

# Package ‘pema’

May 9, 2026

**Title** Penalized Meta-Analysis

**Version** 0.1.5

**Description** Conduct penalized meta-analysis, see Van Lissa, Van Erp, & Clapper (2023) <[doi:10.31234/osf.io/6phs5](https://doi.org/10.31234/osf.io/6phs5)>. In meta-analysis, there are often between-study differences. These can be coded as moderator variables, and controlled for using meta-regression. However, if the number of moderators is large relative to the number of studies, such an analysis may be overfit. Penalized meta-regression is useful in these cases, because it shrinks the regression slopes of irrelevant moderators towards zero.

**License** GPL (>= 3)

**Encoding** UTF-8

**LazyData** true

**URL** <https://github.com/cjvanlissa/pema>,  
<https://cjvanlissa.github.io/pema/>

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**VignetteBuilder** knitr

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## Contents

pema-package . . . . .	2
as.stan . . . . .	3
bonapersona . . . . .	3
brma . . . . .	4
check_workshop_data . . . . .	7
curry . . . . .	8
I2 . . . . .	9
maxap . . . . .	9
plot_sensitivity . . . . .	10
sample_prior . . . . .	11
shiny_prior . . . . .	11
simulate_smd . . . . .	12
<b>Index</b>	<b>14</b>

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pema-package	<i>pema: Conduct penalized meta-regression.</i>
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## Description

Penalized meta-regression shrinks the regression slopes of irrelevant moderators towards zero (Van Lissa & Van Erp, 2021).

## Author(s)

**Maintainer:** Caspar J van Lissa <c.j.vanlissa@tilburguniversity.edu> ([ORCID](#))

Authors:

- Sara J van Erp

## References

Van Lissa, C. J., van Erp, S., & Clapper, E. B. (2023). Selecting relevant moderators with Bayesian regularized meta-regression. *Research Synthesis Methods*. doi:10.31234/osf.io/6phs5

Stan Development Team (NA). RStan: the R interface to Stan. R package version 2.26.2. <https://mc-stan.org>

**See Also**

Useful links:

- <https://github.com/cjvanlissa/pema>
- <https://cjvanlissa.github.io/pema/>

---

as.stan

*Convert an object to stanfit*

---

**Description**

Create a stanfit object from an object for which a method exists, so that all methods for stanfit objects can be used.

**Usage**

```
as.stan(x, ...)
```

**Arguments**

x                    An object for which a method exists.  
...                   Arguments passed to or from other methods.

**Value**

An object of class stanfit, as documented in [rstan::stan](#).

**Examples**

```
stanfit <- "a"  
class(stanfit) <- "stanfit"  
converted <- as.stan(stanfit)
```

---

bonapersona

*Data from 'The behavioral phenotype of early life adversity'*

---

**Description**

This meta-analysis of rodent studies examined whether early life adversity (ELA) alters cognitive performance in several domains. The data include over 400 independent experiments, involving approximately 8600 animals.

**Usage**

```
data(bonapersona)
```

**Format**

A data.frame with 734 rows and 65 columns.

**References**

Bonapersona, V., Kentrop, J., Van Lissa, C. J., van der Veen, R., Joels, M., & Sarabdjitsingh, R. A. (2019). The behavioral phenotype of early life adversity: A 3-level meta-analysis of rodent studies. *Neuroscience & Biobehavioral Reviews*, 102, 299–307. doi:10.1016/j.neubiorev.2019.04.021

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brma

*Conduct Bayesian Regularized Meta-Analysis*


---

**Description**

This function conducts Bayesian regularized meta-regression (Van Lissa & Van Erp, 2021). It uses the stan function `rstan::sampling` to fit the model. A lasso or horseshoe prior is used to shrink the regression coefficients of irrelevant moderators towards zero. See Details.

