prior_sigma	prior for error terms in linear regression models ("rubin_full" or "mutau_full")
prior	alternative way to specify all priors as a named list with <code>hypermean</code> , <code>hypersd</code> , <code>hypercor</code> , <code>beta</code> , analogous to <code>prior_</code> arguments above, e.g. <code>prior = list(hypermean = normal(0, 10), beta = uniform(-50, 50))</code>
ppd	logical; use prior predictive distribution? ( <i>p.p.d.</i> ) If <code>ppd=TRUE</code> , Stan model will sample from the prior distribution(s) and ignore data in inference. However, <code>data</code> argument might still be used to infer the correct model (if <code>model=NULL</code> ) and to set the default priors, therefore you must specify it.
pooling_control	Pooling for group-specific control mean terms in models using individual-level data. Either "none" or "partial".
test_data	data for cross-validation; NULL for no validation, otherwise a data frame with the same columns as <code>data</code> argument. See "Cross-validation" section below.
quantiles	if <code>model = "quantiles"</code> , a vector indicating which quantiles of data to use (with values between 0 and 1)
outcome	character; column name in (individual-level) data with outcome variable values
group	character; column name in data with grouping factor; it's necessary for individual-level data, for summarised data it will be used as labels for groups when displaying results

treatment	character; column name in (individual-level) data with treatment factor;
silent	Whether to silence messages about prior settings and about other automatic behaviour.
warn	print an additional warning if Rhat exceeds 1.05
...	extra options passed to Stan function, e.g. <code>control = list(adapt_delta = 0.99)</code> , number of iterations etc.

## Details

Below we briefly discuss 1/ data preparation, 2/ choice of model, 3/ choice of priors. All three are discussed in more depth in the package vignette, `vignette("baggr")`.

**Data.** For aggregate data models you need a data frame with columns `tau` and `se` (Rubin model) or `tau`, `mu`, `se.tau`, `se.mu` ("mu & tau" model). An additional column can be used to provide labels for each group (by default column `group` is used if available, but this can be customised – see the example below). For individual level data three columns are needed: `outcome`, `treatment`, `group`. These are identified by using the `outcome`, `treatment` and `group` arguments.

Many data preparation steps can be done through a helper function `prepare_ma`. It can convert individual to summary-level data, calculate odds/risk ratios (with/without corrections) in binary data, standardise variables and more. Using it will automatically format data inputs to work with `baggr()`.

**Models.** Available models are:

- for the **continuous variable** means: "rubin" model for average treatment effect (using summary data), "mutau" version which takes into account means of control groups (also using summary data), "rubin\_full", which is the same model as "rubin" but works with individual-level data
- for **continuous variable quantiles**: "quantiles" model (see Meager, 2019 in references)
- for *mixture data*: "sslabs" (experimental)
- for **binary data**: "logit" model can be used on individual-level data; you can also analyse continuous statistics such as log odds ratios and logs risk ratios using the models listed above; see `vignette("baggr_binary")` for tutorial with examples

If no model is specified, the function tries to infer the appropriate model automatically. Additionally, the user must specify type of pooling. The default is always partial pooling.

**Covariates.** Both aggregate and individual-level data can include extra columns, given by `covariates` argument (specified as a character vector of column names) to be used in regression models. We also refer to impact of these covariates as *fixed effects*.

Two types of covariates may be present in your data:

- In "rubin" and "mutau" models, covariates that **change according to group unit**. In that case, the model accounting for the group covariates is a **meta-regression** model. It can be modelled on summary-level data.
- In "logit" and "rubin\_full" models, covariates that **change according to individual unit**. Then, such a model is commonly referred to as a **mixed model**. It has to be fitted to individual-level data. Note that meta-regression is a special case of a mixed model for individual-level data.

**Priors.** It is optional to specify priors yourself, as the package will try propose an appropriate prior for the input data if you do not pass a prior argument. To set the priors yourself, use `prior_` arguments. For specifying many priors at once (or re-using between models), a single `prior = list(...)` argument can be used instead. Meaning of the prior parameters may slightly change from model to model. Details and examples are given in `vignette("baggr")`. Setting `ppd=TRUE` can be used to obtain prior predictive distributions, which is useful for understanding the prior assumptions, especially useful in conjunction with `effect_plot`. You can also `baggr_compare` different priors by setting `baggr_compare(..., compare="prior")`.

**Cross-validation.** When `test_data` are specified, an extra parameter, the log predictive density, will be returned by the model. (The fitted model itself is the same regardless of whether there are `test_data`.) To understand this parameter, see documentation of `loocv`, a function that can be used to assess out of sample prediction of the model using all available data. If using individual-level data model, `test_data` should only include treatment arms of the groups of interest. (This is because in cross-validation we are not typically interested in the model's ability to fit heterogeneity in control arms, but only heterogeneity in treatment arms.) For using aggregate level data, there is no such restriction.

**Outputs.** By default, some outputs are printed. There is also a plot method for `baggr` objects which you can access via `baggr_plot` (or simply `plot()`). Other standard functions for working with `baggr` object are

- `treatment_effect` for distribution of hyperparameters
- `group_effects` for distributions of group-specific parameters
- `fixed_effects` for coefficients in (meta-)regression
- `effect_draw` and `effect_plot` for posterior predictive distributions
- `baggr_compare` for comparing multiple `baggr` models
- `loocv` for cross-validation
- `pp_check` for posterior predictive checks

## Value

`baggr` class structure: a list including Stan model fit alongside input data, pooling metrics, various model properties. If test data is used, mean value of  $-2 \times \text{lpd}$  is reported as `mean_lpd`

## Author(s)

Witold Wiecek, Rachael Meager

## Examples

```
df_pooled <- data.frame("tau" = c(1, -1, .5, -.5, .7, -.7, 1.3, -1.3),
                        "se" = rep(1, 8),
                        "state" = datasets::state.name[1:8])
baggr(df_pooled) #baggr automatically detects the input data
# same model, but with correct labels,
# different pooling & passing some options to Stan
baggr(df_pooled, group = "state", pooling = "full", iter = 500)
# model with non-default (and very informative) priors
```

```

baggr(df_pooled, prior_hypersd = normal(0, 2))

# "mu & tau" model, using a built-in dataset
# prepare_ma() can summarise individual-level data
ms <- microcredit_simplified
microcredit_summary_data <- prepare_ma(ms, outcome = "consumption")
baggr(microcredit_summary_data, model = "mutau",
      iter = 500, #this is just for illustration -- don't set it this low normally!
      pooling = "partial", prior_hypercor = lkj(1),
      prior_hypersd = normal(0,10),
      prior_hypermean = multinormal(c(0,0),matrix(c(10,3,3,10),2,2)))

```

---

baggr\_compare

*(Run and) compare multiple baggr models*


---

## Description

Compare multiple [baggr](#) models by either providing multiple already existing models as (named) arguments or passing parameters necessary to run a [baggr](#) model.

## Usage

```

baggr_compare(
  ...,
  what = "pooling",
  compare = c("groups", "hyperpars", "effects"),
  transform = NULL,
  prob = 0.95,
  plot = FALSE
)

```

## Arguments

...	Either some (at least 1) objects of class <code>baggr</code> (you should name your objects, see the example below) or the same arguments you'd pass to <a href="#">baggr</a> . In the latter case you must specify what to compare.
what	One of "pooling" (comparison between no, partial and full pooling) or "prior" (comparison between prior and posterior predictive). If pre-existing <code>baggr</code> models are passed to ..., this argument is ignored.
compare	When plotting, choose between comparison of "groups" (default), "hyperpars" (to omit group-specific estimates) or (predicted) "effects". The "groups" option is not available when what = "prior".



transform	a function (e.g. <code>exp()</code> , <code>log()</code> ) to apply to the the sample of group (and hyper, if <code>hyper=TRUE</code> ) effects before plotting; when working with effects that are on log scale, exponent transform is used automatically, you can plot on log scale by setting <code>transform = identity</code>
prob	Width of uncertainty interval (defaults to 95%)
plot	logical; calls <a href="#">plot.baggr_compare</a> when running <code>baggr_compare</code>

### Details

If you pass parameters to the function you must specify what kind of comparison you want, either "pooling", which will run fully/partially/un-pooled models and then compare them, or "prior" which will generate estimates without the data and compare them to the model with the full data. For more details see [baggr](#), specifically the `ppd` argument.

