

Package ‘SAMTx’

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Type Package

Title Sensitivity Assessment to Unmeasured Confounding with Multiple Treatments

Version 0.3.0

Description

A sensitivity analysis approach for unmeasured confounding in observational data with multiple treatments and a binary outcome. This approach derives the general bias formula and provides adjusted causal effect estimates in response to various assumptions about the degree of unmeasured confounding. Nested multiple imputation is embedded within the Bayesian framework to integrate uncertainty about the sensitivity parameters and sampling variability. Bayesian Additive Regression Model (BART) is used for outcome modeling. The causal estimands are the conditional average treatment effects (CATE) based on the risk difference. For more details, see paper: Hu L et al. (2020) A flexible sensitivity analysis approach for unmeasured confounding with multiple treatments and a binary outcome with application to SEER-Medicare lung cancer data <doi:10.48550/arXiv.2012.06093>.

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Imports BART

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Author Liangyuan Hu [aut],
Jungang Zou [aut],
Jiayi Ji [aut, cre]

Maintainer Jiayi Ji <Jiayi.Ji@mountsinai.org>

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sensitivity_analysis *Sensitivity Assessment to Unmeasured Confounding with Multiple Treatments*

Description

This function implements the nested multiple imputation using Bayesian Additive Regression Trees (BART)

Usage

```
sensitivity_analysis(
  covariates,
  y,
  A,
  alpha,
  n_p,
  nposterior = 1000,
  sensitivity_correction = TRUE
)
```

Arguments

covariates	Dataframe including all the covariates
y	Numeric vector for the binary outcome
A	Numeric vector for the treatment indicator
alpha	Priors for sensitivity parameters
n_p	Number of nested imputations to conduct
nposterior	Number of posterior samples, default is 1000
sensitivity_correction	Whether to use sensitivity correction algorithm, default is TRUE

Value

A list of dataframes for each ATE between different treatments. If number of treatments = 3, it contains

ATE12:	A dataframe with number of rows = $n_p * nrow(alpha)$ and number of columns = $length(y)$
ATE23:	A dataframe with number of rows = $n_p * nrow(alpha)$ and number of columns = $length(y)$
ATE13:	A dataframe with number of rows = $n_p * nrow(alpha)$ and number of columns = $length(y)$

Examples

```

sample_size = 10
x1 = rbinom(sample_size, 1, prob=0.4)
x2 = rbinom(sample_size, 1, prob=0.5)
lp.A = 0.2 * x1 + 0.4 * x2 + rnorm(sample_size, 0, 0.1)
lp.B = -0.3 * x1 + 0.8 * x2 + rnorm(sample_size, 0, 0.1)
lp.C = 0.1 * x1 + 0.5 * x2 + rnorm(sample_size, 0, 0.1)
# calculate the true probability of assignment
p.A1 <- exp(lp.A)/(exp(lp.A)+exp(lp.B)+exp(lp.C))
p.A2 <- exp(lp.B)/(exp(lp.A)+exp(lp.B)+exp(lp.C))
p.A3 <- exp(lp.C)/(exp(lp.A)+exp(lp.B)+exp(lp.C))
p.A <- matrix(c(p.A1,p.A2,p.A3),ncol = 3)
A = NULL
for (m in 1:sample_size) { # assign treatment
  A[m] <- sample(c(1, 2, 3),
                size = 1,
                replace = TRUE,
                prob = p.A[m, ])
}
table(A)
# set the binary outcome
Y2 = 0.3 * x1 + 0.2 * x1 * x2 + 1.3 * x2
Y1 = -0.6 * x1 + 0.5 * x2 + 0.3 * x1 * x2
Y0 = -0.8 * x1 - 1.2 * x2 + 1.5 * x2 * x1
Y2 = rbinom(sample_size, 1, exp(Y2)/(1+exp(Y2)))
Y1 = rbinom(sample_size, 1, exp(Y1)/(1+exp(Y1)))
Y0 = rbinom(sample_size, 1, exp(Y0)/(1+exp(Y0)))
dat = cbind(Y0, Y1, Y2, A)
Yobs <- apply(dat, 1, function(x)
  x[1:3][x[4]]) #observed when trt is received
n = 1
alpha = cbind(
  runif(n, mean(Y0[A ==1])-mean(Y0[A ==2]) - 0.001, mean(Y0[A ==1])-mean(Y0[A ==2]) + 0.001),
  runif(n, mean(Y1[A ==2])-mean(Y1[A ==1]) - 0.001, mean(Y1[A ==2])-mean(Y1[A ==1]) + 0.001),
  runif(n, mean(Y1[A ==2])-mean(Y1[A ==3]) - 0.001, mean(Y1[A ==2])-mean(Y1[A ==3]) + 0.001),
  runif(n, mean(Y0[A ==1])-mean(Y0[A ==3]) - 0.001, mean(Y0[A ==1])-mean(Y0[A ==3]) + 0.001),
  runif(n, mean(Y2[A ==3])-mean(Y2[A ==1]) - 0.001, mean(Y2[A ==3])-mean(Y2[A ==1]) + 0.001),
  runif(n, mean(Y2[A ==3])-mean(Y2[A ==2]) - 0.001, mean(Y2[A ==3])-mean(Y2[A ==2]) + 0.001)
)
y <- Yobs
n_p <- 1
sample_gap <- 10
sensitivity_analysis_result <- sensitivity_analysis(cbind(x1, x2), Yobs,
A, alpha, n_p = 1, sensitivity_correction = TRUE)
mean(sensitivity_analysis_result$ATE_12)
mean(sensitivity_analysis_result$ATE_02)
mean(sensitivity_analysis_result$ATE_01)

```

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