**Usage**

```
brma(x, ...)

## S3 method for class 'formula'
brma(
  formula,
  data,
  vi = "vi",
  study = NULL,
  method = "hs",
  standardize = TRUE,
  prior = switch(method, lasso = c(df = 1, scale = 1), hs = c(df = 1, df_global = 1,
    df_slab = 4, scale_global = 1, scale_slab = 2, relevant_pars = NULL)),
  mute_stan = TRUE,
  ...
)

## Default S3 method:
brma(
  x,
  y,
  vi,
  study = NULL,
  method = "hs",
  standardize,
  prior,
  mute_stan = TRUE,
  intercept,
```

```
    ...
  )
```

## Arguments

<code>x</code>	An $k \times m$ numeric matrix, where $k$ is the number of effect sizes and $m$ is the number of moderators.
<code>...</code>	Additional arguments passed on to <code>rstan::sampling()</code> . Use this, e.g., to override default arguments of that function.
<code>formula</code>	An object of class <code>formula</code> (or one that can be coerced to that class), see <code>lm</code> .
<code>data</code>	Either a <code>data.frame</code> containing the variables in the model, see <code>lm</code> , or a list of multiple imputed <code>data.frames</code> , or an object returned by <code>mice</code> .
<code>vi</code>	Character. Name of the column in the <code>data</code> that contains the variances of the effect sizes. This column will be removed from the <code>data</code> prior to analysis. Defaults to <code>"vi"</code> .
<code>study</code>	Character. Name of the column in the <code>data</code> that contains the study id. Use this when the <code>data</code> includes multiple effect sizes per study. This column can be a vector of integers, or a factor. This column will be removed from the <code>data</code> prior to analysis. See <code>Details</code> for more information about analyzing dependent data.
<code>method</code>	Character, indicating the type of regularizing prior to use. Supports one of <code>c("hs", "lasso")</code> , see <code>Details</code> . Defaults to <code>"hs"</code> .
<code>standardize</code>	Either a logical argument or a list. If <code>standardize</code> is logical, it controls whether all predictors are standardized prior to analysis or not. Parameter estimates are restored to the predictors' original scale. Alternatively, users can provide a list to <code>standardize</code> to gain more control over the standardization process. In this case, it is assumed that the standardization has already taken place. This list must have two elements: <code>list(center = c(mean(X1), mean(X2), mean(X...)), scale = c(sd(X1), sd(X2), sd(X...)))</code> . It is used only to restore parameter estimates to the original scale of the predictors. This is useful, e.g., to standardize continuous and dichotomous variables separately. Defaults to <code>TRUE</code> , which is recommended so that shrinking affects all parameters similarly.
<code>prior</code>	Numeric vector, specifying the prior to use. Note that the different methods require this vector to contain specific named elements.
<code>mute_stan</code>	Logical, indicating whether to mute all 'Stan' output or not.
<code>y</code>	A numeric vector of $k$ effect sizes.
<code>intercept</code>	Logical, indicating whether or not an intercept should be included in the model.

## Details

The Bayesian regularized meta-analysis algorithm (Van Lissa & Van Erp, 2021) penalizes meta-regression coefficients either via the lasso prior (Park & Casella, 2008) or the regularized horseshoe prior (Pironen & Vehtari, 2017).

**lasso** The Bayesian equivalent of the lasso penalty is obtained when placing independent Laplace (i.e., double exponential) priors on the regression coefficients centered around zero. The scale of the Laplace priors is determined by a global scale parameter `scale`, which defaults to 1

and an inverse-tuning parameter  $\frac{1}{\lambda}$  which is given a chi-square prior governed by a degrees of freedom parameter `df` (defaults to 1). If `standardize = TRUE`, shrinkage will affect all coefficients equally and it is not necessary to adapt the scale parameter. Increasing the `df` parameter will allow larger values for the inverse-tuning parameter, leading to less shrinkage.