### Value

an object of class `baggr_compare`

### Author(s)

Witold Wiecek, Brice Green

### See Also

[plot.baggr\\_compare](#) and [print.baggr\\_compare](#) for working with results of this function

### Examples

```
# Most basic comparison between no, partial and full pooling
# (This will run the models)
# run model with just prior and then full data for comparison
# with the same arguments that are passed to baggr
prior_comparison <-
  baggr_compare(schools,
                model = 'rubin',
                #this is just for illustration -- don't set it this low normally!
                iter = 500,
                prior_hypermean = normal(0, 3),
                prior_hypersd = normal(0,2),
                prior_hypercor = lkj(2),
                what = "prior")
# print the aggregated treatment effects
prior_comparison
# plot the comparison of the two distributions
plot(prior_comparison)
# Now compare different types of pooling for the same model
pooling_comparison <-
  baggr_compare(schools,
                model = 'rubin',
                #this is just for illustration -- don't set it this low normally!
```

```

        iter = 500,
        prior_hypermean = normal(0, 3),
        prior_hypersd = normal(0,2),
        prior_hypercor = lkj(2),
        what = "pooling",
        # You can automatically plot:
        plot = TRUE)
# Compare existing models (you don't have to, but best to name them):
bg1 <- baggr(schools, pooling = "partial")
bg2 <- baggr(schools, pooling = "full")
baggr_compare("Partial pooling model" = bg1, "Full pooling" = bg2)

#' ...or simply draw from prior predictive dist (note ppd=T)
bg1 <- baggr(schools, ppd=TRUE)
bg2 <- baggr(schools, prior_hypermean = normal(0, 5), ppd=TRUE)
baggr_compare("Prior A, p.p.d."=bg1,
              "Prior B p.p.d."=bg2,
              compare = "effects")

# Compare how posterior predictive effect varies with e.g. choice of prior
bg1 <- baggr(schools, prior_hypersd = uniform(0, 20))
bg2 <- baggr(schools, prior_hypersd = normal(0, 5))
baggr_compare("Uniform prior on SD"=bg1,
              "Normal prior on SD"=bg2,
              compare = "effects", plot = TRUE)

# Models don't have to be identical. Compare different subsets of input data:
bg1_small <- baggr(schools[1:6,], pooling = "partial")
baggr_compare("8 schools model" = bg1, "First 6 schools" = bg1_small,
              plot = TRUE)

```

---

baggr\_plot

*Plotting method in baggr package*


---

## Description

Extracts study effects from the baggr model and sends them to one of bayesplot package plotting functions.

## Usage

```

baggr_plot(
  bg,
  hyper = FALSE,
  style = "intervals",
  transform = NULL,
  prob = 0.5,
  prob_outer = 0.95,

```

```

    vline = FALSE,
    order = TRUE,
    ...
  )

```

### Arguments

bg	object of class baggr
hyper	logical; show hypereffect as the last row of the plot?
style	either "intervals" or "areas"
transform	a function (e.g. <code>exp()</code> , <code>log()</code> ) to apply to the values of group (and hyper, if <code>hyper=TRUE</code> ) effects before plotting; when working with effects that are on log scale, exponent transform is used automatically, you can plot on log scale by setting <code>transform = identity</code>
prob	Probability mass for the inner interval in visualisation
prob_outer	Probability mass for the outer interval in visualisation
vline	logical; show vertical line through 0 in the plot?
order	logical; sort groups by magnitude of treatment effect?
...	extra arguments to pass to the <code>bayesplot</code> functions

### Value

ggplot2 object

### Author(s)

Witold Wiecek; the visual style is based on *bayesplot* package

### See Also

[bayesplot::MCMC-intervals](#) for more information about *bayesplot* functionality; [forest\\_plot](#) for a typical meta-analysis alternative; [effect\\_plot](#) for plotting treatment effects for a new group

### Examples

```

fit <- baggr(schools, pooling = "none")
plot(fit)
plot(fit, style = "areas", order = FALSE)

```

---

baggr_theme_set	<i>Set, get, and replace themes for baggr plots</i>
-----------------	---

---

### Description

These functions get, set, and modify the ggplot2 themes of the baggr plots. `baggr_theme_get()` returns a ggplot2 theme function for adding themes to a plot. `baggr_theme_set()` assigns a new theme for all plots of baggr objects. `baggr_theme_update()` edits a specific theme element for the current theme while holding the theme's other aspects constant. `baggr_theme_replace()` is used for wholesale replacing aspects of a plot's theme (see [ggplot2::theme\\_get\(\)](#)).

### Usage

```
baggr_theme_set(new = bayesplot::theme_default())  
  
baggr_theme_get()  
  
baggr_theme_update(...)  
  
baggr_theme_replace(...)
```

### Arguments

<code>new</code>	New theme to use for all baggr plots
<code>...</code>	A named list of theme settings

### Details

Under the hood, many of the visualizations rely on the bayesplot package, and thus these leverage the `bayesplot::bayesplot_theme_get()` functions. By default, these match the bayesplot's package theme to make it easier to form cohesive graphs across this package and others. The trickiest of these to use is `baggr_theme_replace`; 9 times out of 10 you want `baggr_theme_update`.

### Value

The get method returns the current theme, but all of the others invisibly return the old theme.

### See Also

[bayesplot::bayesplot\\_theme\\_get](#)

### Examples

```
# make plot look like default ggplots  
  
library(ggplot2)
```

```

fit <- baggr(schools)
baggr_theme_set(theme_grey())
baggr_plot(fit)

# use baggr_theme_get to return theme elements for current theme
qplot(mtcars$mpg) + baggr_theme_get()

# update specific aspect of theme you are interested in
baggr_theme_update(text = element_text(family = "mono"))

# undo that silliness
baggr_theme_update(text = element_text(family = "serif"))

# update and replace are similar, but replace overwrites the
# whole element, update just edits the aspect of the element
# that you give it
# this will error:
# baggr_theme_replace(text = element_text(family = "Times"))
# baggr_plot(fit)
# because it deleted everything else to do with text elements

```

---

binary\_to\_individual *Generate individual-level binary outcome data from an aggregate statistics*

---

## Description

This is a helper function that is typically used automatically by some of *baggr* functions, such as when running `model="logit"` in *baggr*, when summary-level data are supplied.

## Usage

```
binary_to_individual(data, group = "group", rename_group = TRUE)
```

## Arguments

<code>data</code>	A data frame with columns <code>a</code> , <code>c</code> and <code>b/n1</code> , <code>d/n2</code> . (You can also use <code>ai</code> , <code>ci</code> , <code>n1i</code> , <code>n2i</code> instead.)
<code>group</code>	Column name storing group
<code>rename_group</code>	If TRUE (default), this will rename the grouping variable to "group", making it easier to work with <i>baggr</i> See vignette("baggr_binary") for an example of use and notation details.

## Value

A data frame with columns `group`, `outcome` and `treatment`.

