

# Package: yodel (via r-universe)

September 14, 2024

**Title** A General Bayesian Model Averaging Helper

**Version** 1.0.0

**Description** Provides helper functions to perform Bayesian model averaging using Markov chain Monte Carlo samples from separate models. Calculates weights and obtains draws from the model-averaged posterior for quantities of interest specified by the user. Weight calculations can be done using marginal likelihoods or log-predictive likelihoods as in Ando, T., & Tsay, R. (2010) <[doi:10.1016/j.ijforecast.2009.08.001](https://doi.org/10.1016/j.ijforecast.2009.08.001)>.

**License** MIT + file LICENSE

**URL** <https://github.com/rich-payne/yodel>

**Imports** dplyr (>= 1.0), purrr (>= 0.3), rlang (>= 0.4)

**Encoding** UTF-8

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.2.3

**Suggests** testthat

**Repository** <https://rich-payne.r-universe.dev>

**RemoteUrl** <https://github.com/rich-payne/yodel>

**RemoteRef** HEAD

**RemoteSha** 76d3eddc91c60da3e96c88913be1f118c2e625b7

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**Description**

Calculate posterior weights of each model and optionally supply MCMC samples and functions (through the `bma_model()` function) to calculate a quantity of interest from each model using the `posterior()` function.

**Usage**

```
bma(..., seed = sample(.Machine$integer.max, 1))

model_bma_predictive(
  log_post_pred,
  adjustment = 0,
  w_prior = 1,
  mcmc = NULL,
  fun = NULL
)

model_bma_marginal(log_marginal, w_prior = 1, mcmc = NULL, fun = NULL)
```

**Arguments**

<code>...</code>	Named calls to the <code>bma_model()</code> function.
<code>seed</code>	an integer which is used to specify the seed when sampling from the different models (e.g. in <code>posterior()</code> ).
<code>log_post_pred</code>	a matrix containing the log likelihood for each observation on each iteration of the MCMC. The matrix should have dimensions (number-of-MCMC-iteration) by (number of observations).
<code>adjustment</code>	an adjustment to be applied to the posterior log-predictive likelihood. A simple bias correction in Ando & Tsay (2010) is: $-(\text{number of parameters in the model}) / 2$ .
<code>w_prior</code>	the prior weight for the model.
<code>mcmc</code>	a named list (or dataframe) of MCMC samples of model parameters.
<code>fun</code>	a function which takes the MCMC samples and returns a value of interest.
<code>log_marginal</code>	The log marginal likelihood of the model.

**Details**

It is required that if MCMC samples are supplied, that each MCMC run must have the same number of collected samples.

**Value**

`bma`: A list containing the prior and posterior weights for each model, the sampled model (`model_index`) at each MCMC iteration and the arguments supplied to each `bma_model()` call.

`model_bma`: A named list of the arguments, with a "yodel\_bma\_candidate" class attached.

`model_bma`: A named list of the arguments, with a "yodel\_bma\_candidate" class attached.

**References**

Ando, T., & Tsay, R. (2010). Predictive likelihood for Bayesian model selection and averaging. *International Journal of Forecasting*, 26(4), 744-763.

**Examples**

```
# Minimal example
fit <- bma(
  linear = model_bma_predictive(
    # mcmc = data.frame(b1 = 1:5, b2 = 11:15, sigma = seq(.1, .5, .1)),
    log_post_pred = matrix(log(1:100), 5, 20),
    adjustment = - 3 / 2,
    w_prior = .5
  ),
  quad = model_bma_predictive(
    # mcmc = data.frame(b1 = 1:5 / 2, b2 = 11:15 / 2, b3 = 5:1, sigma = seq(.1, .5, .1)),
    log_post_pred = matrix(log(2:101), 5, 20),
    adjustment = - 4 / 2,
    w_prior = .5
  )
)

fit$w_prior
fit$w_post
```

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 posterior

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*Calculate Posterior Quantities*


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**Description**

Calculate posterior quantities specifically of interest for a given model.

**Usage**

```
posterior(x, ...)
```

**Arguments**

`x` MCMC output.  
`...` additional arguments passed to S3 methods.

**Value**

a dataframe or tibble with the posterior probabilities.

**Examples**

```
# functions which calculate the dose response for a linear and quadratic model
fun_linear <- function(x, dose) {
  mean_response <- x$b1 + x$b2 * dose
  data.frame(iter = 1:nrow(x), dose = dose, mean = mean_response)
}
fun_quad <- function(x, dose) {
  mean_response <- x$b1 + x$b2 * dose + x$b3 * dose ^ 2
  data.frame(iter = 1:nrow(x), dose = dose, mean = mean_response)
}

# Bayesian model averaging
fit <- bma(
  linear = model_bma_predictive(
    mcmc = data.frame(b1 = 1:5, b2 = 11:15, sigma = seq(.1, .5, .1)),
    log_post_pred = matrix(log(1:100), 5, 20),
    adjustment = - 3 / 2,
    w_prior = .5,
    fun = fun_linear
  ),
  quad = model_bma_predictive(
    mcmc = data.frame(b1 = 1:5 / 2, b2 = 11:15 / 2, b3 = 5:1, sigma = seq(.1, .5, .1)),
    log_post_pred = matrix(log(2:101), 5, 20),
    adjustment = - 4 / 2,
    w_prior = .5,
    fun = fun_quad
  )
)

# posterior samples using Bayesian model averaging
posterior(fit, dose = 1)
posterior(fit, dose = 2)
```

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posterior.yodel\_bma    *Posterior Samples from Bayesian Model Averaging*

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**Description**

Calculate posterior quantities of interest using Bayesian model averaging.

**Usage**

```
## S3 method for class 'yodel_bma'
posterior(x, ...)
```

**Arguments**

`x` output from a call to `bma()`.

`...` additional arguments to be passed to each of the functions used to calculate the quantity of interest.

**Value**

A dataframe with the posterior samples for each iteration of the MCMC. The dataframe will have, at a minimum, the columns "iter" and "model" indicating the MCMC iteration and the model that was used in the calculations. The functions used for each model are defined within the `model_bma()` function and used in the `bma()` function. See the example below.

**Examples**

```
# functions which calculate the dose response for a linear and quadratic model
fun_linear <- function(x, dose) {
  mean_response <- x$b1 + x$b2 * dose
  data.frame(iter = 1:nrow(x), dose = dose, mean = mean_response)
}
fun_quad <- function(x, dose) {
  mean_response <- x$b1 + x$b2 * dose + x$b3 * dose ^ 2
  data.frame(iter = 1:nrow(x), dose = dose, mean = mean_response)
}

# Bayesian model averaging
fit <- bma(
  linear = model_bma_predictive(
    mcmc = data.frame(b1 = 1:5, b2 = 11:15, sigma = seq(.1, .5, .1)),
    log_post_pred = matrix(log(1:100), 5, 20),
    adjustment = - 3 / 2,
    w_prior = .5,
    fun = fun_linear
  ),
  quad = model_bma_predictive(
    mcmc = data.frame(b1 = 1:5 / 2, b2 = 11:15 / 2, b3 = 5:1, sigma = seq(.1, .5, .1)),
    log_post_pred = matrix(log(2:101), 5, 20),
    adjustment = - 4 / 2,
    w_prior = .5,
    fun = fun_quad
  )
)

# posterior samples using Bayesian model averaging
posterior(fit, dose = 1)
posterior(fit, dose = 2)
```

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