

Package ‘bmabart’

April 29, 2025

Type Package

Title Bayesian Mediation Analysis Using BART

Version 1.0

Date 2025-04-28

Depends R (>= 2.14.1), BART, survival, gplots

Imports lattice, methods

Description

Used for Bayesian mediation analysis based on Bayesian additive Regression Trees (BART).
The analysis method is described in Yu and Li (2025) ``Mediation Analysis with Bayesian Additive Regression Trees'', submitted for publication.

License GPL (>= 2)

URL <https://www.r-project.org>,
https://publichealth.lsuhsu.edu/Faculty_pages/qyu/index.html

RoxygenNote 7.3.2

NeedsCompilation no

Author Qingzhao Yu [aut, cre],
Bin Li [aut]

Maintainer Qingzhao Yu <qyu@lsuhsc.edu>

Repository CRAN

Date/Publication 2025-04-29 08:50:11 UTC

Contents

bmabart-package	2
bma.bart	2
cgd1	5
data_org	6
print.summary.bma.bart	9
summary.bma.bart	10
weight_behavior	12

Index	13
--------------	-----------

bmbart-package	<i>Bayesian Mediation Analysis Using Bayesian Additive Regression Trees</i>
----------------	---

Description

Used for Bayesian mediation analysis based on Bayesian additive Regression Trees (BART). The analysis method is described in Yu and Li (2025) "Mediation Analysis with Bayesian Additive Regression Trees", submitted for publication.

Details

Build BARTs using the R package and perform the Bayesian Mediation Analysis.

Author(s)

Qingzhao Yu and Bin Li

Maintainer: Qingzhao Yu <qyu@lsuhsc.edu>

References

Yu, Q., and Li, B. (2025) <doi:>. "Mediation Analysis with Bayesian Additive Regression Trees," submitted.

bma.bart	<i>Bayesian Mediation Analysis Using Bayesian Additive Regression Trees</i>
----------	---

Description

Build BARTs using the R package and perform the Bayesian Mediation Analysis.

Usage

```
bma.bart(pred, m, y, refy = rep(NA, ncol(data.frame(y))),
  predref = rep(NA, ncol(data.frame(pred))), deltap = NA,
  deltam = NA, mref = rep(NA, ncol(data.frame(m))), cova = NULL,
  cova.ref = list(), mcov = NULL, mcov.ref = list(), mclist = NULL,
  complete = FALSE, ntree = 200L, numcut = 100L, ndpost = 1000L,
  nskip = 100L, keepevery = 1L, nkeeptrain = ndpost, nkeeptest = ndpost,
  nkeeptestmean = ndpost, nkeeptreedraws = ndpost, printevery = 100L,
  seed = sample(1:1e+06, 1))
```

Arguments

pred	The vector/matrix of the exposure/predict variable(s).
m	The dataframe of all potential mediators
y	The vector/matrix of the outcome(s).
refy	The reference groups of y when the corresponding outcome is binary or categorical.
predref	The reference groups of pred when the corresponding outcome is binary or categorical.
deltap	A vector of the length of the number of exposures. The difference in pred when calculate the changing rate by pred. If not set, the difference is 1 for categorical predictor and one tenth of the standard deviation of the predictor if continuous.
deltam	A vector of the length of the number of mediators. The ith item is the difference in the ith mediator when calculate the changing rate by each mediator. If not set, the difference is 1 for categorical mediators and one tenth of the standard deviation of the mediator if continuous.
mref	The reference groups of mediators when the corresponding mediator is binary or categorical.
cova	The covariance data for y.
cova.ref	The reference group for the binary or categorical covariates in cova.
mcov	The covariance data for mediators.
mcov.ref	The reference group if the mcovs are categorical or binary.
mclist	If mclist is null but not mcov, mcov is applied to all mediators. If both mcov and mclist are not NULL, the first item of mclist lists all mediators that are using different mcov, the following items gives the mcov for the mediators in order, NA if no mcov to be used. e.g. mclist=list(c(1,2,4),l1=1,l2=NA,l4=c(1,3)), mediator 1, m[,1], use mcov[,1], 2 uses no covariates, 4 uses mcov[,c(1,3)], all other mediators use all. Can also replace variable names with column numbers in the mclist.
complete	complete=TRUE if only completed cases are used in analysis.
ntree	As in the BART package, the number of trees in the sum.
numcut	See the BART package. The number of possible values of c (see usequants). If a single number is given, this is used for all variables. Otherwise a vector with length equal to ncol(x.train) is required, where the ith element gives the number of c used for the ith variable in x.train. If usequants is false, numcut equally spaced cutoffs are used covering the range of values in the corresponding column of x.train. If usequants is true, then min(numcut, the number of unique values in the corresponding columns of x.train - 1) c values are used.
ndpost	As in the BART package, the number of posterior draws returned.
nskip	As in the BART package, number of MCMC iterations to be treated as burn in.
keepevery	As in the BART package, every keepevery draw is kept to be returned to the user.
nkeeptrain	As in the BART package, number of MCMC iterations to be returned for train data.

