

# Package ‘makemyprior’

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**Type** Package

**Title** Intuitive Construction of Joint Priors for Variance Parameters

**Version** 1.1.0

**Description** Tool for easy prior construction and visualization. It helps to formulate joint prior distributions for variance parameters in latent Gaussian models. The resulting prior is robust and can be created in an intuitive way. A graphical user interface (GUI) can be used to choose the joint prior, where the user can click through the model and select priors. An extensive guide is available in the GUI. The package allows for direct inference with the specified model and prior. Using a hierarchical variance decomposition, we formulate a joint variance prior that takes the whole model structure into account. In this way, existing knowledge can intuitively be incorporated at the level it applies to. Alternatively, one can use independent variance priors for each model component in the latent Gaussian model.

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**Author** Ingeborg Gullikstad Hem [cre, aut],  
Geir-Arne Fuglstad [aut],  
Andrea Riebler [aut]

**Maintainer** Ingeborg Gullikstad Hem <ingeborg.hem@ntnu.no>

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---

compile\_stan

*Compile stan-model*

---

### Description

Function that compiles the stan-code for inference that is included in the model. The compiled version is stored in a .rds-file, which is by default stored in tempdir(). Can also be stored in the package (permanent = TRUE), or in a custom directory. In the latter case, this custom directory must be specified every time `inference_stan` is called. This will also be done by `inference_stan`, but this way can save some time if it is not already pre-compiled.

**Usage**

```
compile_stan(save = FALSE, permanent = FALSE, path = NULL)
```

**Arguments**

save	Whether to save stan-file to location in package or not, defaults to FALSE. Must be in interactive session to save the object to a file.
permanent	If TRUE, the file is stored in the package directory. If FALSE (default), the file is saved in tempdir().
path	Only used if file cannot be saved in the package folder. This is a path to a folder where the file is stored, do not specify a name for the file! (It will be called "full_file.rds", and should not be changed.) This argument makes the permanent argument being ignored.

**Details**

Note that you will get a message saying something about integer division. The PC priors on variance proportions are represented by splines, and to evaluate them in Stan we look up values, and use integer division for this. This does not cause problems.

**Value**

Returns the stan-model invisibly.

**Examples**

```
if (interactive() && requireNamespace("rstan")){
  compile_stan(save = TRUE) # saving in tempdir()
}
```

---

create_stan_file	<i>Create a "skeleton" for custom Stan code</i>
------------------	---

---

**Description**

Makes and saves files with generic code for writing custom Stan code and still use the HD prior.

**Usage**

```
create_stan_file(save = FALSE, location = "")
```

**Arguments**

save	To confirm that files can be saved (default FALSE).
location	Path to location.

**Details**

Must be in an interactive session to store the code. A folder called "my\_stan\_code" will be created in location. If the folder already exists in the specified location, you get an error. The folder contains:

`main_file.stan` Main file. Can put all necessary functions here, but for a cleaner code that is easier to read, we put the functions in separate files.

`jacobian.stan` Function that automatically computes the Jacobian, needed to transform from weights and total variance parameterization to log-variance parameterization.

`prior_distributions.stan` Functions for computing the prior distributions.

The provided code is written so a random intercept model with an intercept, a group effect and a residual effect can be fitted:

`example_custom_stan.R` R script showing how one can fit a random intercept model using the provided code.

The code can be expanded to fit the desired model. This requires some knowledge about Stan. No more documentation is given, as this is merely an offer to users who want to use other models than what are provided in the package already, and will be highly model specific.

**Value**

Nothing.

**Examples**

```
## Not run:
create_stan_file(TRUE, "")

## End(Not run)
```

---

eval_joint_prior	<i>Evaluate the joint variance prior</i>
------------------	--

---

**Description**

Function for evaluating the joint variance prior stored in `prior_obj`. To compute the joint prior, the functions needs to know the transformation from the total variance/variance proportion scale to log-variance scale. This is computed before inference, but is not stored in the `mmp_prior`-object. To avoid having to recompute this for every evaluation and thus improve the speed, we make a condensed data object with the function [make\\_eval\\_prior\\_data](#).

**Usage**

```
eval_joint_prior(theta, prior_data)

make_eval_prior_data(prior_obj)
```

**Arguments**

theta	Vector of log variances. The order of the log variances is the same as specified in the formula, with the residual variance at the end for a Gaussian likelihood. To be sure, you can use <a href="#">get_parameter_order</a> to check the order.
prior_data	An object from <a href="#">make_eval_prior_data</a> .
prior_obj	Object of class mmp_prior, see <a href="#">make_prior</a> .

**Details**

Note that a Jeffreys' prior is improper and sampling with the prior only will not work when it is used. For sampling from the prior (for example for debugging), use a proper prior for all parameters instead.

The `make_eval_prior_data` function is used to create a condensed version of the prior object from `make_prior`, that only contains what is needed to compute the joint prior. Since the HD prior is chosen on total variances and variance proportions, some additional information is needed to compute the Jacobian for the joint prior. To improve the speed, we do this once before evaluating the prior.

