Package ‘bama’

January 21, 2021

Title High Dimensional Bayesian Mediation Analysis

Version 1.2

URL https://github.com/umich-cphds/bama

BugReports https://github.com/umich-cphds/bama/issues

Description Perform mediation analysis in the presence of high-dimensional mediators based on the potential outcome framework. Bayesian Mediation Analysis (BAMA), developed by Song et al (2019) <doi:10.1111/biom.13189> and Song et al (2020) <arXiv:2009.11409>, 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 7.1.1

LinkingTo Rcpp, RcppArmadillo, RcppDist, BH

Imports Rcpp, parallel

Depends R (>= 3.5)

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation yes

Author Alexander Rix [aut], Mike Kleinsasser [aut, cre], Yanyi Song [aut]

Maintainer Mike Kleinsasser <mkleinsa@umich.edu>

Repository CRAN

Date/Publication 2021-01-21 11:20:06 UTC
R topics documented:

- bama ................................................. 2
- bama.data ......................................... 7
- fdr.bama ............................................. 7
- print.bama .......................................... 9
- print.fdr.bama ..................................... 10
- summary.bama ..................................... 10
- summary.fdr.bama ................................ 11

Index 12

---

bama

Bayesian Mediation Analysis

Description

bama is a Bayesian inference method that uses continuous shrinkage priors for high-dimensional Bayesian mediation analysis, developed by Song et al (2019, 2020). bama provides estimates for the regression coefficients as well as the posterior inclusion probability for ranking mediators.

Usage

bama(
  Y, A, M, C1, C2, method, burnin, ndraws, weights = NULL, inits = NULL, control = list(k = 2, lm0 = 1e-04, lm1 = 1, l = 1, lambda0 = 0.04, lambda1 = 0.2, lambda2 = 0.2, phi0 = 0.01, phi1 = 0.01, a0 = 0.01 * ncol(M), a1 = 0.05 * ncol(M), a2 = 0.05 * ncol(M), a3 = 0.89 * ncol(M)), seed = NULL)

Arguments

- Y  Length n numeric outcome vector
- A  Length n numeric exposure vector
- M  n x p numeric matrix of mediators of Y and A
- C1 n x nc1 numeric matrix of extra covariates to include in the outcome model
- C2 n x nc2 numeric matrix of extra covariates to include in the mediator model
method | String indicating which method to use. Options are
| • "BSLMM" - mixture of two normal components; Song et al. 2019
| • "PTG" - product threshold Gaussian prior; Song et al. 2020
| • "GMM" - four-component Gaussian mixture prior; Song et al. 2020
burnin | number of iterations to run the MCMC before sampling
ndraws | number of draws to take from MCMC (includes burnin draws)
weights | Length n numeric vector of weights
inits | list of initial values for the Gibbs sampler. Options are
| • beta.m - Length p numeric vector of initial beta.m in the outcome model. See details for equation
| • alpha.a - Length p numeric vector of initial alpha.a in the mediator model. See details for equation
control | list of Gibbs algorithm control options. These include prior and hyper-prior parameters. Options vary by method selection. If method = "BSLMM"
| • k - Shape parameter prior for inverse gamma
| • lm0 - Scale parameter prior for inverse gamma for the small normal components
| • lm1 - Scale parameter prior for inverse gamma for the large normal components
| • l - Scale parameter prior for the other inverse gamma distributions
| If method = "PTG"
| • lambda0 - threshold parameter for product of alpha.a and beta.m effect
| • lambda1 - threshold parameter for beta.m effect
| • lambda2 - threshold parameter for alpha.a effect
| • ha - inverse gamma shape prior for sigma_sq.a
| • la - inverse gamma scale prior for sigma_sq.a
| • h1 - inverse gamma shape prior for sigma_sq.e
| • l1 - inverse gamma scale prior for sigma_sq.e
| • h2 - inverse gamma shape prior for sigma_sq.g
| • l2 - inverse gamma scale prior for sigma_sq.g
| • km - inverse gamma shape prior for tau_sq.b
| • lm - inverse gamma scale prior for tau_sq.b
| • kma - inverse gamma shape prior for tau_sq.a
| • lma - inverse gamma scale prior for tau_sq.a
| If method = "GMM"
| • phi0 - prior beta.m variance
| • phi1 - prior alpha.a variance
| • a0 - prior count of non-zero beta.m and alpha.a effects
| • a1 - prior count of non-zero beta.m and zero alpha.a effects
| • a2 - prior count of zero beta.m and non-zero alpha.a effects
| • a3 - prior count of zero beta.m and zero alpha.a effects
bama