**hs** One issue with the lasso prior is that it has relatively light tails. As a result, not only does the lasso have the desirable behavior of pulling small coefficients to zero, it also results in too much shrinkage of large coefficients. An alternative prior that improves upon this shrinkage pattern is the horseshoe prior (Carvalho, Polson & Scott, 2010). The horseshoe prior has an infinitely large spike at zero, thereby pulling small coefficients toward zero but in addition has fat tails, which allow substantial coefficients to escape the shrinkage. The regularized horseshoe is an extension of the horseshoe prior that allows the inclusion of prior information regarding the number of relevant predictors and can be more numerically stable in certain cases (Piiroinen & Vehtari, 2017). The regularized horseshoe has a global shrinkage parameter that influences all coefficients similarly and local shrinkage parameters that enable flexible shrinkage patterns for each coefficient separately. The local shrinkage parameters are given a Student's t prior with a default `df` parameter of 1. Larger values for `df` result in lighter tails and a prior that is no longer strictly a horseshoe prior. However, increasing `df` slightly might be necessary to avoid divergent transitions in Stan (see also <https://mc-stan.org/misc/warnings.html>). Similarly, the degrees of freedom for the Student's t prior on the global shrinkage parameter `df_global` can be increased from the default of 1 to, for example, 3 if divergent transitions occur although the resulting prior is then strictly no longer a horseshoe. The scale for the Student's t prior on the global shrinkage parameter `scale_global` defaults to 1 and can be decreased to achieve more shrinkage. Moreover, if prior information regarding the number of relevant moderators is available, it is recommended to include this information via the `relevant_pars` argument by setting it to the expected number of relevant moderators. When `relevant_pars` is specified, `scale_global` is ignored and instead based on the available prior information. Contrary to the horseshoe prior, the regularized horseshoe applies additional regularization on large coefficients which is governed by a Student's t prior with a `scale_slab` defaulting to 2 and `df_slab` defaulting to 4. This additional regularization ensures at least some shrinkage of large coefficients to avoid any sampling problems.

## Value

A list object of class `brma`, with the following structure:

```
list(
  fit          # An object of class stanfit, for compatibility with rstan
  coefficients # A numeric matrix with parameter estimates; these are
              # interpreted as regression coefficients, except tau2 and tau,
              # which are interpreted as the residual variance and standard
              # deviation, respectively.
  formula      # The formula used to estimate the model
  terms       # The predictor terms in the formula
  X           # Numeric matrix of moderator variables
  Y           # Numeric vector with effect sizes
  vi         # Numeric vector with effect size variances
  tau2       # Numeric, estimated tau2
  R2         # Numeric, estimated heterogeneity explained by the moderators
```

```

    k          # Numeric, number of effect sizes
  study      # Numeric vector with study id numbers
)

```

## References

Van Lissa, C. J., van Erp, S., & Clapper, E. B. (2023). Selecting relevant moderators with Bayesian regularized meta-regression. *Research Synthesis Methods*. doi:10.31234/osf.io/6phs5

Park, T., & Casella, G. (2008). The Bayesian Lasso. *Journal of the American Statistical Association*, 103(482), 681–686. doi:10.1198/016214508000000337

Carvalho, C. M., Polson, N. G., & Scott, J. G. (2010). The horseshoe estimator for sparse signals. *Biometrika*, 97(2), 465–480. doi:10.1093/biomet/asq017

Piironen, J., & Vehtari, A. (2017). Sparsity information and regularization in the horseshoe and other shrinkage priors. *Electronic Journal of Statistics*, 11(2). <https://projecteuclid.org/journals/electronic-journal-of-statistics/volume-11/issue-2/Sparsity-information-and-regularization/10.1214/17-EJS1337SI.pdf>

## Examples

```

data("curry")
df <- curry[c(1:5, 50:55), c("d", "vi", "sex", "age", "donorcode")]
suppressWarnings({res <- brma(d~, data = df, iter = 10)})

```

---

check\_workshop\_data    *Check Data for BRMA Workshop*

---

## Description

This function checks that argument `df` is a suitable `data.frame` for completing the workshop on Bayesian Regularized Meta-Regression, and checks that `pema` package dependencies are correctly installed. It suggests how to remedy any failed checks.

## Usage

```
check_workshop_data(df = NULL)
```

## Arguments

`df`                    A `data.frame`.

## Value

Invisibly returns a logical TRUE/FALSE, indicating whether all checks have passed.

## Examples

```
check_workshop_data(bonapersona)
```

---

 curry

*Data from 'Happy to Help?'*


---

### Description

A systematic review and meta-analysis of the effects of performing acts of kindness on the well-being of the actor.

### Usage

```
data(curry)
```

### Format

A data.frame with 56 rows and 18 columns.