**Value**

Logarithm of the prior density

**Examples**

```
ex_model <- makemyprior_example_model()
get_parameter_order(ex_model) # a, b, eps
prior_data <- make_eval_prior_data(ex_model)
eval_joint_prior(c(0, 0, 0), prior_data)
eval_joint_prior(c(-1, 0, 1), prior_data)

# a model with only 2 variance parameters
if (interactive()){

  data <- list(
    a = rep(1:10, each = 10)
  )
  set.seed(1); data$y <- rnorm(10, 0, 0.4)[data$a] + rnorm(100, 0, 1)

  # random intercept model
  ex_model2 <- make_prior(y ~ mc(a), data, family = "gaussian",
    prior = list(tree = "s2 = (a, eps)",
      w = list(s2 = list(prior = "pc0", param = 0.25)),
      V = list(s2 = list(prior = "pc", param = c(3, 0.05)))),
    intercept_prior = c(0, 1000))

  prior_data2 <- make_eval_prior_data(ex_model2)
  # evaluating the prior in a grid
  theta_a <- seq(-8, 4, 0.1)
  theta_eps <- seq(-8, 4, 0.1)
```

```

res <- matrix(nrow = 0, ncol = 3)
for (ind in 1:length(theta_a)){
  for (jnd in 1:length(theta_eps)){
    res <- rbind(res, c(theta_a[ind], theta_eps[jnd],
                       eval_joint_prior(c(theta_a[ind], theta_eps[jnd]), prior_data2)))
  }
}

# graph showing the prior
if (requireNamespace("ggplot2")){
  res2 <- as.data.frame(res)
  names(res2) <- c("x", "y", "z")
  # Note from the "exp(z)" that we use the posterior, and not log posterior, in this plot
  ggplot(res2, aes(x = x, y = y, z = exp(z), fill = exp(z))) +
    geom_raster() +
    geom_contour(color = "black") +
    scale_fill_viridis_c(option = "E") +
    xlab("Log variance of 'a'") +
    ylab("Log residual variance") +
    labs(fill = "Density") +
    theme_bw()
}
}

```

---

eval\_pc\_prior

*Evaluate PC prior for variance proportion*


---

### Description

Evaluate PC prior for a variance proportion.

### Usage

```
eval_pc_prior(x, obj, param, logitscale = FALSE)
```

### Arguments

x	Values to evaluate prior in.
obj	Prior object from <a href="#">make_prior</a>
param	Which weight to plot, indicated using syntax shown when printing (do not need to include the w[. .] part to indicate that it is a variance proportion, but can be included). Print the prior object to see syntax for each weight.
logitscale	Is the input x on logit-scale? (default FALSE).

### Value

Returns density for the given variance proportion.

**Examples**

```
ex_prior <- makemyprior_example_model()
eval_pc_prior(seq(0, 1, 0.01), ex_prior, "eps/eps_a_b")
# or:
eval_pc_prior(seq(0, 1, 0.01), ex_prior, "w[eps/eps_a_b]")
```

---

expit

*expit*

---

**Description**

Calculates inverse logit,  $\exp(x)/(1+\exp(x)) = 1/(1+\exp(-x))$

**Usage**

```
expit(x)
```

**Arguments**

x                      Real number, or vector of reals

**Value**

expit value

**Examples**

```
expit(2)
expit(seq(-5, 5, 1))
```

---

extract\_posterior\_effect

*Extract the posterior of a random effect*

---

**Description**

Extract the posterior of a random effect in the model for inference done with Stan

**Usage**

```
extract_posterior_effect(obj, effname)
```

**Arguments**

obj            An object from inference\_stan.  
 effname       Name of the random effect, same name as in the data.

**Value**

Returns a matrix with the posterior samples of the chosen effect

**Examples**

```
if (interactive() && requireNamespace("rstan")){
  ex_prior <- makemyprior_example_model()
  res_stan <- inference_stan(ex_prior, iter = 100)
  # Note: For reliable results, increase the number of iterations (e.g., 'iter = 2000')
  extract_posterior_effect(res_stan, "a")
}
```

---

extract\_posterior\_parameter

*Extract the posterior parameter estimate*

---

**Description**

Extract the posterior parameter estimate of a random effect variance or fixed effect coefficient when inference is done with Stan

**Usage**

```
extract_posterior_parameter(obj, param)
```

**Arguments**

obj            An object from inference\_stan.  
 param         Name of the variance parameter, which is the same as the name of the corresponding fixed or random effect in the data. Intercept is denoted 'intercept', and residual variance is denoted 'eps'.

**Value**

Returns a vector with the posterior samples of the chosen parameter, on variance scale for variances parameters and original (the common) scale for fixed effect coefficients

**Examples**

```

if (interactive() && requireNamespace("rstan")){
  ex_prior <- makemyprior_example_model()
  res_stan <- inference_stan(ex_prior, iter = 100)
  # Note: For reliable results, increase the number of iterations (e.g., 'iter = 2000')
  extract_posterior_parameter(res_stan, "intercept")
  extract_posterior_parameter(res_stan, "a")
}

```

---

find\_pc\_prior\_param    *Find suitable PC prior parameters*

---

**Description**

Returns the U value in  $P(U > \sigma) = \alpha$  for a PC prior on standard deviation given an equal-tailed credible interval  $P(\text{lower} < \text{func}(x) < \text{upper}) = \text{prob}$  where  $x$  is a Gaussian variable with zero mean standard deviation  $\sigma$ . Note that this function uses sampling.

