

Package ‘tbd’

January 5, 2019

Title Estimation of causal effects with outcomes truncated by death

Version 0.0.0.9000

Author Zhixuan Shao [cre],
Bo Liu [ctb],
Linbo Wang [aut]

Maintainer Zhixuan Shao <shaozhixuansh@pku.edu.cn>

Description Estimation of the survivor average causal effect under outcomes truncated by death, which requires the existence of a substitution variable. It can be applied to both experimental and observational data.

Depends R (>= 3.3.2), numDeriv, stats

License GPL-3

Encoding UTF-8

URL <https://github.com/KillingVectorField/causal-inference-truncated-by-death>

LazyData true

RoxygenNote 5.0.1

R topics documented:

boot.ci	1
print.sace	2
sace	3
selectSV	5
summary.sace	6
Index	7

boot.ci	<i>Estimate the confidence interval of SACE using bootstrap.</i>
---------	--

Description

Give quantiles of bootstrap samples SACE.

Usage

```
boot.ci(object, nboot = 1000, seed = 100:(100 + nboot - 1), alpha = 0.05,
        max.step = 1000, singular.ok = FALSE, print.progress = TRUE)
```

Arguments

object	an object of class <code>sace</code> .
nboot	a positive integer. The number of bootstrap samples desired.
seed	an integer vector with length <code>nboot</code> . Seed to generate samples.
alpha	confidence level.
max.step	see documentation of sace .
singular.ok	see documentation of sace .
print.progress	logical. Need progress be printed?

Value

a list with 4 elements:

nskip	number of failures during bootstrap.
sace.boot.record	a vector with length <code>nboot-skip</code> . SACE estimates of all bootstrap samples.
boot.sd	scaler. Standard deviation of SACE estimates of all bootstrap samples.
ci	a vector with length 2. Estimated confidence interval.

Author(s)

Zhixuan Shao <shaozhixuansh@pku.edu.cn>

print.sace	<i>Print results of sace</i>
------------	------------------------------

Description

`print.sace` prints estimation of the SACE (survivor average causal effect).

Usage

```
## S3 method for class 'sace'
print(x, ...)
```

Arguments

x	an object of class <code>sace</code> .
...	additional arguments.

Value

the input object is returned silently.

Author(s)

Zhixuan Shao <shaozhixuansh@pku.edu.cn>

sace

*Estimation of causal effects with outcomes truncated by death***Description**

sace estimates survivor average causal effects (SACE) with outcomes truncated by death.

Usage

```
sace(Z, S, Y, X, A, subset, optim.method = "BFGS", max.step = 1000,
     singular.ok = TRUE, need.variance = TRUE, hessian = TRUE)
```

Arguments

Z	a logical vector. Exposure indicator. Conventionally, 1 means treatment and 0 means control. Must not have missing values.
S	a logical vector. Survival indicator. 1 means survival and 0 means death. Must not have missing values.
Y	a numeric vector. (Univariate) outcomes. May have NA where $S = 0$ (since Y is not well-defined where $S = 0$).
X	an optional numeric matrix or vector. Baseline covariates.
A	an optional numeric matrix or vector. Substitution variable(s) which satisfies the assumptions of "exclusion restriction" and "substitution relevance". See references. If $A == \text{NULL}$, then the naive method, namely OLS, will be used.
subset	an optional vector specifying a subset of observations to be used.
optim.method	The method to be used for maximum likelihood optimization. See optim .
max.step	integer. Maximum iterating steps of maximum likelihood optimization.
singular.ok	logical. Refers to the OLS estimation of the coefficients α_1 and α_2 using lm . If FALSE (default), a singular fit raises an error.
need.variance	logical. Is variance of parameters and estimators needed? See details.
hessian	logical. If TRUE, the hessian returned by optim will be used to compute the information matrix. If FALSE, the matrix will be calculated by an explicit formula.

Details

This function `sace`, gives estimation of average causal effects (ACE) with outcomes truncated by death, based on the assumptions of monotonicity, ignorability and exclusion restriction. While the naive estimates given by the coefficient of Z from $\text{lm}(Y \sim Z + X + A, \text{subset} = S == 1)$ are restricted among survivors and therefore may be subject to selection bias, this method gives consistent estimates of the SACE (survivor average causal effect), defined as the average causal effect among the subgroup consisting of subjects who would survive under either exposure, i.e. among the always-survivor group ($G = LL$). See references.

Parameters β and γ are estimated by MLE, using [optim](#).

If `need.variance == TRUE`, the asymptotic variance estimators of both parameters and estimators will be given. This requires the "numDeriv" package, and may be time-consuming.