**See Also**

[prepare\\_ma](#) uses this function

**Examples**

```
df_yusuf <- read.table(text="
  trial      a n1i  c n2i
  Balcon     14  56 15  58
  Clausen    18  66 19  64
  Multicentre 15 100 12  95
  Barber     10  52 12  47
  Norris     21 226 24 228
  Kahler      3  38  6  31
  Ledwich     2  20  3  20
", header=TRUE)
bti <- binary_to_individual(df_yusuf, group = "trial")
head(bti)
# to go back to summary-level data
prepare_ma(bti, effect = "logOR")
# the last operation is equivalent to simply doing
prepare_ma(df_yusuf, group="trial", effect="logOR")
```

---

 chicks

*Chickens: impact of electromagnetic field on calcium ion efflux in chicken brains*

---

**Description**

An experiment conducted by Blackman et al. (1988) and documented in the following [GitHub repository](#) by Vakar and Gelman. The dataset consists of a large number of experiments (tau, se.tau) repeated at varying wave frequencies. Sham experiments (mu, se.mu) are also included, allowing us to compare performance of models with and without control measurements.

**Usage**

```
chicks
```

**Format**

An object of class `data.frame` with 38 rows and 7 columns.

**References**

Blackman, C. F., S. G. Benane, D. J. Elliott, D. E. House, and M. M. Pollock. "Influence of Electromagnetic Fields on the Efflux of Calcium Ions from Brain Tissue in Vitro: A Three-Model Analysis Consistent with the Frequency Response up to 510 Hz." *Bioelectromagnetics* 9, no. 3 (1988): 215–27.

---

convert_inputs	<i>Convert inputs for baggr models</i>
----------------	--

---

### Description

Converts data to a list of inputs suitable for Stan models, checks integrity of data and suggests the appropriate default model if needed. Typically all of this is done automatically by [baggr](#), so **this function is only for debugging** or running models "by hand".

### Usage

```
convert_inputs(
  data,
  model,
  quantiles,
  group = "group",
  outcome = "outcome",
  treatment = "treatment",
  covariates = c(),
  test_data = NULL,
  silent = FALSE
)
```

### Arguments

data	‘data.frame’ with desired modelling input
model	valid model name used by baggr; see <a href="#">baggr</a> for allowed models if model = NULL, this function will try to find appropriate model automatically
quantiles	vector of quantiles to use (only applicable if model = "quantiles")
group	name of the column with grouping variable
outcome	name of column with outcome variable (designated as string)
treatment	name of column with treatment variable
covariates	Character vector with column names in data. The corresponding columns are used as covariates (fixed effects) in the meta-regression model.
test_data	same format as data argument, gets left aside for testing purposes (see <a href="#">baggr</a> )
silent	Whether to print messages when evaluated

### Details

Typically this function is only called within [baggr](#) and you do not need to use it yourself. It can be useful to understand inputs or to run models which you modified yourself.

### Value

R structure that’s appropriate for use by [baggr](#) Stan models; group\_label, model and n\_groups are included as attributes and are necessary for [baggr](#) to work correctly

**Author(s)**

Witold Wiecek

**Examples**

```
# simple meta-analysis example,
# this is the formatted input for Stan models in baggr():
convert_inputs(schools, "rubin")
```

---

data_spike	<i>Spike &amp; slab example dataset</i>
------------	---

---

**Description**

Spike &amp; slab example dataset

**Usage**

data\_spike

**Format**An object of class `data.frame` with 1500 rows and 4 columns.

---

effect_draw	<i>Make predictive draws from baggr model</i>
-------------	---

---

**Description**

This function takes the samples of hyperparameters from a [baggr](#) model (typically hypermean and hyper-SD, which you can see using [treatment\\_effect](#)) and draws values of new realisations of treatment effect, i.e. an additional draw from the "population of studies". This can be used for both prior and posterior draws, depending on [baggr](#) model.

**Usage**

```
effect_draw(
  x,
  n,
  transform = NULL,
  summary = FALSE,
  message = TRUE,
  interval = 0.95
)
```



**Arguments**

x	A baggr class object.
n	How many values to draw? The default is as long as the number of samples in the baggr object (see <i>Details</i> ).
transform	a transformation (an R function) to apply to the result of a draw.
summary	logical; if TRUE returns summary statistics rather than samples from the distribution;
message	logical; use to disable messages prompted by using with no pooling models
interval	uncertainty interval width (numeric between 0 and 1), if summary=TRUE

**Details**

The predictive distribution can be used to "combine" heterogeneity between treatment effects and uncertainty in the mean treatment effect. This is useful both in understanding impact of heterogeneity (see Riley et al, 2011, for a simple introduction) and for study design e.g. as priors in analysis of future data (since the draws can be seen as an expected treatment effect in a hypothetical study).

The default number of samples is the same as what is returned by Stan model implemented in [baggr](#), (depending on such options as `iter`, `chains`, `thin`). If `n` is larger than what is available in Stan model, we draw values with replacement. This is not recommended and warning is printed in these cases.

Under default settings in [baggr](#), a *posterior* predictive distribution is obtained. But `effect_draw` can also be used for *prior* predictive distributions when setting `ppd=T` in [baggr](#). The two outputs work exactly the same way.

**Value**

A vector (with `n` values) for models with one treatment effect parameter, a matrix (`n` rows and same number of columns as number of parameters) otherwise.

**References**

Riley, Richard D., Julian P. T. Higgins, and Jonathan J. Deeks. "Interpretation of Random Effects Meta-Analyses". *BMJ* 342 (10 February 2011)..

**See Also**

[treatment\\_effect](#) returns samples of hypermean and hyper-SD which are used by this function

---

 effect\_plot

*Plot predictive draws from baggr model*


---

### Description

This function plots values from [effect\\_draw](#), the predictive distribution (under default settings, *posterior* predictive), for one or more baggr objects.

### Usage

```
effect_plot(..., transform = NULL)
```

### Arguments

...	Object(s) of class <a href="#">baggr</a> . If there is more than one, a comparison will be plotted and names of objects will be used as a plot legend (see examples).
transform	a transformation to apply to the result, should be an R function; (this is commonly used when calling <code>group_effects</code> from other plotting or printing functions)

### Details

Under default settings in [baggr](#) posterior predictive is obtained. But `effect_plot` can also be used for *prior* predictive distributions when setting `ppd=T` in [baggr](#). The two outputs work exactly the same, but labels will change to indicate this difference.

### Value

A ggplot object.

### See Also

[effect\\_draw](#) documents the process of drawing values; [baggr\\_compare](#) can be used as a shortcut for `effect_plot` with argument `compare = "effects"`

### Examples

```
# A single effects plot
bg1 <- baggr(schools, prior_hypersd = uniform(0, 20))
effect_plot(bg1)

# Compare how posterior depends on the prior choice
bg2 <- baggr(schools, prior_hypersd = normal(0, 5))
effect_plot("Uniform prior on SD"=bg1,
           "Normal prior on SD"=bg2)
```

```
# Compare the priors themselves (ppd=T)
bg1_ppd <- baggr(schools, prior_hypersd = uniform(0, 20), ppd=TRUE)
bg2_ppd <- baggr(schools, prior_hypersd = normal(0, 5), ppd=TRUE)
effect_plot("Uniform prior on SD"=bg1_ppd,
            "Normal prior on SD"=bg2_ppd)
```

---

fixed_effects	<i>Effects of covariates on outcome in baggr models</i>
---------------	---

---

## Description

Effects of covariates on outcome in baggr models

## Usage

```
fixed_effects(bg, summary = FALSE, transform = NULL, interval = 0.95)
```

## Arguments

bg	a <a href="#">baggr</a> model
summary	logical; if TRUE returns summary statistic instead of all MCMC samples
transform	a transformation (R function) to apply to the result; (this is commonly used when calling from other plotting or printing functions)
interval	uncertainty interval width (numeric between 0 and 1), if summary=TRUE

## Value

A list with 2 vectors (corresponding to MCMC samples) tau (mean effect) and sigma\_tau (SD). If summary=TRUE, both vectors are summarised as mean and lower/upper bounds according to interval

## See Also

[treatment\\_effect](#) for overall treatment effect across groups, [group\\_effects](#) for effects within each group, [effect\\_draw](#) and [effect\\_plot](#) for predicted treatment effect in new group

---

 forest\_plot

*Draw a forest plot for a baggr model*


---

### Description

The forest plot functionality in *baggr* is a simple interface for calling the [forestplot](#) function. By default the forest plot displays raw (unpooled) estimates for groups and the treatment effect estimate underneath. This behaviour can be modified to display pooled group estimates.