**Usage**

```

find_pc_prior_param(
  lower,
  upper,
  alpha = 0.05,
  func = exp,
  N = 10000,
  prob = 0.95
)

```

**Arguments**

lower	lower end of credible interval
upper	upper end of credible interval
alpha	tail probability of the PC prior (default = 0.05)
func	function to scale Gaussian variables to match desired credible interval scale, default is the exponential function
N	number of samples to use when sampling sigma and x, default is 1e4
prob	amount of mass to put in the credible interval, default is 0.95

**Value**

The U-value to pass to the PC prior. NB! Store result to avoid rerunning this function, as it uses sampling. The function also prints (sampled) quantiles for the U-value that is returned.

**Examples**

```
find_pc_prior_param(0.1, 10)
```

---

`get_parameter_order`     *Internal variance parameter order*

---

**Description**

Returns the internal order of the variance parameters related to each random effect in the model.

**Usage**

```
get_parameter_order(prior_obj)
```

**Arguments**

`prior_obj`     Object of class `mmp_prior`, see [make\\_prior](#).

**Value**

Names of the random effects in the model in the order the prior object reads them.

**Examples**

```
ex_model <- makemyprior_example_model()
get_parameter_order(ex_model)
```

---

`inference_inla`     *Run inference*

---

**Description**

This function helps you run inference with INLA using a prior object from [make\\_prior](#). You must have INLA installed to run this. INLA can be installed with: `install.packages("INLA", repos = c(getOption("repos"), INLA = "https://inla.r-inla-download.org/R/stable"), dep = TRUE)`. Also see [r-inla.org](http://r-inla.org).

**Usage**

```
inference_inla(prior_obj, use_likelihoood = TRUE, print_prior = TRUE, ...)
```

**Arguments**

prior_obj	An object from <a href="#">make_prior</a> , from <a href="#">makemyprior_gui</a> , from <a href="#">inference_stan</a> , or from <a href="#">inference_inla</a> (for refitting model)
use_likelihoood	Whether to sample from the prior only (FALSE, can be used for e.g. debugging or to look at the priors on variance parameters when using an HD prior, see also <a href="#">Details</a> ), or to use the likelihood and data to get the posterior (TRUE, default).
print_prior	Whether to print a text with the chosen prior or not (default TRUE)
...	Other values to be sent to INLA. Useful arguments include <code>Ntrials</code> for the binomial likelihood. We set the default value of <code>num.threads</code> to 1 (this can however be changed). See <a href="#">inla</a> for details. Can be anything sent to <a href="#">inla</a> except for <code>control.expert</code> and arguments that specify priors.

**Details**

Jeffreys' prior is improper. If `use_likelihoood = FALSE` and Jeffreys' prior is used for the total variance, the prior will be changed to a Gaussian(0,1) prior on the log total variance. This means that it does not make sense to look at the variances/standard deviations/precisions, but the variance proportions will be correct. Note that this is only an issue when sampling from the prior (i.e., not using the likelihood).

**Value**

A named list with a prior object (`prior`), an `inla`-object (`inla`) and some data `inla` requires (`inla_data`).

**Examples**

```
## Not run:

vignette("make_prior", package = "makemyprior")

## End(Not run)

ex_prior <- makemyprior_example_model()
if (interactive() && requireNamespace("INLA")){
  posterior <- inference_inla(ex_prior)
  plot(posterior)
}
```

---

inference\_stan

*Run inference*


---

**Description**

This function helps you run inference with [rstan](#) using a prior object from [make\\_prior](#). Note that you must install Stan: `install.packages("rstan")`, see [mc-stan.org](#).

**Usage**

```
inference_stan(
  prior_obj,
  use_likelihoood = TRUE,
  print_prior = TRUE,
  path = NULL,
  ...
)
```

**Arguments**

prior_obj	An object from <a href="#">make_prior</a> , from <a href="#">makemyprior_gui</a> , from <a href="#">inference_stan</a> , or from <a href="#">inference_inla</a> (for refitting model)
use_likelihoood	Whether to sample from the prior only (FALSE, can be used for e.g. debugging or to look at the priors on variance parameters when using an HD prior, see also Details), or to use the likelihood and data to get the posterior (TRUE, default).
print_prior	Whether to print a text with the chosen prior or not (default TRUE)
path	Path to folder. See <a href="#">compile_stan</a> . Only necessary if compiled code is stored somewhere else than in <code>tempdir()</code> or the package directory (checking <code>tempdir()</code> first).
...	Other arguments to be sent to <a href="#">sampling</a> . Useful arguments include: <ul style="list-style-type: none"> <li><code>iter</code> number of iterations for each chain (including burn-in, 2000 is the default)</li> <li><code>warmup</code> number of iterations for the burn-in (default is <code>iter/2</code>)</li> <li><code>chains</code> number of chains</li> <li><code>init</code> initial value of the model parameters on internal parameterization (log-variances and covariate coefficients)</li> <li><code>seed</code> seed value for random number generation</li> </ul> <p>See <a href="#">sampling</a> for more details. Note that for inference with <code>stan</code>, the <code>Ntrials</code> argument must be included in the data object, and cannot be provided to this function.</p>

**Details**

We cannot sample from a Jeffreys' prior since it is improper. If `use_likelihoood = FALSE` and Jeffreys' prior is used for the total variance, the prior will be changed to a Gaussian(0,1) prior on the log total variance. This means that it does not make sense to look at the variances/standard deviations/precisions, but the variance proportions will be correct. Note that this is only an issue when sampling from the prior (i.e., not using the likelihood).