Details

bama uses two regression models for the two conditional relationships, \( Y | A, M, C \) and \( M | A, C \). For the outcome model, bama uses

\[
Y = M \beta_M + A * \beta_A + C * \beta_C + \epsilon_Y
\]

For the mediator model, bama uses the model

\[
M = A * \alpha_A + C * \alpha_C + \epsilon_M
\]

For high dimensional tractability, bama 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). bama uses a Metropolis-Hastings within Gibbs MCMC to generate posterior samples from the model.

Value

If method = "BSLMM", then bama returns a object of type "bama" with 12 elements:

- **beta.m** \( n \text{draws} \times p \) matrix containing outcome model mediator coefficients.
- **r1** \( n \text{draws} \times p \) matrix indicating whether or not each beta.m belongs to the larger normal component (1) or smaller normal component (0).
- **alpha.a** \( n \text{draws} \times p \) matrix containing the mediator model exposure coefficients.
- **r3** \( n \text{draws} \times p \) matrix indicating whether or not each alpha.a belongs to the larger normal component (1) or smaller normal component (0).
- **beta.a** Vector of length \( n \text{draws} \) containing the beta.a coefficient.
- **pi.m** Vector of length \( n \text{draws} \) containing the proportion of non zero beta.m coefficients.
- **pi.a** Vector of length \( n \text{draws} \) containing the proportion of non zero alpha.a coefficients.
- **sigma.m0** Vector of length \( n \text{draws} \) containing the standard deviation of the smaller normal component for mediator-outcome coefficients (beta.m).
- **sigma.m1** Vector of length \( n \text{draws} \) containing standard deviation of the larger normal component for mediator-outcome coefficients (beta.m).
- **sigma.ma0** Vector of length \( n \text{draws} \) containing standard deviation of the smaller normal component for exposure-mediator coefficients (alpha.a).
- **sigma.ma1** Vector of length \( n \text{draws} \) containing standard deviation of the larger normal component for exposure-mediator coefficients (alpha.a).
call The R call that generated the output.

If method = "GMM", then bama returns a object of type "bama" with:

**beta.m** ndraws x p matrix containing outcome model mediator coefficients.

**alpha.a** ndraws x p matrix containing the mediator model exposure coefficients.

**betam_member** ndraws x p matrix of 1’s and 0’s where item = 1 only if beta.m is non-zero.

**alphaa_member** ndraws x p matrix of 1’s and 0’s where item = 1 only if alpha.a is non-zero.

**alpha.c** ndraws x (q2 + p) matrix containing alpha_c coefficients. Since alpha.c is a matrix of dimension q2 x p, the draws are indexed as alpha_c(w, j) = w * p + j

**beta.c** ndraws x q1 matrix containing beta_c coefficients. Since beta.c is a matrix of dimension q1 x p

**beta.a** Vector of length ndraws containing the beta.a coefficient.

**sigma.sq.a** Vector of length ndraws variance of beta.a effect

**sigma.sq.e** Vector of length ndraws variance of outcome model error

**sigma.sq.g** Vector of length ndraws variance of mediator model error

If method = "PTG", then bama returns a object of type "bama" with:

**beta.m** ndraws x p matrix containing outcome model mediator coefficients.

**alpha.a** ndraws x p matrix containing the mediator model exposure coefficients.

**alpha.c** ndraws x (q2 + p) matrix containing alpha_c coefficients. Since alpha.c is a matrix of dimension q2 x p, the draws are indexed as alpha_c(w, j) = w * p + j