### Usage

```
forest_plot(
  bg,
  show = c("inputs", "posterior", "both", "covariates"),
  print = show,
  prob = 0.95,
  digits = 3,
  ...
)
```

### Arguments

<code>bg</code>	a <a href="#">baggr</a> class object
<code>show</code>	if "inputs", then plotted points and lines correspond to raw inputs for each group; if "posterior" – to posterior distribution; you can also plot "both" inputs and posteriors; if "covariates", then fixed effect coefficients are plotted
<code>print</code>	which values to print next to the plot: values of "inputs" or "posterior" means? (if show="covariates", it must be "posterior")
<code>prob</code>	width of the intervals (lines) for the plot
<code>digits</code>	number of digits to display when printing out mean and SD in the plot
<code>...</code>	other arguments passed to <a href="#">forestplot</a>

### See Also

[forestplot](#) function and its vignette for examples; [effect\\_plot](#) and [baggr\\_plot](#) for non-forest plots of baggr results

### Examples

```
bg <- baggr(schools, iter = 500)
forest_plot(bg)
forest_plot(bg, show = "posterior", print = "inputs", digits = 2)
```

---

get_n_samples	<i>Extract number of samples from a baggr object</i>
---------------	--

---

**Description**

Extract number of samples from a baggr object

**Usage**

```
get_n_samples(x)
```

**Arguments**

x	baggr fit to get samples from
---	-------------------------------

**Details**

Checks for number of iterations and number of Markov chains, returns maximum number of valid samples

---

get_order	<i>Separate out ordering so we can test directly</i>
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---

**Description**

Separate out ordering so we can test directly

**Usage**

```
get_order(df_groups, hyper)
```

**Arguments**

df_groups	data.frame of group effects used in <a href="#">plot.baggr_compare</a>
hyper	show parameter estimate? same as in <a href="#">plot.baggr_compare</a>

**Details**

Given a set of effects measured by models, identifies the model which has the biggest range of estimates and ranks groups by those estimates, returning the order

---

group\_effects      *Extract baggr study effects*

---

### Description

Given a baggr object, returns the raw MCMC draws of the posterior for each group's effect or a summary of these draws. If there are no covariates in the model, this effect is a single random variable. If there are covariates, the group effect is a sum of effect of covariates (fixed effects) and the study-specific random variable (random effects). This is an internal function currently used as a helper for plotting and printing of results.

### Usage

```
group_effects(
  bg,
  summary = FALSE,
  transform = NULL,
  interval = 0.95,
  random_only = FALSE,
  rename_int = FALSE
)
```

### Arguments

bg	baggr object
summary	logical; if TRUE returns summary statistics as explained below.
transform	a transformation to apply to the result, should be an R function; (this is commonly used when calling group_effects from other plotting or printing functions)
interval	uncertainty interval width (numeric between 0 and 1), if summarising
random_only	logical; for meta-regression models, should <a href="#">fixed_effects</a> be included in the returned group effect?
rename_int	logical; if TRUE then rather than returning median, lci and uci columns they are renamed to e.g. 50%, 2.5%, 97.5%; this only works if summary=TRUE

### Details

If summary = TRUE, the returned object contains, for each study or group, the following 5 values: the posterior medians, the lower and upper bounds of the uncertainty intervals using the central posterior credible interval of width specified in the argument interval, the posterior mean, and the posterior standard deviation.

### Value

Either an array with MCMC samples (if summary = FALSE) or a summary of these samples (if summary = TRUE). For arrays the three dimensions are: N samples, N groups and N effects (equal to 1 for the basic models).

**See Also**

[fixed\\_effects](#) for effects of covariates on outcome. To extract random effects when covariates are present, you can use either [random\\_effects](#) or, equivalently, `group_effects(random_only=TRUE)`.

**Examples**

```
fit1 <- baggr(schools)
group_effects(fit1, summary = TRUE, interval = 0.5)
```

---

is.baggr_cv	<i>Check if something is a baggr_cv object</i>
-------------	--

---

**Description**

Check if something is a baggr\_cv object

**Usage**

```
is.baggr_cv(x)
```

**Arguments**

x                    object to check

---

labbe	<i>L'Abbe plot for binary data</i>
-------	------------------------------------

---

**Description**

This plot shows relationship between proportions of events in control and treatment groups in binary data.

**Usage**

```
labbe(
  data,
  group = "group",
  plot_model = FALSE,
  labels = TRUE,
  shade_se = c("rr", "or", "none")
)
```

**Arguments**

data	a data frame with binary data (must have columns a, c, b/n1, d/n2)
group	a character string specifying group names (e.g. study names), used for labels;
plot_model	if TRUE, then odds ratios and risk ratios <a href="#">baggr</a> models are estimated (using default settings) and their mean estimates of effects are plotted as lines
labels	if TRUE, names from the group column are displayed
shade_se	if "none", nothing is plotted, if "or" or "rr", a shaded area corresponding to inverse of effect's (OR or RR) SE is added to each data point; the default is "rr"

**Value**

A ggplot object

**See Also**

`vignette("baggr_binary")` for an illustrative example

---

loocv

*Leave one group out cross-validation for baggr models*


---

**Description**

Performs exact leave-one-group-out cross-validation on a baggr model.

**Usage**

```
loocv(data, return_models = FALSE, ...)
```

**Arguments**

data	Input data frame - same as for <a href="#">baggr</a> function.
return_models	logical; if FALSE, summary statistics will be returned and the models discarded; if TRUE, a list of models will be returned alongside summaries
...	Additional arguments passed to <a href="#">baggr</a> .

**Details**

The values returned by `loocv()` can be used to understand how excluding any one group affects the overall result, as well as how well the model predicts the omitted group. LOO-CV approaches are a good general practice for comparing Bayesian models, not only in meta-analysis.

This function automatically runs  $K$  baggr models, where  $K$  is number of groups (e.g. studies), leaving out one group at a time. For each run, it calculates *expected log predictive density* (ELPD) for that group (see Gelman et al 2013). (In the logistic model, where the proportion in control group is unknown, each of the groups is divided into data for controls, which is kept for estimation, and



data for treated units, which is not used for estimation but only for calculating predictive density. This is akin to fixing the baseline risk and only trying to infer the odds ratio.)

The main output is the cross-validation information criterion, or -2 times the ELPD summed over  $K$  models. (We sum the terms as we are working with logarithms.) This is related to, and often approximated by, the Watanabe-Akaike Information Criterion. When comparing models, smaller values mean a better fit. For more information on cross-validation see [this overview article](#)

For running more computation-intensive models, consider setting the `mc.cores` option before running `loocv`, e.g. `options(mc.cores = 4)` (by default `baggr` runs 4 MCMC chains in parallel). As a default, `rstan` runs "silently" (`refresh=0`). To see sampling progress, please set e.g. `loocv(data, refresh = 500)`.