**Value**

A named list with a prior object (`prior`), a stan-object (`stan`) and some data stan requires (`stan_data`).

**Examples**

```
## Not run:

vignette("make_prior", package = "makemyprior")

## End(Not run)

ex_prior <- makemyprior_example_model()
if (interactive() && requireNamespace("rstan")){
  posterior <- inference_stan(ex_prior, iter = 100)
  # Note: For reliable results, increase the number of iterations (e.g., 'iter = 2000')
  plot(posterior)
}

## Not run:

posterior <- inference_stan(ex_prior, use_likelihoood = TRUE, iter = 1e4, chains = 1, seed = 1)
plot(posterior)

## End(Not run)
```

---

latin\_data

*Latin square experiment data*

---

**Description**

Simulated dataset for latin square experiment with 81 observations.

**Usage**

```
latin_data
```

**Format**

A list with the following variables:

**y** Response

**lin** Covariate for linear effect of treatment

**row** Row indexes

**col** Column indexes

**treat\_iid, treat\_rw2** Treatment indexes

**Examples**

```

## Not run:

vignette("latin_square", package = "makemyprior")

## End(Not run)

if (interactive() && requireNamespace("rstan")){

  formula <- y ~ lin + mc(row) + mc(col) + mc(iid) +
    mc(rw2, model = "rw2", constr = TRUE, lin_constr = TRUE)

  prior <- make_prior(
    formula, latin_data,
    prior = list(tree = "s1 = (rw2, iid);
                  s2 = (row, col, s1); s3 = (s2, eps)",
                  w = list(s1 = list(prior = "pc0", param = 0.25),
                          s2 = list(prior = "dirichlet"),
                          s3 = list(prior = "pc0", param = 0.25))))

  posterior <- inference_stan(prior, iter = 150, warmup = 50,
                             seed = 1, init = "0", chains = 1)
  # Note: For reliable results, increase the number of iterations

  plot(prior)
  plot_tree_structure(prior)
  plot_posterior_fixed(posterior)
  plot_posterior_stan(posterior, param = "prior", prior = TRUE)
}

## Not run:

posterior <- inference_stan(prior, iter = 15000, warmup = 5000,
                           seed = 1, init = "0", chains = 1)

plot(prior)
plot_tree_structure(prior)
plot_posterior_fixed(posterior)
plot_posterior_stan(posterior, param = "prior", prior = TRUE)

## End(Not run)

```

---

logit

logit

---

**Description**

Calculates logit,  $\log(x/(1-x)) = \log(x) - \log(1-x)$

**Usage**

`logit(x)`

**Arguments**

`x` Value between 0 and 1, or vector of such values

**Value**

logit value

**Examples**

```
logit(0.5)
logit(seq(0, 1, 0.1))
```

---

`makemyprior_example_model`

*Returning a simple example prior object*

---

**Description**

Creating a simple prior object using [make\\_prior](#). Used in examples of other functions in the package.

**Usage**

```
makemyprior_example_model(seed = 1)
```

**Arguments**

`seed` A seed value for reproducing the data (default seed = 1).

**Details**

See the example for what model is made.

**Value**

An object of class `mmp_prior`.

## Examples

```

ex_model <- makemyprior_example_model()

## Not run:
# The function corresponds to the following model call:

set.seed(1)

data <- list(
  a = rep(1:10, each = 10),
  b = rep(1:10, times = 10)
)
data$y <- rnorm(10, 0, 0.4)[data$a] + rnorm(10, 0, 0.6)[data$b] + rnorm(100, 0, 1)

formula <- y ~ mc(a) + mc(b)

prior <- make_prior(formula, data, family = "gaussian",
  prior = list(tree = "s1 = (a, b); s2 = (s1, eps)",
    w = list(s2 = list(prior = "pc0", param = 0.25)),
    V = list(s2 = list(prior = "pc", param = c(3, 0.05))))),
  intercept_prior = c(0, 1000))

## End(Not run)

```

---

makemyprior\_gui

*Graphical prior construction*


---

## Description

This functions opens a shiny app where the specified prior can be seen, and changed.

## Usage

```
makemyprior_gui(prior, guide = FALSE, no_pc = FALSE)
```

## Arguments

prior	An object from <a href="#">make_prior</a> .
guide	Logical, whether to open the guide directly when the app is started. Default is FALSE. The guide can be opened in the app at any time.
no_pc	Turn off computation of the PC prior on splits when using the shiny-app, to avoid slow computations. Upon closing, the PC priors will be computed. Default is FALSE.

**Value**

Returns an object that can be sent to [inference\\_stan](#) or [inference\\_inla](#). Can also be sent to [make-myprior\\_gui](#) again.

