Package 'abima'

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Title Adaptive Bootstrap Inference for Mediation Analysis with Enhanced Statistical Power

Version 1.1

Description

Assess whether and how a specific continuous or categorical exposure affects the outcome of interest through one- or multi-dimensional mediators using an adaptive bootstrap (AB) approach. The AB method allows to make inference for composite null hypotheses of no mediation effect, providing valid type I error control and thus optimizes statistical power. For more technical details, refer to He, Song and Xu (2024) <doi:10.1093/jrsssb/qkad129>.

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Encoding UTF-8

RoxygenNote 7.2.3

Imports boot, stats

URL https://websites.umich.edu/~songlab/software.html#ABIMA, https://github.com/canyi-chen/abima

BugReports https://github.com/canyi-chen/abima/issues

Suggests testthat (>= 3.0.0)

Config/testthat/edition 3

NeedsCompilation no

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abYlm.Mglm   *Adaptive Bootstrap Test in Mediation Analysis with Linear Models or*
                              Generalized Linear Models

Description

abYlm.Mglm conducts an adaptive bootstrap test in a mediation analysis in which mediator M is
modeled by a generalized linear model (GLM) and outcome Y is modeled by a linear model (LM).
The family of the generalized linear model is specified according to M.family.

Usage

```
abYlm.Mglm(
  S,
  M,
  Y,
  X = NULL,
  covariates_cfder = NULL,
  M.family = stats::gaussian(),
  s = 1,
  s_star = 0,
  B = 199,
  lambda = 2
)
```

Arguments

S	an n-by-1 vector for exposure.
M	an n-by-1 vector for mediator.
Y	an n-by-1 vector for outcome.
X	an n-by-p matrix for p confounders. Do not include intercept in matrix X. In the absence of confounders, matrix is not required to be specified.
covariates_cfder	
	a vector of p confounders to adjust mediation effects, and default is zero (or void). The length of this vector is p, the same as the column dimension of X.
M.family	the error distribution and link function for the mediator model. The default family is gaussian().
s	exposure level with default set at 1.
s_star	baseline exposure level with default set at 0.
B	the number of bootstrap samples with default set at 199.
lambda	the tuning parameter used in the adaptive bootstrap procedure with default set at 2.

Value

NIE refers to natural indirect effect, which is the estimated when a change of exposure S occurs from s_star to s.

p_value_NIE refers to the AB p value for NIE.

NDE refers to natural direct effect, which is estimated when exposure S changes from s_star to s.

p_value_NDE is the p value for NDE.

NTE is the estimated natural total effect when exposure S changes from s_star to s.

p_value_NTE is the p value for NTE.

References

He, Y., Song, P. X. K., and Xu, G. (2023), "Adaptive bootstrap tests for composite null hypotheses in the mediation pathway analysis," Journal of the Royal Statistical Society Series B: Statistical Methodology, qkad129. doi:10.1093/jrsssb/qkad129.

Examples

```
## Load libraries
library(abima)

set.seed(2)

## Set up parameters
M.family <- poisson()

simulation <- function(alpha_S = 0, beta_M = 0) {
  data <- generate_all_data(
    n = 500,
    alpha_S = alpha_S,
    beta_M = beta_M,
    M.family = M.family
  )
  S <- data$S
  M <- data$M
  Y <- data$Y
  X <- data$X

  out <- abYlm.Mglm(S,
                    M,
                    Y,
                    X,
                    M.family = M.family,
                    lambda = 2,
                    B = 199)
  out
}


simulation(1 / 8, 1 / 8)
```

```
simulation(0, 0)
```

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abYlm.Mlm   *Adaptive Bootstrap Test in Mediation Analysis with Linear Models*

Description

`abYlm.Mlm` performs an adaptive bootstrap test in mediation analysis in which both mediator M and outcome Y are modeled by linear models. The mediators can be multi-dimensional.

Usage

```
abYlm.Mlm(S, M, Y, X = NULL, s = 1, s_star = 0, B = 199, lambda = 2)
```

Arguments

S	an n-by-1 vector for exposure.
M	an n-by-m matrix for m mediators, where each row corresponds to a m-element vector of mediators for one subject. The dimension m can be 1 or an integer larger than 1.
Y	an n-by-1 vector for outcome.
X	an n-by-p matrix for p confounders. Do not include intercept in matrix X. In the absence of confounders, matrix is not required to be specified.
s	exposure level with default set at 1.
s_star	baseline exposure level with default set at 0.
B	the number of bootstrap samples with default set at 199.
lambda	the tuning parameter used in the adaptive bootstrap procedure with default set at 2.

Value

NIE refers to natural indirect effect, which is the estimated when a change of exposure S occurs from s_star to s.

p_value_NIE refers to the AB p value for NIE.

NDE refers to natural direct effect, which is estimated when exposure S changes from s_star to s.

p_value_NDE is the p value for NDE.

NTE is the estimated natural total effect when exposure S changes from s_star to s.

p_value_NTE is the p value for NTE.

References

He, Y., Song, P. X. K., and Xu, G. (2023), "Adaptive bootstrap tests for composite null hypotheses in the mediation pathway analysis," Journal of the Royal Statistical Society Series B: Statistical Methodology, qkad129. doi:10.1093/jrsssb/qkad129.

Examples

```
## Load libraries
library(abima)

set.seed(2)


## Set up parameters
M.family <- gaussian()
Y.family <- gaussian()

simulation <- function(alpha_S = 0, beta_M = 0) {
  data <- generate_all_data(
    n = 200,
    alpha_S = alpha_S,
    beta_M = beta_M,
    M.family = M.family,
    Y.family = Y.family
  )
  S <- data$S
  M <- data$M
  Y <- data$Y
  X <- data$X

  out <- abYlm.Mlm(S, M, Y, X, lambda = 2, B = 199)
  out
}


simulation(1 / 8, 1 / 8)

simulation(0, 0)
```

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generate_all_data *Data simulated from a directed acyclic graph (DAG) model*

Description

Simulate data from a directed acyclic graph (DAG) model.

Usage

```
generate_all_data(
  n = 200,
  alpha_S = 0,
  beta_M = 0,
  tau_S = 1,
  alpha_vec = rep(1, 3),
  beta_vec = rep(1, 3),
  M.family = stats::gaussian(),
  Y.family = stats::gaussian(),
  sigma_M = 0.5,
  sigma_Y = 0.5
)
```

Arguments

n	a sample size
alpha_S	a parameter in mediator model M~S+X for S
beta_M	a parameter in outcome model Y~S+M+X for M
tau_S	a parameter in outcome model Y~S+M+X for S
alpha_vec	a parameter vector in mediator model M~S+X for X
beta_vec	a parameter vector in outcome model Y~S+M+X for X
M.family	an error distribution and link function to be used in the mediator model. See [family](#) for details of family functions. The default family is [gaussian](#).
Y.family	an error distribution and link function to be used in the outcome model. See [family](#) for details of family functions. The default family is [gaussian](#).
sigma_M	the variance of the error term in the mediator model M~S+X
sigma_Y	the variance of the error term in the outcome model Y~S+M+X

Value

A list with the following components:

S	exposure
M	mediator
Y	outcome
X	confounder

Examples

```
out <- generate_all_data(n = 200)
summary(out$S)
summary(out$M)
summary(out$Y)
summary(out$X)
```

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