nkeepertest	As in the BART package, number of MCMC iterations to be returned for test data.
nkeepertestmean	As in the BART package, number of MCMC iterations to be returned for test mean.
nkeepreedraws	As in the BART package, number of MCMC iterations to be returned for tree draws.
printevery	As in the BART package, as the MCMC runs, a message is printed every print-every draws.
seed	A seed number to keep the results repeatable.

Details

Please refer to the reference for the details of model fitting and inferences of mediation effects.

Value

aiex	posterior samples of average indirect effects using method X. method 2 to show the results from the partial differences, method 3 to show the results from the G-computation, and method 4 for G-computation with non-parametric method (binary exposures only).
adeX	posterior samples of average direct effects using method X.
ateX	posterior samples of average total effects using method X.
ieX, deX, teX	posterior samples of indirect effects, direct effects and total effects using method X.
apart.ie	posterior samples of the a-part:changing rate of mediators with pred, using method 2.
bpert.ie	posterior samples of the b-part:changing rate of outcomes with mediators, using method 2.
data0	the output from data_org.
y.type	the type of outcomes.
y.model	the BART model of outcomes.
m.models	the BART model of each mediator.
DIC	the estimated DIC, deviances, D_bar, Var_D, and p_D.

Note

data_org is run automatically in bma.bart. No need to run it separately.

Author(s)

Qingzhao Yu and Bin Li

References

Yu, Q., and Li, B. (2025) <doi:>. "Mediation Analysis with Bayesian Additive Regression Trees," submitted.

Examples

```

data(weight_behavior)
#number of mcmc iterations are set to 3 to reduce time. Need to bring it up to reasonable times.
#binary predictor
try0= bma.bart(pred=weight_behavior[,3], m=weight_behavior[,c(2,4:14)],
               y=weight_behavior[,15], refy = 0, predref = "F",nskip=0,ndpost=2)
summary(try0)

#add covariate for mediators
try1= bma.bart(pred=weight_behavior[,3], m=weight_behavior[,c(2,4:13)],
               mcov=weight_behavior[,14], mclist=append(list(var=1:10),rep(NA,10)),
               #"sweater" is used as a cov for "exercices" only
               y=weight_behavior[,15], refy = 0, predref = "F",nskip=0,ndpost=2)
summary(try1)
summary(try1,trim=0)
#multiple predictor
try2= bma.bart(pred=weight_behavior[,4], m=weight_behavior[,c(2:3,5:14)],
               y=weight_behavior[,15], refy = 0, predref = "OTHER",nskip=0,ndpost=2)
summary(try2)
try3= bma.bart(pred=weight_behavior[,c(1,4)], m=weight_behavior[,c(2:3,5:14)],
               y=weight_behavior[,15], refy = 0, predref = "OTHER",nskip=0,ndpost=2)
summary(try3)
#continuous y
try4= bma.bart(pred=weight_behavior[,4], m=weight_behavior[,c(2:3,5)],
               y=weight_behavior[,1], refy = 0, predref = "OTHER",nskip=0,ndpost=2)
summary(try4)
#categorical y
try5= bma.bart(pred=weight_behavior[,1], m=weight_behavior[,c(2:3,5)],
               y=weight_behavior[,4], refy = "",nskip=0,ndpost=2)
summary(try5)
#add covariates for y and for mediators
try6= bma.bart(pred=weight_behavior[,4], m=weight_behavior[,c(5:12)],
               cova=weight_behavior[,2:3], mcov=weight_behavior[,13:14],
               mclist=c(list(var=1:7),rep(NA,6),list(1)),
               y=weight_behavior[,1], refy = 0, predref = "OTHER",nskip=0,ndpost=2)
#cova and mcov needs to be binarized and numerized
summary(try6)

##Surv class outcome (survival analysis)
data(cgd1)      #a dataset in the survival package
x=cgd1[,c(4:5,7:12)]
pred=cgd1[,6]
status<-ifelse(is.na(cgd1$etime1),0,1)
y=Surv(cgd1$futime,status)
#for continuous predictor
try7= bma.bart(pred=pred,m=x,y=y,nskip=0,ndpost=3)
#summary(try7)