**Examples**

```
## Not run:

vignette("make_prior", package = "makemyprior")

## End(Not run)

if (interactive()){
  ex_prior <- makemyprior_example_model()
  new_prior <- makemyprior_gui(ex_prior)
}
```

---

`makemyprior_models`      *List available priors, latent models and likelihoods*

---

**Description**

Prints available priors, latent models and likelihoods to use with [make\\_prior](#).

**Usage**

```
makemyprior_models(type = c("prior", "latent", "likelihood"), select = NULL)
```

**Arguments**

<code>type</code>	Which of priors, latent models and likelihoods to list. Options are prior, latent and likelihood
<code>select</code>	Which in each group to show details about. NULL gives only list what exists (default), all gives detailed information about everything in that category. Can also ask for one or more specific priors/latent models/likelihoods

**Value**

None.

**Examples**

```
makemyprior_models("prior", c("pc0", "pc1"))
makemyprior_models("latent")
makemyprior_models("likelihood", "all")
```

---

makemyprior\_plotting *List of available plotting functions*

---

## Description

Directs to this help page.

## Usage

```
makemyprior_plotting()
```

## Details

The available plotting functions are:

- [plot\\_marginal\\_prior](#)
- [plot\\_posterior\\_fixed](#)
- [plot\\_posterior\\_precision](#)
- [plot\\_posterior\\_stan](#)
- [plot\\_posterior\\_stdev](#)
- [plot\\_posterior\\_variance](#)
- [plot\\_prior](#)
- [plot\\_several\\_posterior\\_stan](#)
- [plot\\_tree\\_structure](#)

In addition the following functions can be used to extract posterior samples of effects and parameters:

- [extract\\_posterior\\_effect](#)
- [extract\\_posterior\\_parameter](#)

[eval\\_pc\\_prior](#) can be used to evaluate a PC prior for a weight parameter, and [eval\\_joint\\_prior](#) to evaluate the whole joint prior.

## Value

None.

---

make\_prior

*Making a prior object*


---

### Description

Make a prior object with all necessary information about the prior and model. The object can either be sent to [makemyprior\\_gui](#) or used directly for inference with Stan ([inference\\_stan](#)) or INLA ([inference\\_inla](#)).

### Usage

```
make_prior(
  formula,
  data,
  family = "gaussian",
  prior = list(),
  intercept_prior = c(),
  covariate_prior = list()
)
```

### Arguments

formula	A formula object, using the function <a href="#">mc</a> .
data	The data used in the model, as a <code>data.frame</code> or <code>list</code> . All elements must have the same length.
family	A string indicating the likelihood family. <code>gaussian</code> with identity link is the default. <code>binomial</code> with logit link and <code>poisson</code> with log link are also possible.
prior	tree The tree structure as a string. A split is specified as <code>s1 = (a,b)</code> , where <code>(s1)</code> represents a split node and can be any name except names of the input data in <code>data</code> and the reserved <code>(eps)</code> , which is used for residuals for a Gaussian likelihood. Short names are recommended. Note that these split names are just used in the initial specification, and will not be used later as they are changed by the function automatically. The child nodes for each split are included in parentheses separated by commas, and each split is separated by semicolons. Singletons are included as <code>(a)</code> . V A named list with information on the priors on each top node and singleton, i.e., all variances. The names in the list are the top node and singleton names from the tree argument. Syntax is <code>V = list(s1 = list(prior = prior_name, param = parameter_vector))</code> . w A named list with information on the priors on each split, i.e., all variance proportions. The names in the list are the split node names from the tree argument, and is specified in the same way as the variance priors in V. Prior on residuals can be defined using <code>eps</code> in this list in the case of a Gaussian likelihood.

`intercept_prior` Parameters for Gaussian prior on intercept, specified as a vector with mean and standard deviation. Default is (0, 1000).

`covariate_prior` Parameters for Gaussian prior on coefficients of covariates, specified as named list, each element is a vector with mean and standard deviation. Default is (0, 1000).

### Details

See [makemyprior\\_models](#) for details on available priors and likelihoods.

### Value

Prior object.

### Examples

```
## Not run:

vignette("make_prior", package = "makemyprior")

## End(Not run)

p <- 10
m <- 10
n <- m*p

set.seed(1)
data <- list(a = rep(1:p, each = m),
            b = rep(1:m, times = p),
            x = runif(n))
data$y <- data$x + rnorm(p, 0, 0.5)[data$a] +
  rnorm(m, 0, 0.3)[data$b] + rnorm(n, 0, 1)

formula <- y ~ x + mc(a) + mc(b)

prior <- make_prior(formula, data, family = "gaussian",
                  intercept_prior = c(0, 1000),
                  covariate_prior = list(x = c(0, 100)))

prior
plot(prior)
```

## Description

Function for defining a latent component for the HD prior package. All model components must be specified, and if an HD prior is used, this is specified later. See [make\\_prior](#) for more details and examples.