**beta.c** ndraws x q1 matrix containing beta_c coefficients. Since beta.c is a matrix of dimension q1 x p

**betam_member** ndraws x p matrix of 1’s and 0’s where item = 1 only if beta.m is non-zero.

**alphaa_member** ndraws x p matrix of 1’s and 0’s where item = 1 only if alpha.a is non-zero.

**beta.a** Vector of length ndraws containing the beta.a coefficient.

**sigma.sq.a** Vector of length ndraws variance of beta.a effect

**sigma.sq.e** Vector of length ndraws variance of outcome model error

**sigma.sq.g** Vector of length ndraws variance of mediator model error

References


Examples

```r
library(bama)

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

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

# We just include the intercept term in this example as we have no covariates
C1 <- matrix(1, 1000, 1)
C2 <- matrix(1, 1000, 1)
beta.m <- rep(0, 100)
alpha.a <- rep(0, 100)

out <- bama(Y = Y, A = A, M = M, C1 = C1, C2 = C2, method = "BSLMM", seed = 1234,
            burnin = 1000, ndraws = 1100, weights = NULL, inits = NULL,
            control = list(k = 2, l0 = 1e-04, l1 = 1, l = 1))

# The package includes a function to summarise output from 'bama'
sweep <- summary(out)
head(sweep)

# Product Threshold Gaussian
ptgmod <- bama(Y = Y, A = A, M = M, C1 = C1, C2 = C2, method = "PTG", seed = 1234,
               burnin = 1000, ndraws = 1100, weights = NULL, inits = NULL,
               control = list(lambda0 = 0.04, lambda1 = 0.2, lambda2 = 0.2))

mean(ptgmod$beta.a)
apply(ptgmod$beta.m, 2, mean)
apply(ptgmod$alpha.a, 2, mean)
apply(ptgmod$alpha_member, 2, mean)

# Gaussian Mixture Model
gmmmod <- bama(Y = Y, A = A, M = M, C1 = C1, C2 = C2, method = "GMM", seed = 1234,
                burnin = 1000, ndraws = 1100, weights = NULL, inits = NULL,
                control = list(phi0 = 0.01, phi1 = 0.01))

mean(gmmmod$beta.a)
apply(gmmmod$beta.m, 2, mean)
apply(gmmmod$alpha.a, 2, mean)

mean(gmmmod$sigma.sq.a)
mean(gmmmod$sigma.sq.e)
mean(gmmmod$sigma.sq.g)
```
**bama.data**

*Synthetic example data for bama*

**Description**

Synthetic example data for bama

**Usage**

```r
bama.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

---

**fdr.bama**

*Bayesian Mediation Analysis Controlling For False Discovery*

**Description**

`fdr.bama` uses the permutation test to estimate the null PIP distribution for each mediator and determines a threshold (based off of the `fdr` parameter) for significance.

**Usage**

```r
fdr.bama(
  Y,
  A,
  M,
  C1,
  C2,
  beta.m,
  alpha.a,
  burnin,
  ndraws,
  weights = NULL,
  npermutations = 200,
  fdr = 0.1,
  k = 2,
  lm0 = 1e-04,
  lm1 = 1,
)```
fdr.bama

l = 1,
mc.cores = 1,
type = "PSOCK"
)

Arguments

Y
Length n numeric outcome vector
A
Length n numeric exposure vector
M
n x p numeric matrix of mediators of Y and A
C1
n x nc1 numeric matrix of extra covariates to include in the outcome model
C2
n x nc2 numeric matrix of extra covariates to include in the mediator model
beta.m
Length p numeric vector of initial beta.m in the outcome model
alpha.a
Length p 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
weights
Length n numeric vector of weights
npermutations
The number of permutations to generate while estimating the null pip distribution. Default is 200
fdr
False discovery rate. Default is 0.1
k
Shape parameter prior for inverse gamma. Default is 2.0
l\textsubscript{m0}
Scale parameter prior for inverse gamma for the small normal components. Default is 1e-4
l\textsubscript{m1}
Scale parameter prior for inverse gamma for the large normal components. Default is 1.0
l
Scale parameter prior for the other inverse gamma distributions. Default is 1.0
mc.cores
The number of cores to use while running fdr.bama. fdr.bama uses the parallel package for parallelization, so see that for more information. Default is 1 core
type
Type of cluster to make when mc.cores > 1. See makeCluster in the parallel package for more details. Default is "PSOCK"