### Value

log predictive density value, an object of class `baggr_cv`; full model, prior values and *lpd* of each model are also returned. These can be examined by using `attributes()` function.

### Author(s)

Witold Wiecek

### References

Gelman, Andrew, Jessica Hwang, and Aki Vehtari. "Understanding Predictive Information Criteria for Bayesian Models." *Statistics and Computing* 24, no. 6 (November 2014): 997–1016.

### See Also

[loo\\_compare](#) for comparison of many LOO CV results; you can print and plot output via `plot.baggr_cv` and `print.baggr_cv`

### Examples

```
## Not run:
# even simple examples may take a while
cv <- loocv(schools, pooling = "partial")
print(cv)      # returns the lpd value
attributes(cv) # more information is included in the object

## End(Not run)
```

---

loo\_compare

*Compare LOO CV models*

---

### Description

Given multiple `loocv` outputs, calculate differences in their expected log predictive density.

**Usage**

```
loo_compare(x, ...)
```

**Arguments**

```
x          An object of class baggr_cv or a list of such objects.
...        Additional objects of class "baggr_cv"
```

**See Also**

[loocv](#) for fitting LOO CV objects and explanation of the procedure

**Examples**

```
## Not run:
# 2 models with more/less informative priors -- this will take a while to run
cv_1 <- loocv(schools, model = "rubin", pooling = "partial")
cv_2 <- loocv(schools, model = "rubin", pooling = "partial",
             prior_hypermean = normal(0, 5), prior_hypersd = cauchy(0,4))
loo_compare(cv_1, cv_2)

## End(Not run)
```

---

microcredit

*7 studies on effect of microcredit supply*

---

**Description**

This dataframe contains the data used in Meager (2019) to estimate hierarchical models on the data from 7 randomized controlled trials of expanding access to microcredit.

**Usage**

```
microcredit
```

**Format**

A data frame with 40267 rows, 7 study identifiers and 7 outcomes

**Details**

The columns include the group indicator which gives the name of the lead author on each of the respective studies, the value of the 6 outcome variables of most interest (consumer durables spending, business expenditures, business profit, business revenues, temptation goods spending and consumption spending) all of which are standardised to USD PPP in 2009 dollars per two weeks (these are flow variables), and finally a treatment assignment status indicator.

The dataset has not otherwise been cleaned and therefore includes NAs and other issues common to real-world datasets.

For more information on how and why these variables were chosen and standardised, see Meager (2019) or consult the associated code repository which includes the standardisation scripts: [link](#)

## References

Meager, Rachael (2019) Understanding the average impact of microcredit expansions: A Bayesian hierarchical analysis of seven randomized experiments. *American Economic Journal: Applied Economics*, 11(1), 57-91.

---

microcredit\_simplified

*Simplified version of the microcredit dataset.*

---

## Description

This dataframe contains the data used in Meager (2019) to estimate hierarchical models on the data from 7 randomized controlled trials of expanding access to microcredit.

## Usage

microcredit\_simplified

## Format

A data frame with 14224 rows, 7 study identifiers and 1 outcome

## Details

The columns include the group indicator which gives the name of the lead author on each of the respective studies, the value of the household consumption spending standardised to USD PPP in 2009 dollars per two weeks (these are flow variables), and finally a treatment assignment status indicator.

The dataset has not otherwise been cleaned and therefore includes NAs and other issues common to real data.

For more information on how and why these variables were chosen and standardised, see Meager (2019) or consult the associated code repository: [link](#)

This dataset includes only complete cases and only the consumption outcome variable.

## References

Meager, Rachael (2019) Understanding the average impact of microcredit expansions: A Bayesian hierarchical analysis of seven randomized experiments. *American Economic Journal: Applied Economics*, 11(1), 57-91.

---

mint	<i>"Mean and interval" function, including other summaries, calculated for matrix (by column) or vector</i>
------	---

---

### Description

This function is just a convenient shorthand for getting typical summary statistics.

### Usage

```
mint(y, int = 0.95, digits = NULL, median = FALSE, sd = FALSE)
```

### Arguments

y	matrix or a vector; for matrices, mint is done by-column
int	probability interval (default is 95 percent) to calculate
digits	number of significant digits to <a href="#">round</a> values by.
median	return median value?
sd	return SD?

### Examples

```
mint(rnorm(100, 12, 5))
```

---

mutau_cor	<i>Correlation between mu and tau in a baggr model</i>
-----------	--

---

### Description

Correlation between mu and tau in a baggr model

### Usage

```
mutau_cor(bg, summary = FALSE, interval = 0.95)
```

### Arguments

bg	a <a href="#">baggr</a> model where model = "mutau"
summary	logical; if TRUE returns summary statistics as explained below.
interval	uncertainty interval width (numeric between 0 and 1), if summarising

### Value

a vector of values

---

plot.baggr	<i>Plotting method for baggr outputs</i>
------------	--

---

**Description**

Using generic plot() on baggr output invokes `baggr_plot` visual. See therein for customisation options. Note that plot output is ggplot2 object.

**Usage**

```
## S3 method for class 'baggr'  
plot(x, ...)
```

**Arguments**

x	object of class baggr
...	optional arguments, see baggr_plot

**Value**

ggplot2 object from baggr\_plot

**Author(s)**

Witold Wiecek

---

plot.baggr_compare	<i>Plot method for baggr_compare models</i>
--------------------	---

---

**Description**

Allows plots that compare multiple baggr models that were passed for comparison purposes to baggr\_compare or run automatically by baggr\_compare

**Usage**

```
## S3 method for class 'baggr_compare'  
plot(  
  x,  
  compare = x$compare,  
  style = "areas",  
  grid_models = FALSE,  
  grid_parameters = TRUE,  
  prob = x$prob,  
  hyper = TRUE,
```

```

transform = NULL,
order = F,
vline = FALSE,
add_values = FALSE,
values_digits = 2,
values_size = 2,
...
)

```

### Arguments

x	baggr_compare model to plot
compare	When plotting, choose between comparison of "groups" (default), "hyperpars" (to omit group-specific estimates) or (predicted) "effects". The "groups" option is not available when what = "prior".
style	What kind of plot to display (if grid_models = TRUE), passed to the style argument in <a href="#">baggr_plot</a> .
grid_models	If FALSE (default), generate a single comparison plot; if TRUE, display each model (using individual <a href="#">baggr_plot</a> 's) side-by-side.
grid_parameters	if TRUE, uses ggplot-style faceting when plotting models with many parameters (especially "quantiles", "sslab"); if FALSE, returns separate plot for each parameter
prob	Width of uncertainty interval (defaults to 95%)
hyper	Whether to plot pooled treatment effect in addition to group treatment effects when compare = "groups"
transform	a function (e.g. exp(), log()) to apply to the values of group (and hyper, if hyper=TRUE) effects before plotting
order	Whether to sort by median treatment effect by group. If yes, medians from the model with largest range of estimates are used for sorting. If not, groups are shown alphabetically.
vline	logical; show vertical line through 0 in the plot?
add_values	logical; if TRUE, values will be printed next to the plot, in a style that's similar to what is done for forest plots
values_digits	number of significant digits to use when printing values,
values_size	size of font for the values, if add_values == TRUE
...	ignored for now, may be used in the future

---

plot.baggr_cv	<i>Plotting method for results of baggr LOO analyses</i>
---------------	--

---

**Description**

Plotting method for results of baggr LOO analyses

**Usage**

```
## S3 method for class 'baggr_cv'
plot(x, y, ..., add_values = TRUE)
```

**Arguments**

x	output from <a href="#">loocv</a> that has return_models = TRUE
y	Unused, ignore
...	Unused, ignore
add_values	logical; if TRUE, values of <i>elpd</i> are printed next to each study

**Value**

ggplot2 plot in similar style to [baggr\\_compare](#) default plots

---

plot_quantiles	<i>plot quantiles</i>
----------------	-----------------------

---

**Description**

Plot results for baggr quantile models. Displays results faceted per group. Results are ggplot2 plots and can be modified.

