

# Package ‘hdbm’

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**Title** High Dimensional Bayesian Mediation Analysis

**Version** 0.9.0

**Description** Perform mediation analysis in the presence of high-dimensional mediators based on the potential outcome framework. High dimensional Bayesian mediation (HDBM), developed by Song et al (2018) [<doi:10.1101/467399>](https://doi.org/10.1101/467399), relies on two Bayesian sparse linear mixed models to simultaneously analyze a relatively large number of mediators for a continuous exposure and outcome assuming a small number of mediators are truly active. This sparsity assumption also allows the extension of univariate mediator analysis by casting the identification of active mediators as a variable selection problem and applying Bayesian methods with continuous shrinkage priors on the effects.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.1.1

**LinkingTo** Rcpp, RcppArmadillo

**Imports** Rcpp

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** yes

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**Repository** CRAN

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hdbm

*High Dimensional Bayesian Mediation***Description**

hdbm is a Bayesian inference method that uses continuous shrinkage priors for high-dimensional mediation analysis, developed by Song et al (2018). hdbm provides estimates for the regression coefficients as well as the posterior inclusion probability for ranking mediators.

**Usage**

```
hdbm(Y, A, M, C1, C2, beta.m, alpha.a, burnin, ndraws)
```

**Arguments**

|         |                                                           |
|---------|-----------------------------------------------------------|
| Y       | numeric outcome vector.                                   |
| A       | numeric exposure vector.                                  |
| M       | numeric matrix of mediators of Y and A.                   |
| C1      | numeric matrix of extra covariates in the outcome model   |
| C2      | numeric matrix of extra covariates in the mediator model  |
| beta.m  | numeric vector of initial beta.m in the outcome model     |
| alpha.a | numeric vector of initial alpha.a in the mediator model   |
| burnin  | number of iterations to run the MCMC before sampling      |
| ndraws  | number of draws to take from MCMC after the burnin period |

**Details**

hdbm uses two regression models for the two conditional relationships,  $Y|A, M, C1$  and  $M|A, C2$ . For the outcome model, hdbm uses

$$Y = M\beta_M + A * \beta_A + C1 * \beta_C Y + \epsilon_Y$$

For the mediator model, hdbm uses the model

$$M = A * \alpha_A + C2 * \alpha_C 2 + \epsilon_M$$

For high dimensional tractability, hdbm employs continuous Bayesian shrinkage priors to select mediators and makes the two following assumptions: First, it assumes that all the potential mediators contribute small effects in mediating the exposure-outcome relationship. Second, it assumes that only a small proportion of mediators exhibit large effects ("active" mediators). hdbm uses a Metropolis-Hastings within Gibbs MCMC to generate posterior samples from the model.

**Value**

hdbm returns a list with 11 elements (each of length `ndraws`), sampled from the burned in MCMC:

**beta.m** Outcome model mediator coefficients

**r1** Whether or not each `beta.m` belongs to the larger normal component (1) or smaller normal component (0)

**alpha.a** Mediator model exposure coefficients

**r3** Whether or not each `alpha.a` belongs to the larger normal component (1) or smaller normal component (0)

**beta.a** `beta.a` coefficient

**pi.m** Proportion of non zero `beta.m` coefficients

**pi.a** Proportion of non zero `alpha.a` coefficients

**sigma.m0** standard deviation of the smaller normal component for mediator-outcome coefficients (`beta.m`)

**sigma.m1** standard deviation of the larger normal component for mediator-outcome coefficients (`beta.m`)

**sigma.ma0** Standard deviation of the smaller normal component for exposure-mediator coefficients (`alpha.a`)

**sigma.ma1** Standard deviation of the larger normal component for exposure-mediator coefficients (`alpha.a`)

**Author(s)**

Alexander Rix

**References**

Yanyi Song, Xiang Zhou et al. Bayesian Shrinkage Estimation of High Dimensional Causal Mediation Effects in Omics Studies. *bioRxiv* [10.1101/467399](https://doi.org/10.1101/467399)

**Examples**

```
library(hdbm)

Y <- hdbm.data$y
A <- hdbm.data$a

# grab the mediators from the example data.frame
M <- as.matrix(hdbm.data[, paste0("m", 1:100)], nrow(hdbm.data))

# We just include the intercept term in this example.
C <- matrix(1, 1000, 1)
beta.m <- rep(0, 100)
alpha.a <- rep(0, 100)

set.seed(12345)
hdbm.out <- hdbm(Y, A, M, C, C, beta.m, alpha.a,
```

```

burnin = 1000, ndraws = 100)

# Which mediators are active?
active <- which(colSums(hdbm.out$r1 * hdbm.out$r3) > 50)
colnames(M)[active]

```

---

hdbm.data

*Synthetic example data for hdbm*


---

### Description

Synthetic example data for hdbm

### Usage

```
hdbm.data
```

### Format

A data.frame with 1000 observations on 102 variables:

**y** Numeric response variable.

**a** Numeric exposure variable.

**m[1-100 ]** Numeric mediator variables

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## \* **datasets**

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