## Usage

```
mc(
  label,
  model = "iid",
  constr = NULL,
  lin_constr = FALSE,
  Cmatrix = NULL,
  graph = NULL,
  ...
)
```

## Arguments

label	Name of the component (short names is an advantage as they are used in the app), no default (MUST be provided)
model	Type of model, default is "iid" (see list of models: <a href="#">makemyprior_models</a> ).
constr	Sum-to-zero constraints on component (default TRUE)
lin_constr	Linear sum-to-zero constraint, TRUE/FALSE (only for rw2 and only for Stan)
Cmatrix	Precision for this component when model = "generic0". We recommend that the matrixes are scaled to the typical variance of the corresponding covariance matrix is 1. This can be done with <a href="#">scale_precmat</a> before sending matrix to <a href="#">mc</a> .
graph	Path to graph file for besag effect (see details).
...	Additional arguments used for inference. For inference with <a href="#">rstan</a> or <a href="#">inla</a> , the following is useful (especially for the Besag model):  scale.model if TRUE, the models are scaled so the geometric mean of the variance (typical variance) is 1  And some additional arguments that can be used by <a href="#">inla</a> . Useful arguments include:  rankdef number defining rank deficiency of the model extraconstr extra linear constraints (in addition to constr)  See <a href="#">f</a> for details.

## Details

The graph argument is a path to a file describing neighbouring relationship on the following form:  
First row: number of elements  
The rest: First number is the index of this element, second is the number of neighbours, the rest is the index numbers of all neighbours for this element. If element 1 and 4 are neighbours, 1 should have 4 in its neighbour list, and 4 should have 1.

**Value**

For specifying details on this latent component.

**Examples**

```
## Not run:

vignette("make_prior", package = "makemyprior")

## End(Not run)
```

---

neonatal_data	<i>Neonatal mortality data</i>
---------------	--------------------------------

---

**Description**

Simulated neonatal mortality data with 323 observations.

**Usage**

```
neonatal_data
```

**Format**

A list with the following variables:

**y** Response

**Ntrials** Number of trials for each cluster

**urban** Covariate indicating if cluster is urban (1) or rural (0)

**nu** Cluster effect indexes

**v** County effect indexes for iid effect

**u** County effect indexes for Besag effect

**Examples**

```
## Not run:

vignette("neonatal_mortality", package = "makemyprior")

## End(Not run)

if (interactive() && requireNamespace("rstan")){

  graph_path <- paste0(path.package("makemyprior"), "/neonatal.graph")

  formula <- y ~ urban + mc(nu) + mc(v) +
```

```

    mc(u, model = "besag", graph = graph_path, scale.model = TRUE)

set.seed(1)
find_pc_prior_param(lower = 0.1, upper = 10, prob = 0.9, N = 2e5)

prior <- make_prior(
  formula, neonatal_data, family = "binomial",
  prior = list(tree = "s1 = (u, v); s2 = (s1, nu)",
    w = list(s1 = list(prior = "pc0", param = 0.25),
      s2 = list(prior = "pc1", param = 0.75)),
    V = list(s2 = list(prior = "pc",
      param = c(3.35, 0.05))))))

posterior <- inference_stan(prior, iter = 150, warmup = 50,
  seed = 1, init = "0", chains = 1)
# Note: For reliable results, increase the number of iterations

plot(prior)
plot_tree_structure(prior)
plot_posterior_fixed(posterior)
plot_posterior_stan(posterior, param = "prior", prior = TRUE)
}

## Not run:

posterior <- inference_stan(prior, iter = 15000, warmup = 5000,
  seed = 1, init = "0", chains = 1)

plot(prior)
plot_tree_structure(prior)
plot_posterior_fixed(posterior)
plot_posterior_stan(posterior, param = "prior", prior = TRUE)

## End(Not run)

```

---

plot.mmp\_prior

*Plotting*


---

## Description

Plotting

## Usage

```

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

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

```

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

### Arguments

`x` Object of class `mmp_prior`, `mmp_inla` or `mmp_stan`.  
`...` Additional arguments to plotting functions. Varies with what object is sent to function.

### Details

See [plot\\_prior](#) (objects of class `mmp_prior`), [plot\\_posterior\\_stan](#) (objects of class `mmp_stan`), and [plot\\_posterior\\_variance](#) (objects of class `mmp_inla`),

### Value

None.

### Examples

```
pri <- makemyprior_example_model()
plot(pri)

if (interactive() && requireNamespace("rstan")){
  res_stan <- inference_stan(ex_prior, iter = 100)
  # Note: For reliable results, increase the number of iterations (e.g., 'iter = 2000')
  plot(res_stan)
}

if (interactive() && requireNamespace("INLA")){
  res_inla <- inference_inla(pri)
  plot(res_inla)
}
```

---

`plot_marginal_prior` *Plotting prior for a single parameter (weight or variance (not standard deviation))*

---

### Description

Following the parameterization of the prior.

### Usage

```
plot_marginal_prior(x, obj, param, sd = FALSE)
```

**Arguments**

x	Values to evaluate prior in.
obj	An object from <code>make_prior</code> , <code>inference_stan</code> , <code>inference_inla</code> , or <code>makemyprior_gui</code>
param	Name of parameter to plot (see <code>print(obj)</code> for syntax). Note that only variances will be plotted, so <code>V[. .]</code> and <code>sigma^2[. .]</code> must be used to indicate those parameters.
sd	Whether to plot variance parameters on the standard deviation (TRUE) or variance (FALSE, default) scale

**Value**

A `ggplot` with the posterior distribution. See also [makemyprior\\_plotting](#).