**Usage**

```
plot_quantiles(fit, ncol, hline = TRUE)
```

**Arguments**

fit	an object of class baggr
ncol	number of columns for the plot; defaults to half of number of groups
hline	logical; plots a line through 0

**Value**

ggplot2 object

**Examples**

```
## Not run:
bg <- baggr(microcredit_simplified, model = "quantiles",
            quantiles = c(0.25, 0.50, 0.75),
            iter = 1000, refresh = 0,
            outcome = "consumption")
#vanilla plot
plot_quantiles(bg)[[1]]
plot_quantiles(bg, hline = TRUE)[[2]] +
  ggplot2::coord_cartesian(ylim = c(-2, 5)) +
  ggplot2::ggtitle("Works like a ggplot2 plot!")

## End(Not run)
```

---

pooling

*Pooling metrics and related statistics for baggr*


---

**Description**

Compute statistics relating to pooling in a given [baggr](#) meta-analysis model returns statistics, for either the entire model or individual groups, such as pooling statistic by Gelman & Pardoe (2006), *I-squared*, *H-squared*, or study weights; heterogeneity is a shorthand for pooling(`type = "total"`) weights is shorthand for pooling(`metric = "weights"`)

**Usage**

```
pooling(
  bg,
  metric = c("pooling", "isq", "hsq", "weights"),
  type = c("groups", "total"),
  summary = TRUE
)

heterogeneity(
  bg,
  metric = c("pooling", "isq", "hsq", "weights"),
  summary = TRUE
)

## S3 method for class 'baggr'
weights(object, ...)
```

**Arguments**

`bg` a [baggr](#) model



metric	"pooling" for Gelman & Pardoe statistic $P$ , "isq" for I-squared statistic ( $I-P$ , Higgins & Thompson, 2002) "hsq" for H squared statistic ( $I/P$ , <i>ibid.</i> ); "weights" for study weights; also see <i>Details</i>
type	In pooling calculation is done for each of the "groups" (default) or for "total" hypereffect(s).
summary	logical; if FALSE a whole vector of pooling values is returned, otherwise only the means and intervals
object	<code>baggr</code> model for which to calculate group (study) weights
...	Unused, please ignore.

### Details

Pooling statistic (Gelman & Pardoe, 2006) describes the extent to which group-level estimates of treatment effect are "pooled" toward average treatment effect in the meta-analysis model. If pooling = "none" or "full" (which you specify when calling `baggr`), then the values are always 0 or 1, respectively. If pooling = "partial", the value is somewhere between 0 and 1. We can distinguish between pooling of individual groups and overall pooling in the model.

In many contexts, i.e. medical statistics, it is typical to report  $I-P$ , called  $I^2$  (see Higgins and Thompson, 2002; sometimes another statistic,  $H^2 = 1/P$ , is used). Higher values of *I-squared* indicate higher heterogeneity; Von Hippel (2015) provides useful details for *I-squared* calculations (and some issues related to it, especially in frequentist models). See Gelman & Pardoe (2006) Section 1.1 for a short explanation of how  $R^2$  statistic relates to the pooling metric.

### Group pooling

This is the calculation done by `pooling()` if `type = "groups"` (default). In a partial pooling model (see `baggr` and above), group  $k$  (e.g. study) has standard error of treatment effect estimate,  $se_k$ . The treatment effect (across  $k$  groups) is variable across groups, with hyper-SD parameter  $\sigma_\tau$ .

The quantity of interest is ratio of variation in treatment effects to the total variation. By convention, we subtract it from 1, to obtain a *pooling metric*  $P$ .

$$p = 1 - (\sigma_\tau)^2 / (\sigma_\tau)^2 + se_k^2$$

- If  $p < 0.5$ , the variation across studies is higher than variation within studies.
- Values close to 1 indicate nearly full pooling. Variation across studies dominates.
- Values close to 0 indicate no pooling. Variation within studies dominates.

Note that, since  $\sigma_\tau^2$  is a Bayesian parameter (rather than a single fixed value),  $P$  is also a parameter. It is typical for  $P$  to have very high dispersion, as in many cases we cannot precisely estimate  $\sigma_\tau$ . To obtain samples from the distribution of  $P$  (rather than summarised values), set `summary=FALSE`.

### Study weights

Contributions of each group (e.g. each study) to the mean meta-analysis estimate can be calculated by calculating for each study  $w_k$  the inverse of sum of group-specific SE squared and between-study variation. To obtain weights, this vector (across all studies) has to be normalised to 1, i.e.  $w_k / \text{sum}(w_k)$  for each  $k$ .

SE is typically treated as a fixed quantity (and usually reported on the reported point estimate), but between-study variance is a model parameter, hence the weights themselves are also random variables.

### Overall pooling in the model

Typically researchers want to report a single measure from the model, relating to heterogeneity across groups. This is calculated by either `pooling(mymodel, type = "total")` or simply `heterogeneity(mymodel)`

Formulae for the calculations below are provided in main package vignette and almost analogous to the group calculation above, but using mean variance across all studies. In other words, pooling  $P$  is simply ratio of the expected within-study variance term to total variance.

To obtain such single estimate we need to substitute average variability of group-specific treatment effects and then calculate the same way we would calculate  $p$ . By default we use the mean across  $k$   $se_k^2$  values. Typically, implementations of  $I^2$  in statistical packages use a different calculation for this quantity, which may make  $I$ 's not comparable when different studies have different SE's.

Same as for group-specific estimates,  $P$  is a Bayesian parameter and its dispersion can be high.

### Value

Matrix with mean and intervals for chosen pooling metric, each row corresponding to one meta-analysis group.

### References

Gelman, Andrew, and Iain Pardoe. "Bayesian Measures of Explained Variance and Pooling in Multilevel (Hierarchical) Models." *Technometrics* 48, no. 2 (May 2006): 241-51.

Higgins, Julian P. T., and Simon G. Thompson. "Quantifying Heterogeneity in a Meta-Analysis." *Statistics in Medicine*, vol. 21, no. 11, June 2002, pp. 1539-58.

Hippel, Paul T von. "The Heterogeneity Statistic  $I^2$  Can Be Biased in Small Meta-Analyses." *BMC Medical Research Methodology* 15 (April 14, 2015).

---

pp\_check.baggr

*Posterior predictive checks for baggr model*

---

### Description

Performs posterior predictive checks with the **bayesplot** package.

### Usage

```
## S3 method for class 'baggr'
pp_check(x, type = "dens_overlay", nsamples = 40)
```

**Arguments**

x	Model to check
type	type of pp_check. For a list see <a href="#">here</a> .
nsamples	number of samples to compare

**Details**

For a detailed explanation of each of the ppc functions, see the [PPC](#) documentation of the bayesplot package.

