

Package ‘sreg’

March 20, 2024

Type Package

Title ATE Estimation under CAR and Cluster-Level Treatment Assignment

Version 2.1.0

Author Juri Trifonov <jutrifonov@uchicago.edu>

Maintainer Juri Trifonov <jutrifonov@uchicago.edu>

Description The 'sreg' package offers a robust toolkit for estimating average treatment effects (ATEs) within the context of a stratified block randomization design under the covariate-adaptive randomization (CAR). Designed to accommodate scenarios with multiple treatments and cluster-level treatment assignments, the 'sreg' package not only provides ATE estimators but also includes sophisticated features for calculating adjusted variance estimators developed in papers (Bugni, Canay, Shaikh; 2017), (Bugni, Canay, Shaikh, Tabord-Meehan; 2023) and (Jiang, Linton, Tang, Zhang, 2023).

License MIT + file LICENSE

Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

Imports dplyr, extraDistr, haven, tidyr

Depends R (>= 2.10)

NeedsCompilation no

R topics documented:

AEJapp	2
sreg	2
sreg.rgen	4
Index	6

AEJapp	<i>Replication data for: Iron Deficiency and Schooling Attainment in Peru (Chong et al, 2016)</i>
--------	---

Description

The data is taken from Chong et al. (2016), who study the effect of iron deficiency anemia (i.e., anemia caused by a lack of iron) on school-age children's educational attainment and cognitive ability in Peru.

Usage

```
data("AEJapp")
```

Format

A data frame with 215 observations on the 62 variables.

Source

Chong, Alberto, Cohen, Isabelle, Field, Erica, Nakasone, Eduardo, and Torero, Maximo. Replication data for: Iron Deficiency and Schooling Attainment in Peru. Nashville, TN: American Economic Association [publisher], 2016. Ann Arbor, MI: Inter-university Consortium for Political and Social Research [distributor], 2019-10-12. <https://doi.org/10.3886/E113624V1>.

References

Chong, Alberto, Isabelle Cohen, Erica Field, Eduardo Nakasone, and Maximo Torero. "Iron Deficiency and Schooling Attainment in Peru." *American Economic Journal: Applied Economics* 8, no. 4 (October 2016): 222–55. <https://doi.org/10.1257/app.20140494>.

Examples

```
data(AEJapp)
```

sreg	<i>Estimate Average Treatment Effects (ATEs) and corresponding Standard Errors</i>
------	--

Description

The function estimates the ATE(s) and the corresponding standard error(s) given the data provided. Multiple treatments, strata-based treatments, cluster-level treatments, and linear adjustments are supported. The function implements the appropriate estimator(s) given the data provided.

Usage

```
sreg(Y, S = NULL, D, G.id = NULL, Ng = NULL, X = NULL, HC1 = TRUE)
```

Arguments

Y	a numeric vector of the observed outcomes
S	a numeric vector of strata indicators; if S = NULL then the estimator without strata is applied
D	a numeric vector of treatments
G.id	a numeric vector of cluster indicators; if G.id = NULL then the estimator without clusters is applied
Ng	a numeric vector of cluster sizes; if Ng = NULL then the estimator without clusters is applied
X	a data frame with columns representing the covariate values for every observation; if X = NULL then the estimator without linear adjustments is applied
HC1	a TRUE/FALSE argument indicating whether the small sample correction should be applied to the variance estimator

Value

An object of class `sreg` that is a list containing the following elements:

- `tau.hat`: a $1 \times |\mathcal{A}|$ vector of ATE estimates, where $|\mathcal{A}|$ represents the number of treatments
- `se.rob`: a $1 \times |\mathcal{A}|$ vector of standard errors estimates, where $|\mathcal{A}|$ represents the number of treatments
- `t.stat`: a $1 \times |\mathcal{A}|$ vector of t -statistics, where $|\mathcal{A}|$ represents the number of treatments
- `p.value`: a $1 \times |\mathcal{A}|$ vector of corresponding p -values, where $|\mathcal{A}|$ represents the number of treatments
- `CI.left`: a $1 \times |\mathcal{A}|$ vector of the left bounds of the 95% as. confidence interval
- `CI.right`: a $1 \times |\mathcal{A}|$ vector of the right bounds of the 95% as. confidence interval
- `data`: an original data of the form `data.frame(Y, S, D, G.id, Ng, X)`
- `lin.adj`: a data frame representing the covariates that were used in implementing linear adjustments

Examples

```
library("sreg")
library("dplyr")
library("haven")
### Example 1. Simulated Data.
data <- sreg.rgen(n = 1000, tau.vec = c(0), n.strata = 4, cluster = FALSE)
Y <- data$Y
S <- data$S
D <- data$D
X <- data.frame("x_1" = data$x_1, "x_2" = data$x_2)
result <- sreg(Y, S, D, G.id = NULL, Ng = NULL, X)
### Example 2. Data taken from Chong et al. (2016).
## Data description
?AEJapp
## Upload the data from the package
data("AEJapp")
data <- AEJapp
head(data)
## Replicate the empirical illustration from (Bugni et al, 2019)
```

```

# Prepare the data
Y <- data$gradesq34
D <- data$treatment
S <- data$class_level
data.clean <- data.frame(Y, D, S)
data.clean <- data.clean %>%
  mutate(D = ifelse(D == 3, 0, D))
Y <- data.clean$Y
D <- data.clean$D
S <- data.clean$S
# Look at the frequency table
table(D = data.clean$D, S = data.clean$S)
# Replicate the results from (Bugni et al, 2019)
result <- sreg::sreg(Y, S, D)

## Besides that, it is possible to add linear adjustments (covariates)
pills <- data$pills_taken
age <- data$age_months
data.clean <- data.frame(Y, D, S, pills, age)
data.clean <- data.clean %>%
  mutate(D = ifelse(D == 3, 0, D))
Y <- data.clean$Y
D <- data.clean$D
S <- data.clean$S
X <- data.frame("pills" = data.clean$pills, "age" = data.clean$age)
result <- sreg::sreg(Y, S, D, X)

```

sreg.rgen

Generates a pseudo-random sample for estimating ATE

Description

Generates a pseudo-random sample for estimating ATE

Usage

```

sreg.rgen(
  n,
  Nmax = 50,
  n.strata,
  tau.vec = c(0),
  gamma.vec = c(0.4, 0.2, 1),
  cluster = TRUE,
  is.cov = TRUE
)

```

Arguments

n	number of observations
Nmax	maximum size of clusters
n.strata	number of strata
tau.vec	a numeric vector of treatment effects

<code>gamma.vec</code>	a numeric vector of parameters
<code>cluster</code>	a TRUE/FALSE argument indicating whether the dgp should include clusters or not
<code>is.cov</code>	a TRUE/FALSE argument indicating whether the dgp should include covariates or not

Value

a data frame containing the results

Examples

```
data <- sreg.rgen(n = 1000, tau.vec = c(0), n.strata = 4, cluster = TRUE)
```

Index

* **datasets**

AEJapp, [2](#)

AEJapp, [2](#)

sreg, [2](#)

sreg.rgen, [4](#)