Value

fdr.bama returns a object of type "fdr.bama" with 5 elements:

bama.out Output from the bama run.
pip.null A \textit{p x npermutations} matrices containing the estimated null PIP distribution for each mediator.
threshold The cutoff significance threshold for each PIP controlling for the false discovery rate.
fdr The false discovery rate used to calculate threshold.
call The R call that generated the output.
Author(s)
Alexander Rix

References

Examples
library(bama)
Y <- bama.data$y
A <- bama.data$a

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

# We just include the intercept term in this example as we have no covariates
C1 <- matrix(1, 1000, 1)
C2 <- matrix(1, 1000, 1)
beta.m <- rep(0, 100)
alpha.a <- rep(0, 100)

set.seed(12345)
out <- fdr.bama(Y, A, M, C1, C2, beta.m, alpha.a, burnin = 100,
    ndraws = 120, npermutations = 10)

# The package includes a function to summarise output from 'fdr.bama'
summary(out)

print.bama

Printing bama objects

Description
Print a bama object.

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

Arguments
x An object of class 'bama'.
... Additional arguments to pass to print.data.frame or summary.bama
print.fdr.bama  Printing bama objects

Description

Print a bama object.

Usage

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

Arguments

x          An object of class 'bama'.
...        Additional arguments to pass to print.data.frame or summary.bama

summary.bama  Summarize objects of type "bama"

Description

summary.bama summarizes the 'beta.m' estimates from bama and generates an overall estimate, credible interval, and posterior inclusion probability.

Usage

## S3 method for class 'bama'
summary(object, rank = F, ci = c(0.025, 0.975), ...)

Arguments

object     An object of class "bama".
rank       Whether or not to rank the output by posterior inclusion probability. Default is TRUE.
.ci        The credible interval to calculate. ci should be a length 2 numeric vector specifying the upper and lower bounds of the CI. By default, ci = c(0.025, .975).
...        Additional optional arguments to summary

Value

A data.frame with 4 elements. The beta.m estimates, the estimates’ credible interval (which by default is 95\% inclusion probability (pip) of each 'beta.m').
**summary.fdr.bama**  
*Summarize objects of type "fdr.bama"*

**Description**

`summary.fdr.bama` summarizes the `beta.m` estimates from `fdr.bama` and for each mediator generates an overall estimate, credible interval, posterior inclusion probability (PIP), and PIP threshold for significance controlling for the specified false discovery rate (FDR).

**Usage**

```r
## S3 method for class 'fdr.bama'
summary(
  object,
  rank = F,
  ci = c(0.025, 0.975),
  fdr = object$fdr,
  filter = T,
  ...
)
```

**Arguments**

- `object`: An object of class "bama".
- `rank`: Whether or not to rank the output by posterior inclusion probability. Default is `TRUE`.
- `ci`: The credible interval to calculate. `ci` should be a length 2 numeric vector specifying the upper and lower bounds of the CI. By default, `ci = c(0.025, 0.975)`.
- `fdr`: False discovery rate. By default, it is set to whatever the `fdr` of `object` is. However, it can be changed to recalculate the PIP cutoff threshold.
- `filter`: Whether or not to filter out mediators with PIP less than the PIP threshold.
- `...`: Additional optional arguments to `summary`

**Value**

A data.frame with 4 elements. The `beta.m` estimates, the estimates’ credible interval (which by default is 95\% inclusion probability (pip) of each 'beta.m').
Index

* datasets
  bama.data, 7

bama, 2
bama.data, 7

fdr.bama, 7

print.bama, 9
print.fdr.bama, 10

summary.bama, 10
summary.fdr.bama, 11