---

predict.baggr	<i>Predict method for baggr objects</i>
---------------	---

---

**Description**

Predict method for baggr objects

**Usage**

```
## S3 method for class 'baggr'
predict(object, nsamples, newdata = NULL, allow_new_levels = TRUE, ...)
```

**Arguments**

object	model to predict from
nsamples	Number of samples to draw from the posterior. Cannot exceed the number of samples in the fitted model.
newdata	optional, new data to predict observations from
allow_new_levels	whether to allow the model to make predictions about unobserved groups. Without additional group-level information the model will use the unconditional, pooled estimate.
...	other arguments to pass to predict function (currently not used)

---

predict_mutau	<i>Predict function for the mu &amp; tau model</i>
---------------	--

---

**Description**

Predict function for the mu & tau model

**Usage**

```
predict_mutau(x, nsamples, newdata = NULL, allow_new_levels = TRUE)
```

**Arguments**

x	model to predict from
nsamples	number of samples to predict
newdata	new data to predict, defaults to NULL
allow_new_levels	allow the predictive of new, unobserved groups

---

predict_quantiles	<i>Predict function for the quantiles model</i>
-------------------	---

---

**Description**

Predict function for the quantiles model

**Usage**

```
predict_quantiles(x, nsamples, newdata = NULL, allow_new_levels = TRUE)
```

**Arguments**

x	model to predict from
nsamples	number of samples to predict
newdata	new data to predict, defaults to NULL
allow_new_levels	allow the predictive of new, unobserved groups

---

predict_rubin	<i>Predict function for the rubin model</i>
---------------	---

---

**Description**

Predict function for the rubin model

**Usage**

```
predict_rubin(x, nsamples, newdata = NULL, allow_new_levels = TRUE)
```

**Arguments**

x	model to predict from
nsamples	number of samples to predict
newdata	new data to predict, defaults to NULL
allow_new_levels	allow the predictive of new, unobserved groups

---

predict_unknown	<i>Predict method for model that is unknown or not implemented</i>
-----------------	--

---

**Description**

Predict method for model that is unknown or not implemented

**Usage**

```
predict_unknown(x)
```

**Arguments**

x	baggr model to generate predictions from
---	--

prepare\_ma

*Convert from individual to summary data in meta-analyses***Description**

Allows for one-way conversion from full to summary data or for calculation of effects for binary data. Input must be pre-formatted appropriately.

**Usage**

```
prepare_ma(
  data,
  effect = c("mean", "logOR", "logRR", "RD"),
  rare_event_correction = 0.25,
  correction_type = c("single", "all"),
  log = FALSE,
  cfb = FALSE,
  summarise = TRUE,
  treatment = "treatment",
  baseline = NULL,
  group = "group",
  outcome = "outcome",
  pooling = FALSE
)
```

**Arguments**

data	<b>either</b> a data.frame of individual-level observations with columns for outcome (numeric), treatment (values 0 and 1) and group (numeric, character or factor); <b>or</b> , a data frame with binary data (must have columns a, c, b/n1, d/n2).
effect	what effect to calculate? a mean (and SE) of outcome in groups or (for binary data) logOR (odds ratio), logRR (risk ratio), RD (risk difference);
rare_event_correction	This correction is used when working with binary data (effect logOR or logRR) The value of correction is added to all cells in either some or all rows (groups), depending on correction_type. Using corrections may bias results but is the only alternative to avoid infinite values.
correction_type	If "single" then rare event correction is only applied to the particular rows that have 0 cells, if "all", then to all studies
log	logical; log-transform the outcome variable?
cfb	logical; calculate change from baseline? If yes, the outcome variable is taken as a difference between values in outcome and baseline columns
summarise	logical; TRUE by default, but you can disable it to obtain converted (e.g. logged) data with columns renamed

treatment	name of column with treatment variable
baseline	name of column with baseline variable
group	name of the column with grouping variable
outcome	name of column with outcome variable
pooling	Internal use only, please ignore

## Details

The conversions done by this function are not typically needed and may happen automatically when data is given to [baggr](#). However, this function can be used to explicitly convert from full to reduced (summarised) data without analysing it in any model. It can be useful for examining your data and generating summary tables.

If multiple operations are performed, they are taken in this order:

1. conversion to log scale,
2. calculating change from baseline,
3. summarising data (using appropriate effect)

## Value

- If you summarise: a data.frame with columns for group, tau and se.tau (for effect = "mean", also baseline means; for "logRR" or "logOR" also a, b, c, d, which correspond to typical contingency table notation, that is: a = events in exposed; b = no events in exposed, c = events in unexposed, d = no events in unexposed).
- If you do not summarise data, individual level data will be returned, but some columns may be renamed or transformed (see the arguments above).

## Author(s)

Witold Wiecek

## See Also

[convert\\_inputs](#) for how any type of data is (internally) converted into a list of Stan inputs; vignette [baggr\\_binary](#) for more details about rare event corrections

## Examples

```
# Example of working with binary outcomes data
# Make up some individual-level data first:
df_rare <- data.frame(group = paste("Study", LETTERS[1:5]),
  a = c(0, 2, 1, 3, 1), c = c(2, 2, 3, 3, 5),
  n1i = c(120, 300, 110, 250, 95),
  n2i = c(120, 300, 110, 250, 95))
df_rare_ind <- binary_to_individual(df_rare)
# Calculate ORs; default rare event correction will be applied
prepare_ma(df_rare_ind, effect = "logOR")
```

```
# Add 0.5 to all rows
prepare_ma(df_rare_ind, effect = "logOR",
           correction_type = "all",
           rare_event_correction = 0.5)
```

---

```
prepare_prior
```

---

*Prepare prior values for Stan models in baggr*

---

## Description

This is an internal function called by [baggr](#). You can use it for debugging or to run modified models. It extracts and prepares priors passed by the user. Then, if any necessary priors are missing, it sets them automatically and notifies user about these automatic choices.

## Usage

```
prepare_prior(
  prior,
  data,
  stan_data,
  model,
  pooling,
  covariates,
  quantiles = c(),
  silent = FALSE
)
```

## Arguments

prior	prior argument passed from <a href="#">baggr</a> call
data	data another argument in <a href="#">baggr</a>
stan_data	list of inputs that will be used by sampler this is already pre-obtained through <a href="#">convert_inputs</a>
model	same as in <a href="#">baggr</a>
pooling	same as in <a href="#">baggr</a>
covariates	same as in <a href="#">baggr</a>
quantiles	same as in <a href="#">baggr</a>
silent	same as in <a href="#">baggr</a>

## Value

A named list with prior values that can be appended to `stan_data` and passed to a Stan model.



---

print.baggr	<i>S3 print method for objects of class baggr (model fits)</i>
-------------	--

---

**Description**

This prints a concise summary of the main `baggr` model features. More info is included in the summary of the model and its attributes.

**Usage**

```
## S3 method for class 'baggr'
print(x, exponent = FALSE, digits = 2, prob = 0.95, group, fixed = TRUE, ...)
```

**Arguments**

<code>x</code>	object of class <code>baggr</code>
<code>exponent</code>	if TRUE, results (for means) are converted to exp scale
<code>digits</code>	Number of significant digits to print.
<code>prob</code>	Width of uncertainty interval (defaults to 95%)
<code>group</code>	logical; print group effects? If unspecified, they are printed only if less than 20 groups are present
<code>fixed</code>	logical: print fixed effects?
<code>...</code>	currently unused by this package: further arguments passed to or from other methods (print requirement)

---

print.baggr_compare	<i>Print method for baggr_compare models</i>
---------------------	--

---

**Description**

Print method for `baggr_compare` models

**Usage**

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

**Arguments**

<code>x</code>	<code>baggr_compare</code> model
<code>digits</code>	number of significant digits for effect estimates
<code>...</code>	other parameters passed to print

---

print\_baggr\_cv      *Print baggr\_cv objects nicely*

---

**Description**

Print baggr\_cv objects nicely

**Usage**

```
## S3 method for class 'baggr_cv'  
print(x, digits = 3, ...)
```

**Arguments**

x	baggr_cv object obtained from <a href="#">loocv</a> to print
digits	number of digits to print
...	Unused, ignore

---

print.compare\_baggr\_cv      *Print baggr\_cv comparisons*

---

**Description**

Print baggr\_cv comparisons

**Usage**

```
## S3 method for class 'compare_baggr_cv'  
print(x, digits = 3, ...)
```

**Arguments**

x	baggr_cv comparison to print
digits	number of digits to print
...	additional arguments for s3 consistency

---

print_dist	<i>Output a distribution as a string</i>
------------	--

---

**Description**

Used for printing nicely formatted outputs when reporting results etc.

