

# Package: FusioMR (via r-universe)

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**Type** Package

**Title** Flexible, Unified and Versatile Mendelian Randomization

**Version** 2.0.0

**Description** A Bayesian Mendelian Randomization framework for causal effect estimation from GWAS summary statistics. Supports single and multiple exposure/outcome analyses with optional correlated horizontal pleiotropy.

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**Encoding** UTF-8

**LazyData** true

**Depends** R (>= 4.3.0)

**Imports** Rcpp (>= 1.0.10), invgamma (>= 1.1), stats

**LinkingTo** Rcpp, RcppArmadillo (>= 0.12.0.0)

**Suggests** testthat (>= 3.0.0)

**Config/testthat/edition** 3

**RoxygenNote** 7.3.3

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

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**RemoteUrl** <https://github.com/kangbw702/FusioMR>

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fusiomr	<i>FusioMR: A Flexible and unified MR framework using summary statistics for single- and multi-outcome, tailored for molecular trait exposures while also applicable to complex trait exposures.</i>
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## Description

Main function of the FusioMR package. Offer robust estimates the causal effect of an exposure on an outcome from GWAS summary statistics, using Bayesian hierarchical model and uses Gibbs sampling.

## Usage

```
fusiomr(
  b_exp,
  se_exp,
  b_out,
  se_out,
  model = c("seso_uhp_only", "seso_with_chp", "semo", "memo"),
  control = parameter_control(),
  verbose = FALSE
)
```

## Arguments

b_exp	Numeric vector of SNP-exposure effect estimates.
se_exp	Numeric vector of standard errors of b_exp.
b_out	Numeric vector of SNP-outcome effect estimates.
se_out	Numeric vector of standard errors of b_out.
model	Character string. One of "seso_uhp_only", "seso_with_chp", "semo", "memo".
control	A list of advanced prior hyper-parameters returned by <a href="#">parameter_control</a> . Defaults are suitable for most uses.
verbose	Logical; if TRUE, print progress messages.

## Value

A list with components

**est** causal effect estimation

**se** sd of the causal effect.

**pval** two-sided p-value

**ci** 95% empirical credible interval.

**model** The model used.

**Examples**

```
## Not run:
set.seed(1)
K <- 50
b_exp <- rnorm(K, 0, 0.1); se_exp <- rep(0.01, K)
b_out <- 0.3 * b_exp + rnorm(K, 0, 0.01); se_out <- rep(0.01, K)
model <- fusiomr(b_exp, se_exp, b_out, se_out,
               model = "seso_uhp_only")
model$est; model$se; model$ci;

## End(Not run)
```

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parameter\_control      *Control advanced parameters for FusioMR models*

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**Description**

Bundles advanced hyper-parameters for the MCMC settings, IV-selection thresholds, and empirical-Bayes variance priors setting ups. Typically, users never need to touch this: `fusiomr()` uses `parameter_control()` with sensible defaults tuned for estimation. Pass a customized value of parameters only when needed, e.g., to shorten MCMC niter, burnin prop, tighten IV selection, or correct for winner's curse via `z_thresh`, account for sample overlap via `rho_ov`, or tune prior strength via `c_gamma/c_theta`.

**Usage**

```
parameter_control(
  niter = 20000,
  burnin_prop = 0.5,
  c_gamma = 0.5,
  c_theta = 0.8,
  kappa_gamma = 1,
  kappa_theta = 1,
  Kmin = 5,
  Kmax = 20,
  rho_ov = 0,
  z_thresh = NULL,
  trim = 0.1,
  hybrid = FALSE,
  kappa_hybrid = 5,
  global_mean_gamma = NULL,
  global_mean_theta = NULL,
  global_Sigma_gamma = NULL,
  global_Sigma_theta = NULL
)
```

**Arguments**

niter	Number of Gibbs iterations. Default 20000 is calibrated for stable posterior estimates;
burnin_prop	Burn-in proportion in [0, 1).
c_gamma	Prior weight per IV for $\sigma^2_{\text{gamma}}$ ( $a_{\text{gamma}} = 1 + c_{\text{gamma}} * K/2$ ), Larger values make the inverse-gamma prior more concentrated around its mean. Default= 0.5;
c_theta	Prior weight per IV for $\sigma^2_{\text{theta}}$ ( $a_{\text{theta}} = 1 + c_{\text{theta}} * K/2$ ), Larger values make the inverse-gamma prior more concentrated around its mean. Default = 0.8;
kappa_gamma	Tunning parameter for prior mean of $\sigma^2_{\text{gamma}}$ ;
kappa_theta	Tunning parameter for prior mean of $\sigma^2_{\text{theta}}$ ;
Kmin, Kmax	Lower and upper bound on K used when computing prior shape.
rho_ov	Sampling correlation between exposure and outcome due to sample overlap, in [-1, 1]. Default = 0;
z_thresh	Optional  Z  selection threshold used to pick QTLs (winner's-curse fix). Example: for $p=5e-8$ two-sided, use $qnorm(1 - 5e-8/2)$ .
trim	Tail probability for winsor.
hybrid	Logical; if TRUE, blend local with a global: prior mean = $\eta * \text{local} + (1 - \eta) * \text{global}$ ( $\eta = K/(K + \text{kappa\_hybrid})$ );
kappa_hybrid	Pooling control; larger values shrink more toward the global.
global_mean_gamma, global_mean_theta	Global EB centers for hybrid mode.
global_Sigma_gamma	2x2 numeric matrix. Global empirical-Bayes mean of the SNP-effect covariance Sigma_gamma. Required when hybrid = TRUE for the "memo" model.
global_Sigma_theta	2x2 numeric matrix. Global empirical-Bayes mean of the pleiotropy covariance Sigma_theta. Required when hybrid = TRUE for the "semo" or "memo" model.

**Value**

A named list of parameters for more advanced setting.

**Examples**

```
# defaults
ctrl <- parameter_control()
```

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