```

Description

This database was obtained from the survival package containing a time-to-event data.

Usage

```
data(weight_behavior)
```

Format

The data set contains many variables.

Examples

```
data(cgd1)
names(cgd1)
```

data_org

Prepare Variables for Bayesian Mediation Analysis with BART

Description

Read in exposure, mediators, outcome, and covariates, and transform them into formats fit for BART fitting.

Usage

```
data_org(pred, m, y, refy = rep(NA, ncol(data.frame(y))),
  predref = rep(NA, ncol(data.frame(pred))), deltap = NA,
  deltam = NA, mref = rep(NA, ncol(data.frame(m))), cova = NULL,
  cova.ref = list(), mcov = NULL, mcov.ref = list(), mclist = NULL,
  complete = FALSE)
```

Arguments

pred	The vector/matrix of the exposure/predict variable(s).
m	The dataframe of all potential mediators
y	The vector/matrix of the outcome(s).
refy	The reference groups of y when the corresponding outcome is binary or categorical.
predref	The reference groups of pred when the corresponding outcome is binary or categorical.
deltap	A vector of the length of the number of exposures. The difference in pred when calculate the changing rate by pred. If not set, the difference is 1 for categorical predictor and one tenth of the standard deviation of the predictor if continuous.

deltam	A vector of the length of the number of mediators. The ith item is the difference in the ith mediator when calculate the changing rate by each mediator. If not set, the difference is 1 for categorical mediators and one tenth of the standard deviation of the mediator if continuous.
mref	The reference groups of mediators when the corresponding mediator is binary or categorical.
cova	The covariance data for y.
cova.ref	The reference group for the binary or categorical covariates in cova.
mcov	The covariance data for mediators.
mcov.ref	The reference group if the mcovs are categorical or binary.
mclist	If mclist is null but not mcov, mcov is applied to all mediators. If both mcov and mclist are not NULL, the first item of mclist lists all mediators that are using different mcov, the following items gives the mcov for the mediators in order, NA if no mcov to be used. e.g. mclist=list(c(1,2,4),l1=1,l2=NA,l4=c(1,3)), mediator 1, m[,1], use mcov[,1], 2 uses no covariates, 4 uses mcov[,c(1,3)], all other mediators use all. Can also replace variable names with column numbers in the mclist.
complete	complete=TRUE if only completed cases are used in analysis.

Details

The function helps organize input data into formats readable to the BART package for building BART. It also recognize the type of the response variable(s), so that different functions and methods will be used for the mediation effect inferences.

Value

Return the cleaned up dataset and organized by types, which is ready for the Bayesian Mediation Analysis.

N	The total number of observations.
y_type	The format of the response variable(s): 1 for continuous, 2 binary, 3 categorical, and 4 time-to-event. It is the same length as the number of outcomes.
y	The original y with observations of missing data removed, if complete=T.
y1	The outcome variables where binary or categorical variables are replaced with dummy design matrix.
cova	The covariates for y, where binary or categorical variables are replaced with dummy design matrix.
npred	The number of predictors/exposures, where a categorical exposure of k levels has k-1 dummy predictors.
nm	The number of original mediators, ncol(m).
mcov	Reformatted mcov.
mind	If mcov is not NULL, mind is a matrix of (# of mediator)*ncol(mcov), cell (i,j) is the indicator of whether the jth column of mcov should be used for mediator i in m1.