<b>study_id</b>	factor	Unique identifier of the study
<b>effect_id</b>	integer	Unique identifier of the effect size
<b>d</b>	numeric	Standardized mean difference between the control group and intervention group
<b>vi</b>	numeric	Variance of the effect size
<b>n1i</b>	numeric	Number of participants in the intervention group
<b>n1c</b>	numeric	Number of participants in the control group
<b>sex</b>	numeric	Percentage of male participants
<b>age</b>	numeric	Mean age of participants
<b>location</b>	character	Geographical location of the study
<b>donor</b>	character	From what population did the donors (helpers) originate?
<b>donorcode</b>	factor	From what population did the donors (helpers) originate? Dichotomized to Anxious or Typ
<b>interventioniv</b>	character	Description of the intervention / independent variable
<b>interventioncode</b>	factor	Description of the intervention / independent variable, categorized to Acts of Kindness, Pro
<b>control</b>	character	Description of the control condition
<b>controlcode</b>	factor	Description of the control condition, categorized to Neutral Activity, Nothing, or Self Help
<b>recipients</b>	character	Who were the recipients of the act of kindness?
<b>outcomedv</b>	character	What was the outcome, or dependent variable, of the study?
<b>outcomecode</b>	factor	What was the outcome, or dependent variable, of the study? Categorized into Happiness, L

### References

Curry, O. S., Rowland, L. A., Van Lissa, C. J., Zlotowitz, S., McAlaney, J., & Whitehouse, H. (2018). Happy to help? A systematic review and meta-analysis of the effects of performing acts of kindness on the well-being of the actor. *Journal of Experimental Social Psychology*, 76, 320-329. [doi:10.1016/j.jecresq.2007.04.005](https://doi.org/10.1016/j.jecresq.2007.04.005)

---

I2	<i>Compute I2</i>
----	-------------------

---

**Description**

I2 represents the amount of heterogeneity relative to the total amount of variance in the observed effect sizes (Higgins & Thompson, 2002). For three-level meta-analyses, it is additionally broken down into I2\_w (amount of within-cluster heterogeneity) and I2\_b (amount of between-cluster heterogeneity).

**Usage**

```
I2(x, ...)
```

**Arguments**

x	An object for which a method exists.
...	Arguments passed to other functions.

**Value**

Numeric matrix, with rows corresponding to I2 (total heterogeneity), and optionally I2\_w and I2\_b (within- and between-cluster heterogeneity).

**Examples**

```
I2(matrix(1:20, ncol = 1))
```

---

maxap	<i>Maximum a posteriori parameter estimate</i>
-------	--

---

**Description**

Find the parameter estimate with the highest posterior probability density given a vector of samples.

**Usage**

```
maxap(x, dens = NULL, ...)
```

**Arguments**

x	Numeric vector.
dens	Optional object of class density. Defaults to NULL.
...	Arguments passed to <a href="#">density</a>

**Value**

Atomic numeric vector with the maximum a-posteriori estimate of vector  $x$ .

**Examples**

```
maxap(c(1,2,3,4,5))
```

---

plot_sensitivity	<i>Plot posterior distributions for BRMA models</i>
------------------	---

---

**Description**

To perform a rudimentary sensitivity analysis, plot the posterior distributions of multiple BRMA models and compare them visually.

**Usage**

```
plot_sensitivity(..., parameters = NULL, model_names = NULL)
```

**Arguments**

...	Objects of class <code>brma</code> . If the argument <code>model_names</code> is <code>NULL</code> , the names of these objects are used to label the plot.
<code>parameters</code>	Optional character vector with the names of parameters that exist in the models in ..., Default: <code>NULL</code> .
<code>model_names</code>	Optional character vector with the names used to label the models in ..., Default: <code>NULL</code> .

**Value**

An object of class `ggplot`

**Examples**

```
plot_sensitivity(samples = list(
  data.frame(Parameter = "b",
    Value = rnorm(10),
    Model = "M1"),
  data.frame(Parameter = "b",
    Value = rnorm(10, mean = 2),
    Model = "M2")),
  parameters = "b")
```

---

sample_prior	<i>Sample from the Prior Distribution</i>
--------------	---

---

**Description**

Samples from a prior distribution with parameters defined in `prior`. The result can be plotted using the `plot` function.

**Usage**

```
sample_prior(  
  method = c("hs", "lasso"),  
  prior = switch(method, lasso = c(df = 1, scale = 1), hs = c(df = 1, df_global = 1,  
    df_slab = 4, scale_global = 1, scale_slab = 2, par_ratio = NULL)),  
  iter = 1000  
)
```

**Arguments**

<code>method</code>	Character string, indicating which prior to sample from. Default: first element of <code>c("hs", "lasso")</code> .
<code>prior</code>	Numeric vector, specifying the prior to use. See <a href="#">brma</a> for more details.
<code>iter</code>	A positive integer specifying the number of iterations to sample. Default: 1000

**Value**

NULL, function is called for its side-effect of plotting to the graphics device.

