Package: hdbm (via r-universe)

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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>, 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.

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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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Contents

`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)

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References

Yanyi Song, Xiang Zhou et al. Bayesian Shrinkage Estimation of High Dimensional Causal Mediation Effects in Omics Studies. bioRxiv 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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