pred1	The original pred with observations of missing data removed, if complete=T.
pred2	The pred1 with all categorical or binary variables are turned into dummies.
binpred1	The column numbers of binary predictors in pred1.
binpred2	The column numbers of binary predictors in pred2.
catpred1	The column numbers of categorical predictors in pred1.
catpred2	The column numbers of categorical predictors in pred2.
contpred1	The column numbers of continuous predictors in pred1.
contpred2	The column numbers of continuous predictors in pred2.
m1	The original m with observations of missing data removed, if complete=T.
m2	The m1 with all categorical or binary variables are turned into dummies.
m3.1	The m2 with all continuous variables minus a $\text{deltam}[i]/2$, where i is the i th mediator.
m3.2	The m2 with all continuous variables add a $\text{deltam}[i]/2$, where i is the i th mediator.
p1	The number of continuous mediators.
p2	The number of binary mediators.
p3	The number of categorical mediators.
binm1	The column number of binary mediators in m1.
binm2	The column number of binary mediators in m2.
catm1	The column number of categorical mediators in m1.
catm2	A matrix with the number of rows the number of categorical mediators by the order of catm1. Each row has the start (first column) and end (second column) column numbers of the categorical variable's design matrix in m2.
contm1	The column number of continuous mediators in m1.
contm2	The column number of continuous mediators in m2.
deltap	A vector of the length of the number of exposures. The difference in pred when calculate the changing rate by pred. If not input, the difference is 1 for categorical predictor and one tenth of the standard deviation of the predictor if continuous.
deltam	A vector of the length of the number of mediators. The i th item is the difference in the i th mediator when calculate the changing rate by each mediator. If not set, the difference is 1 for categorical mediators and one tenth of the standard deviation of the mediator if continuous.

Note

data_org is run within bma.bart function. Users do not have to run data_org separately.

Author(s)

Qingzhao Yu and Bin Li

References

Yu, Q., and Li, B. (2025) <doi>. "Mediation Analysis with Bayesian Additive Regression Trees," submitted.

Examples

```
data("weight_behavior")
#binary predictor
try0= data_org(pred=weight_behavior[,3], m=weight_behavior[,c(2,4:14)],
               y=weight_behavior[,15], refy = 0, predref = "F")
#add covariate for mediators
try1= data_org(pred=weight_behavior[,3], m=weight_behavior[,c(2,4:13)],
               mcov=weight_behavior[,14], mclist=append(list(var=1:10),rep(NA,10)),
               #"sweater" is used as a cov for "excercises" only
               y=weight_behavior[,15], refy = 0, predref = "F") #,complete=T
#multiple predictor
try2= data_org(pred=weight_behavior[,4], m=weight_behavior[,c(2:3,5:14)],
               y=weight_behavior[,15], refy = 0, predref = "OTHER")
try3= data_org(pred=weight_behavior[,c(1,4)], m=weight_behavior[,c(2:3,5:14)],
               y=weight_behavior[,15], refy = 0, predref = "OTHER")
#continuous y
try4= data_org(pred=weight_behavior[,4], m=weight_behavior[,c(2:3,5:14)],
               y=weight_behavior[,1], refy = 0, predref = "OTHER")
#categorical y
try5= data_org(pred=weight_behavior[,1], m=weight_behavior[,c(2:3,5:14)],
               y=weight_behavior[,4], refy = "", predref = "OTHER")
#add covariates for y and for mediators
try6= data_org(pred=weight_behavior[,4], m=weight_behavior[,c(5:12)],
               cova=weight_behavior[,2:3],mcov=weight_behavior[,13:14],
               mclist=c(list(var=1:7),rep(NA,6),list(1)),
               y=weight_behavior[,1], refy = 0, predref = "OTHER")
#time-to-event outcome
data(cgd1)      #a dataset in the survival package
x=cgd1[,c(4:5,7:12)]
pred=cgd1[,6]
status<-ifelse(is.na(cgd1$etime1),0,1)
y=Surv(cgd1$futime,status)
#for continuous predictor
try7<-data_org(pred=pred,m=x,y=y)
```

```
print.summary.bma.bart
```

Print the summary results for bma.bart object.

Description

Print and plot the inference results.