Value

a list with following elements:

CALL	function call.
data	data used (within the specified subset).
optim.method	method used for optimization.
need.variance	is variance of parameters and estimators needed?
n	sample size.
mu_0_LL	average potential outcomes among control group, $E[Y(0) G = LL]$.
mu_1_LL	average potential outcomes among treatment group, $E[Y(1) G = LL]$.
sace	survivor average causal effect, equals $\mu_{1_LL} - \mu_{0_LL}$.
beta	$PrS(1) = 1 X, A = \text{expit}(\beta_0 + X'\beta_1 + A\beta_2)$, estimated by MLE.
gamma	$PrS(0) = 1 X, A / PrS(1) = 1 X, A = \text{expit}(\gamma_0 + X'\gamma_1 + A\gamma_2)$, estimated by MLE.
beta_gamma.convergence	indicator of convergence of MLE optimization of beta and gamma. 0 means convergence. See optim .
alpha_1	$E[Y(0) Z = 0, G = LL, X, A] = \alpha_{00} + X'\alpha_{01} + A\alpha_{02}$, coefficients of $\text{lm}(Y \sim 1 + X + A, \text{subset} = Z == 0)$.
alpha_2	$E[Y(1) Z = 1, G = LL, X, A] = \alpha_{10} + X'\alpha_{11} + A\alpha_{12}$, coefficients of $\text{lm}(Y \sim 1 + X + W.\text{expit}, \text{subset} = (Z == 1 \& S == 1))$.

The following items will be given only if `need.variance == TRUE`:

beta.var	estimated asymptotic covariance matrix of beta.
gamma.var	estimated asymptotic covariance matrix of gamma.
alpha_1.var	estimated asymptotic covariance matrix of alpha_1.
alpha_2.var	estimated asymptotic covariance matrix of alpha_2.
mu_0_LL.var	estimated asymptotic variance of mu_0_LL.
mu_1_LL.var	estimated asymptotic variance of mu_1_LL.
sace.var	estimated asymptotic variance of the SACE.

Note

The length of vectors Z, Y, S, as well as the row number of matrix X and A must equal the sample size n.

Author(s)

Linbo Wang <linbo.wang@utoronto.ca>

Zhixuan Shao <shaozhixuansh@pku.edu.cn>

References

Linbo Wang, Xiao-Hua Zhou, Thomas S. Richardson; Identification and estimation of causal effects with outcomes truncated by death, *Biometrika*, Volume 104, Issue 3, 1 September 2017, Pages 597-612, <https://doi.org/10.1093/biomet/asx034>

selectSV	<i>Select the substitution variable whose impact on survival is the most significant.</i>
----------	---

Description

Provided with a bunch of substitution variables that are all a priori believed to satisfy the assumptions, i.e. exclusion restriction and substitution relevance, `selectSV` chooses the one that most significantly impact survival(S). A whose coefficient has the smallest P-value (against null) will be chosen.

Usage

```
selectSV(Z, S, X, A.candidates, subset, optim.method = "BFGS",
         max.step = 1000)
```

Arguments

<code>Z</code>	a logical vector. Exposure indicator.
<code>S</code>	a logical vector. Survival indicator.
<code>X</code>	an optional numeric matrix or vector. Baseline covariates.
<code>A.candidates</code>	a numeric matrix. Each column represents a possible substitution variable.
<code>subset</code>	an optional vector specifying a subset of observations to be used.
<code>optim.method</code>	The method to be used for maximum likelihood optimization. See optim .
<code>max.step</code>	integer. Maximum iterating steps of maximum likelihood optimization.

Value

a list with 2 elements:

<code>selected.A</code>	column name of the selected substitution variable.
<code>P.values</code>	P-values (against null hypothesis) of every substitution variable's coefficient.

Note

Outcome Y is not needed here. See [sace](#) for the meaning of Z , S , X , A

Author(s)

Zhixuan Shao <shaozhixuansh@pku.edu.cn>

summary.sace	<i>Summarize results of sace</i>
--------------	----------------------------------

Description

summary.sace summary estimation of the SACE (survivor average causal effect) and all other model parameters.

Usage

```
## S3 method for class 'sace'  
summary(object, ...)
```

Arguments

object	an object of class sace.
...	additional arguments.

Value

the input object is returned silently.

Note

If need.variance is TRUE, sace must have been called with need.variance == TRUE, so that the information needed was recorded.

Author(s)

Zhixuan Shao <shaozhixuansh@pku.edu.cn>

Index

`boot.ci`, [1](#)

`lm`, [3](#)

`optim`, [3–5](#)

`print.sace`, [2](#)

`sace`, [2, 3, 5](#)

`selectSV`, [5](#)

`summary.sace`, [6](#)