**Examples**

```
sample_prior("lasso", iter = 10)
```

---

shiny_prior	<i>Interactively Sample from the Prior Distribution</i>
-------------	---

---

**Description**

Launches a Shiny app that allows interactive comparison of different priors for [brma](#).

**Usage**

```
shiny_prior()
```

**Value**

NULL, function is called for its side-effect of launching a Shiny app.

**Examples**

```
## Not run:
shiny_prior()

## End(Not run)
```

---

simulate\_smd

*Simulates a meta-analytic dataset*


---

**Description**

This function simulates a meta-analytic dataset based on the random-effects model. The simulated effect size is Hedges'  $G$ , an estimator of the Standardized Mean Difference (Hedges, 1981; Li, Dusseldorp, & Meulman, 2017). The functional form of the model can be specified, and moderators can be either normally distributed or Bernoulli-distributed. See Van Lissa, in preparation, for a detailed explanation of the simulation procedure.

**Usage**

```
simulate_smd(
  k_train = 20,
  k_test = 100,
  mean_n = 40,
  es = 0.5,
  tau2 = 0.04,
  alpha = 0,
  moderators = 5,
  distribution = "normal",
  model = "es * x[, 1]"
)
```

**Arguments**

<code>k_train</code>	Atomic integer. The number of studies in the training dataset. Defaults to 20.
<code>k_test</code>	Atomic integer. The number of studies in the testing dataset. Defaults to 100.
<code>mean_n</code>	Atomic integer. The mean sample size of each simulated study in the meta-analytic dataset. Defaults to 40. For each simulated study, the sample size $n$ is randomly drawn from a normal distribution with mean <code>mean_n</code> , and sd <code>mean_n/3</code> .
<code>es</code>	Atomic numeric vector. The effect size, also known as beta, used in the model statement. Defaults to .5.
<code>tau2</code>	Atomic numeric vector. The residual heterogeneity. For a range of realistic values encountered in psychological research, see Van Erp, Verhagen, Grasman, & Wagenmakers, 2017. Defaults to 0.04.
<code>alpha</code>	Vector of slant parameters, passed to <a href="#">sn::rsn</a> .

moderators	Atomic integer. The number of moderators to simulate for each study. Make sure that the number of moderators to be simulated is at least as large as the number of moderators referred to in the model parameter. Internally, the matrix of moderators is referred to as "x". Defaults to 5.
distribution	Atomic character. The distribution of the moderators. Can be set to either "normal" or "bernoulli". Defaults to "normal".
model	Expression. An expression to specify the model from which to simulate the mean true effect size, mu. This formula may use the terms "es" (referring to the es parameter of the call to simulate_smd), and "x\[ , \]" (referring to the matrix of moderators, x). Thus, to specify that the mean effect size, mu, is a function of the effect size and the first moderator, one would pass the value model = "es * x\[ , 1\]". Defaults to "es * x\[ , 1\]".

### Value

List of length 4. The "training" element of this list is a data.frame with k\_train rows. The columns are the variance of the effect size, vi; the effect size, yi, and the moderators, X. The "testing" element of this list is a data.frame with k\_test rows. The columns are the effect size, yi, and the moderators, X. The "housekeeping" element of this list is a data.frame with k\_train + k\_test rows. The columns are n, the sample size n for each simulated study; mu\_i, the mean true effect size for each simulated study; and theta\_i, the true effect size for each simulated study.

### Examples

```
set.seed(8)
simulate_smd()
simulate_smd(k_train = 50, distribution = "bernoulli")
simulate_smd(distribution = "bernoulli", model = "es * x[ ,1] * x[ ,2]")
```

# Index

## \* datasets

bonapersona, 3  
curry, 8

as.stan, 3

bonapersona, 3  
brma, 4, 11

check\_workshop\_data, 7  
curry, 8

density, 9

I2, 9

lm, 5

maxap, 9  
mice, 5

pema (pema-package), 2  
pema-package, 2  
plot, 11  
plot\_sensitivity, 10

rstan::sampling, 4  
rstan::sampling(), 5  
rstan::stan, 3

sample\_prior, 11  
shiny\_prior, 11  
simulate\_smd, 12  
sn::rsn, 12