**Usage**

```
print_dist(dist)
```

**Arguments**

dist            distribution name, one of [priors](#)

**Value**

Character string like `normal(0,10^2)`.

---

priors	<i>Prior distributions in baggr</i>
--------	-------------------------------------

---

**Description**

This page provides a list of all available distributions that can be used to specify priors in [baggr\(\)](#). These convenience functions are designed to allow the user to write the priors in the most "natural" way when implementing them in baggr. Apart from passing on the arguments, their only other role is to perform a rudimentary check if the distribution is specified correctly.

**Usage**

```
multinormal(location, Sigma)
```

```
lkj(shape, order = NULL)
```

```
normal(location, scale)
```

```
lognormal(mu, sigma)
```

```
student_t(nu, mu, sigma)
```

```
cauchy(location, scale)
```

```
uniform(lower, upper)
```

**Arguments**

location	Mean for normal and multivariate normal (in which case location is a vector), and median for Cauchy distributions
Sigma	Variance-covariance matrix for multivariate normal.
shape	Shape parameter for LKJ
order	Order of LKJ matrix (typically it does not need to be specified, as it is inferred directly in the model)
scale	SD for Normal, scale for Cauchy
mu	mean of $\ln(X)$ for lognormal or location for Student's generalised T
sigma	SD of $\ln(X)$ for lognormal or scale for Student's generalised T
nu	degrees of freedom for Student's generalised T
lower	Lower bound for Uniform
upper	Upper bound for Uniform

**Details**

The prior choice in [baggr](#) is done via distinct arguments for each type of prior, e.g. `prior_hypermean`, or a named list of several passed to `prior`. See the examples below.

Notation for priors is "plain-text", in that you can write the distributions as `normal(5, 10)`, `uniform(0, 100)` etc.

Different parameters admit different priors (see [baggr](#) for explanations of what the different `prior_` arguments do):

- `prior_hypermean`, `prior_control`, and `prior_beta` will take "normal", "uniform", "lognormal", and "cauchy" input for scalars. For a vector hypermean (see "mutau" model), it will take any of these arguments and apply them independently to each component of the vector, or it can also take a "multinormal" argument (see the example below).
- `prior_hypersd`, `prior_control_sd`, and `prior_sigma` will take "normal", "uniform", and "lognormal" but negative parts of the distribution are truncated
- `prior_hypercor` allows "lkj" input (see Lewandowski *et al.*)

**Author(s)**

Witold Wiecek, Rachael Meager

**References**

Lewandowski, Daniel, Dorota Kurowicka, and Harry Joe. "Generating Random Correlation Matrices Based on Vines and Extended Onion Method." *Journal of Multivariate Analysis* 100, no. 9 (October 1, 2009): 1989-2001.

**Examples**

```
# (these are not the recommended priors -- for syntax illustration only)

# change the priors for 8 schools:
baggr(schools, model = "rubin", pooling = "partial",
      prior_hypermean = normal(5,5),
      prior_hypersd = normal(0,20))

# passing priors as a list
custom_priors <- list(hypercor = lkj(1), hypersd = normal(0,10),
                     hypermean = multinormal(c(0,0),matrix(c(10,3,3,10),2,2)))
microcredit_summary_data <- prepare_ma(microcredit, outcome = "consumption")
baggr(microcredit_summary_data, model = "mutau",
      pooling = "partial", prior = custom_priors)
```

---

random_effects	<i>Extract random effects from a baggr model</i>
----------------	--

---

**Description**

This is a shortcut for writing `group_effects(random_only=TRUE, ...)`

**Usage**

```
random_effects(...)
```

**Arguments**

... arguments passed to [group\\_effects](#)

---

rubin_data	<i>Make model matrix for the rubin data</i>
------------	---

---

**Description**

Make model matrix for the rubin data

**Usage**

```
rubin_data(x, newdata = NULL, allow_new_levels = TRUE)
```

**Arguments**

x	model to get data from
newdata	new data to use with model
allow_new_levels	whether to allow for unobserved groups

---

schools	<i>8 schools example</i>
---------	--------------------------

---

**Description**

A classic example of aggregate level continuous data in Bayesian hierarchical modelling. This dataframe contains a column of estimated treatment effects of an SAT prep program implemented in 8 different schools in the US, and a column of estimated standard errors.

**Usage**

```
schools
```

**Format**

An object of class `data.frame` with 8 rows and 3 columns.

**Details**

See Gelman et al (1995), Chapter 5, for context and applied example.

**References**

Gelman, Andrew, John B. Carlin, Hal S. Stern, and Donald B. Rubin. Bayesian Data Analysis. Taylor & Francis, 1995.

---

set_prior_val	<i>Add prior values to Stan input for baggr</i>
---------------	---

---

**Description**

Add prior values to Stan input for baggr

**Usage**

```
set_prior_val(target, name, prior, p = 1)
```

**Arguments**

target	list object (Stan input) to which prior will be added
name	prior name, like hypermean, hypersd, hypercor
prior	one of prior distributions allowed by baggr like <a href="#">normal</a>
p	number of repeats of the prior, i.e. when P i.i.d. priors are set for P dimensional parameter as in "mu & tau" type of model

---

single\_comp\_plot      *Plot single comparison ggplot in baggr\_compare style*

---

### Description

Plot single comparison ggplot in baggr\_compare style

### Usage

```
single_comp_plot(  
  df,  
  title = "",  
  legend = "top",  
  ylab = "",  
  grid = F,  
  points = FALSE,  
  add_values = FALSE,  
  values_digits = 2,  
  values_size = 2.5  
)
```

### Arguments

df	data.frame with columns group, median, lci, uci, model (character or factor listing compared models) and, optionally, parameter (character or factor with name of parameter)
title	ggtitle argument passed to ggplot
legend	legend.position argument passed to ggplot
ylab	Y axis label
grid	logical; if TRUE, facets the plot by values in the parameter column
points	you can optionally specify a (numeric) column that has values of points to be plotted next to intervals
add_values	logical; if TRUE, values will be printed next to the plot, in a style that's similar to what is done for forest plots
values_digits	number of significant digits to use when printing values,
values_size	size of font for the values, if add_values == TRUE

### Value

a ggplot2 object

---

stop\_not\_implemented    *Stop with informative error*

---

**Description**

Stop with informative error

**Usage**

```
stop_not_implemented()
```

---

treatment\_effect        *Average treatment effect in a baggr model*

---

**Description**

Average treatment effect in a baggr model

**Usage**

```
treatment_effect(  
  bg,  
  summary = FALSE,  
  transform = NULL,  
  interval = 0.95,  
  message = TRUE  
)
```

**Arguments**

bg	a <a href="#">baggr</a> model
summary	logical; if TRUE returns summary statistics as explained below.
transform	a transformation to apply to the result, should be an R function; (this is commonly used when calling <code>treatment_effect</code> from other plotting or printing functions)
interval	uncertainty interval width (numeric between 0 and 1), if summarising
message	logical; use to disable messages prompted by using with no pooling models

**Value**

A list with 2 vectors (corresponding to MCMC samples) `tau` (mean effect) and `sigma_tau` (SD). If `summary=TRUE`, both vectors are summarised as mean and lower/upper bounds according to `interval`



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