**Examples**

```
ex_prior <- makemyprior_example_model()
plot_marginal_prior(seq(0, 1, 0.001), ex_prior, "w[a/a_b]")
plot_marginal_prior(seq(0, 1, 0.001), ex_prior, "w[eps/eps_a_b]")
plot_marginal_prior(seq(0, 5, 0.01), ex_prior, "V[eps_a_b]")
```

---

`plot_posterior_fixed` *Plotting posterior distributions*

---

**Description**

Function for plotting the posterior distributions of the coefficients of the fixed effects

**Usage**

```
plot_posterior_fixed(obj)
```

**Arguments**

obj	An object from <code>inference_stan</code> or <code>inference_inla</code>
-----	---

**Value**

A `ggplot` with the posterior distributions. See also [makemyprior\\_plotting](#).

**Examples**

```
if (interactive() && requireNamespace("rstan")){
  ex_prior <- makemyprior_example_model()
  res_stan <- inference_stan(ex_prior, iter = 100)
  # Note: For reliable results, increase the number of iterations (e.g., 'iter = 2000')
  plot_posterior_fixed(res_stan)
}
```

---

plot\_posterior\_stan    *Plotting posterior distributions*

---

**Description**

Function for plotting the posterior distributions of the random effect variances on the scale of the tree parameterization.

**Usage**

```
plot_posterior_stan(
  obj,
  param = c("prior", "variance", "stdev", "precision"),
  prior = FALSE
)
```

**Arguments**

obj	An object from inference_stan
param	A string indicating parameterization of plot. "prior" for scale of parameters, "variance", "stdev" and "precision" also possible.
prior	Include prior in the plot? Only possible for param = "prior". Note that if Jeffreys' prior is used for the total variance, it will not be included in the plot.

**Value**

A [ggplot](#) with the posterior distributions. See also [makemyprior\\_plotting](#).

**Examples**

```
if (interactive() && requireNamespace("rstan")){
  ex_prior <- makemyprior_example_model()
  res_stan <- inference_stan(ex_prior, iter = 100)
  # Note: For reliable results, increase the number of iterations (e.g., 'iter = 2000')
  plot_posterior_stan(res_stan)
}
```

---

`plot_posterior_variance`*Plotting posterior variances, standard deviations or precisions*

---

**Description**

Plotting posterior variances, standard deviations or precisions

**Usage**`plot_posterior_variance(obj)``plot_posterior_stdev(obj)``plot_posterior_precision(obj)`**Arguments**

`obj` An object from `inference_stan` or `inference_inla`.

**Value**

A `ggplot` object with the plot See also [makemyprior\\_plotting](#).

**Examples**

```
if (interactive() && requireNamespace("rstan")){
  ex_prior <- makemyprior_example_model()
  res_stan <- inference_stan(ex_prior, iter = 100)
  # Note: For reliable results, increase the number of iterations (e.g., 'iter = 2000')
  plot_posterior_variance(res_stan)
}

if (interactive() && requireNamespace("INLA")){
  ex_prior <- makemyprior_example_model()
  res_inla <- inference_inla(ex_prior)
  plot_posterior_variance(res_inla)
}
```

---

 plot\_prior

*Plotting prior distributions*


---

**Description**

Function for plotting the prior distributions of the random effects on the scale of the parameters chosen

**Usage**

```
plot_prior(obj)
```

**Arguments**

obj                    An object from `make_prior`, `inference_stan`, `inference_inla`, or `makemyprior_gui`

**Value**

A [ggplot](#) with the prior distributions. See also [makemyprior\\_plotting](#).

**Examples**

```
ex_prior <- makemyprior_example_model()
plot_prior(ex_prior)
```

---

 plot\_several\_posterior\_stan

*Plotting several posterior distributions*


---

**Description**

Function for plotting the posterior distributions of the random effect variances on the scale of the tree parameterization.

**Usage**

```
plot_several_posterior_stan(
  objs,
  param = c("prior", "variance", "stdev", "precision", "logvariance")
)
```

**Arguments**

objs	A names list with objects of class <code>mmp_stan</code> from <code>inference_stan</code> , can be any length (but typically length two for one prior ( <code>use_likelihoood = FALSE</code> ) and posterior, or two posteriors).
param	A string indicating parameterization of plot. "prior" for scale of parameters, "variance", "stdev", "precision" and "logvariance" are also possible.

**Details**

We cannot sample from a Jeffreys' prior since it is improper. If Jeffreys' prior is used for the total variance, the prior will be changed to a Gaussian(0,1) prior on the log total variance. This means that it does not make sense to look at the variances/standard deviations/precisions, but the variance proportions will be correct. See also [makemyprior\\_plotting](#).

**Value**

A `ggplot` with the posterior distributions.

**Examples**

```
if (interactive() && requireNamespace("rstan")){
  ex_prior1 <- makemyprior_example_model(seed = 1)
  ex_prior2 <- makemyprior_example_model(seed = 2)
  # Note: For reliable results, increase the number of iterations (e.g., 'iter = 2000')
  res_stan1 <- inference_stan(ex_prior1, iter = 100)
  res_stan2 <- inference_stan(ex_prior2, iter = 100)
  plot_several_posterior_stan(list(One = res_stan1, Two = res_stan2))
}
```

---

plot\_tree\_structure     *Plotting the prior tree structure graph*

---

**Description**

Can only be used for visualization in R.