Usage

```
## S3 method for class 'summary.bma.bart'
print(x, ..., digit = x$digit, method = x$method, RE = x$RE)
```

Arguments

x	the summary.bma.bart object from the summary function.
...	other arguments passed to the print function.
digit	the number of decimal digits to keep.
method	method=2 to show the results from the partial differences, method=3 to show the results from the G-computation, and method=4 for G-computation with non-parametric method (binary exposures only).
RE	If ture, print the relative effects.

Value

No return value, called for side effects.

Author(s)

Qingzhao Yu and Bin Li

References

Yu, Q., and Li, B. (2025) <doi:>. "Mediation Analysis with Bayesian Additive Regression Trees," submitted.

See Also

"[bma.bart](#)" for examples.

summary.bma.bart	<i>Summary of a bma.bart object</i>
------------------	-------------------------------------

Description

The bma.bart object is from the bma.bart function. The summary function is to calculate the estimates, standard deviation and credible sets of the mediation effects and relative effects.

Usage

```
## S3 method for class 'bma.bart'
summary(object, ..., plot = TRUE, RE = TRUE,
        quant = c(0.025, 0.25, 0.5, 0.75, 0.975),
        digit = 4, method = 3, trim = 0.05)
```

Arguments

object	a bma.bart object created by bma.bart.
...	other arguments passed to the print function.
plot	default is TRUE, if ture, draw a barplot of the mediation effects with credible sets.
RE	default is FALSE, if ture, show the inferences on relative mediation effects.
quant	show the quantiles defined by quant of the posterior distributions of mediation effects.
digit	the number of decimal digits to keep.
method	method=2 to show the results from the partial differences, method=3 to show the results from the G-computation, and method=4 for G-computation with non-parametric method (binary exposures only).
trim	the percentage of trims to calculate the trimmed average mediation effects. By default, trim=0.5.

Details

Show the posterior distribution of the estimated mediation effects.

Value

resultX	the mediation effect estimates using method X.
resultX.re	the relative effect estimates using method X.

Author(s)

Bin Li and Qingzhao Yu

References

Yu, Q., and Li, B. (2025) <doi:>. "Mediation Analysis with Bayesian Additive Regression Trees," submitted.

See Also

"[bma.bart](#)" for examples.

weight_behavior	<i>Weight_Behavior Data Set</i>
-----------------	---------------------------------

Description

This database was obtained from the Louisiana State University Health Sciences Center, New Orleans, by Dr. Richard Scribner. He explored the relationship between BMI and kids behavior through a survey at children, teachers and parents in Grenada in 2014. This data set includes 691 observations and 15 variables.

Usage

```
data(weight_behavior)
```

Format

The data set contains the following variables:

bmi - body mass index, calculated by $\text{weight(kg)}/\text{height(cm)}^2$, numeric

age - children's age in years at the time of survey, numeric

sex - sex of the children, factor

race - race of the children, factor

numpeople - number of people in family, numeric

car - the number of cars in family, numeric

gotosch - the method used to go to school, factor

snack - eat snack or not in a day, binary

tvhours - number of hours watching TV per week, numeric

cmphours - number of hours using computer per week, numeric

cellhours - number of hours playing with cell phones per week, numeric

sports - join in a sport team or not, 1: yes; and 2: no

exercises - number of hours of exercises per week, numeric

sweat - number of hours of sweating activities per week, numeric

overweigh - the child is overweighed or not, binary

Examples

```
data(weight_behavior)
names(weight_behavior)
```

Index

- * **Bayesian Additive Regression Trees**

- bmabart-package, [2](#)

- * **Bayesian Mediation Analysis**

- bma.bart, [2](#)

- bmabart-package, [2](#)

- print.summary.bma.bart, [9](#)

- summary.bma.bart, [10](#)

- * **Datasets**

- cgd1, [5](#)

- weight_behavior, [12](#)

- * **Mediator Tests**

- bma.bart, [2](#)

- print.summary.bma.bart, [9](#)

- summary.bma.bart, [10](#)

bma.bart, [2](#), [10](#), [11](#)

bmabart (bmabart-package), [2](#)

bmabart-package, [2](#)

cgd1, [5](#)

data_org, [6](#)

print.summary.bma.bart, [9](#)

summary.bma.bart, [10](#)

weight_behavior, [12](#)