**Usage**

```
plot_tree_structure(obj, nodenames)
```

**Arguments**

obj	An object from <code>make_prior</code> , <code>inference_stan</code> , <code>inference_inla</code> , or <code>makemyprior_gui</code>
nodenames	Custom names for each node (optional). Given as a named list with the default names as list names, and the new names as list elements. Do not need to provide all.

**Value**

A [visNetwork](#) with the tree graph See also [makemyprior\\_plotting](#).

**Examples**

```
ex_prior <- makemyprior_example_model()
plot_tree_structure(ex_prior)
```

---

print.mmp_prior	<i>Print</i>
-----------------	--------------

---

**Description**

Print

**Usage**

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

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

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

**Arguments**

`x` Object of class `mmp_prior`, `mmp_inla` or `mmp_stan`.  
`...` For `mmp_stan` and `mmp_inla`, see [print.data.frame](#).

**Value**

Returns input object invisible.

**Examples**

```
pri <- makemyprior_example_model()
pri # or print(pri)

if (interactive() && requireNamespace("rstan")){
  res_stan <- inference_stan(ex_prior, iter = 100)
  # Note: For reliable results, increase the number of iterations (e.g., 'iter = 2000')
  res_stan # or print(res_stan)
}

if (interactive() && requireNamespace("INLA")){
```

```
res_inla <- inference_inla(pri)
res_inla # or print(res_inla)
}
```

---

scale\_precmat            *Scaling precision matrix*

---

### Description

Scaling a precision matrix so the corresponding covariance matrix has typical variance (geometric mean) equal to 1.

### Usage

```
scale_precmat(Q)
```

### Arguments

Q                      Precision matrix

### Value

Precision matrix which is now scaled to have typical variance 1.

### Examples

```
scale_precmat(diag(10))
```

---

summary.mmp\_prior        *Short summary*

---

### Description

Short summary

### Usage

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

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

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

**Arguments**

object            Object of class `mmp_prior`, `mmp_inla` or `mmp_stan`.  
 ...              For `mmp_stan` and `mmp_inla`, see [print.data.frame](#).

**Value**

Returns summary invisible.

**Examples**

```
pri <- makemyprior_example_model()
summary(pri)

if (interactive() && requireNamespace("rstan")){
  res_stan <- inference_stan(ex_prior, iter = 100)
  # Note: For reliable results, increase the number of iterations (e.g., 'iter = 2000')
  summary(res_stan)
}

if (interactive() && requireNamespace("INLA")){
  res_inla <- inference_inla(pri)
  summary(res_inla)
}
```

---

<code>typical_variance</code>	<i>Compute the typical variance</i>
-------------------------------	-------------------------------------

---

**Description**

Computing the typical variance (geometric mean) of a matrix.

**Usage**

```
typical_variance(mat)
```

**Arguments**

mat              Matrix.

**Value**

Typical variance.

**Examples**

```
typical_variance(diag(10))
```

wheat\_data

*Genomic wheat breeding model data***Description**

Simulated wheat yield data with 100 observations.

**Usage**

```
wheat_data
```

**Format**

A list with the following variables

**y** Response

**a, b, x** Indexes for the additive, dominance and epistasis genetic effects, respectively

**Q\_a, Q\_d, Q\_x** Precision matrices for the genetic effects

**Examples**

```
## Not run:

vignette("wheat_breeding", package = "makemyprior")

## End(Not run)

if (interactive() && requireNamespace("rstan")){

  wheat_data_scaled <- wheat_data
  wheat_data_scaled$Q_a <- scale_precmat(wheat_data$Q_a)
  wheat_data_scaled$Q_d <- scale_precmat(wheat_data$Q_d)
  wheat_data_scaled$Q_x <- scale_precmat(wheat_data$Q_x)

  formula <- y ~
    mc(a, model = "generic0", Cmatrix = Q_a, constr = TRUE) +
    mc(d, model = "generic0", Cmatrix = Q_d, constr = TRUE) +
    mc(x, model = "generic0", Cmatrix = Q_x, constr = TRUE)

  prior <- make_prior(formula, wheat_data_scaled, prior = list(
    tree = "s1 = (d, x); s2 = (a, s1); s3 = (s2, eps)",
    w = list(s1 = list(prior = "pcM", param = c(0.67, 0.8)),
            s2 = list(prior = "pcM", param = c(0.85, 0.8)),
            s3 = list(prior = "pc0", param = 0.25)))

  posterior <- inference_stan(prior, iter = 150, warmup = 50,
                             chains = 1, seed = 1)

  # Note: For reliable results, increase the number of iterations
```

```
plot(prior)
plot_tree_structure(prior)
plot_posterior_fixed(posterior)
plot_posterior_stan(posterior, param = "prior", prior = TRUE)
}

## Not run:

posterior <- inference_stan(prior, iter = 150, warmup = 50,
                           chains = 1, seed = 1)

plot(prior)
plot_tree_structure(prior)
plot_posterior_fixed(posterior)
plot_posterior_stan(posterior, param = "prior", prior = TRUE)

## End(Not run)
```

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