

Package ‘sreg’

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Type Package

Title Stratified Randomized Experiments

Version 2.1.0

Description Estimate average treatment effects (ATEs) in stratified randomized experiments. 'sreg' supports a wide range of stratification designs, including matched pairs, n-tuple designs, and larger strata with many units — possibly of unequal size across strata. 'sreg' is designed to accommodate scenarios with multiple treatments and cluster-level treatment assignments, and accommodates optimal linear covariate adjustment based on baseline observable characteristics. 'sreg' computes estimators and standard errors based on Bugni, Canay, Shaikh (2018) [<doi:10.1080/01621459.2017.1375934>](https://doi.org/10.1080/01621459.2017.1375934); Bugni, Canay, Shaikh, Tabord-Meehan (2024+) [<doi:10.48550/arXiv.2204.08356>](https://doi.org/10.48550/arXiv.2204.08356); Jiang, Linton, Tang, Zhang (2023+) [<doi:10.48550/arXiv.2201.13004>](https://doi.org/10.48550/arXiv.2201.13004); Bai, Jiang, Romano, Shaikh, and Zhang (2024) [<doi:10.1016/j.jeconom.2024.105740>](https://doi.org/10.1016/j.jeconom.2024.105740); Bai (2022) [<doi:10.1257/aer.20201856>](https://doi.org/10.1257/aer.20201856); Bai, Romano, and Shaikh (2022) [<doi:10.1080/01621459.2021.1883437>](https://doi.org/10.1080/01621459.2021.1883437); Liu (2024+) [<doi:10.48550/arXiv.2301.09016>](https://doi.org/10.48550/arXiv.2301.09016); and Cytrynbaum (2024) [<doi:10.3982/QE2475>](https://doi.org/10.3982/QE2475).

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AEJapp	<i>Replication data for: Iron Deficiency and Schooling Attainment in Peru (Chong et al, 2016)</i>
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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, A., Cohen, I., Field, E., Nakasone, E., and Torero, M. (2016). 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. [doi:10.3886/E113624V1](https://doi.org/10.3886/E113624V1).

References

Chong, A., Cohen, I., Field, E., Nakasone, E., and Torero, M. (2016). Iron Deficiency and Schooling Attainment in Peru. *American Economic Journal: Applied Economics*, 8(4), 222–255. doi:[10.1257/app.20140494](https://doi.org/10.1257/app.20140494).

Examples

```
data(AEJapp)
```

plot.sreg	<i>Plot Method for 'sreg' Objects</i>
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Description

Visualize estimated ATEs and confidence intervals for objects of class `sreg`.

Usage

```
## S3 method for class 'sreg'
plot(
  x,
  treatment_labels = NULL,
  title = "Estimated ATEs with Confidence Intervals",
  bar_fill = NULL,
  point_shape = 23,
  point_size = 3,
  point_fill = "white",
  point_stroke = 1.2,
  point_color = "black",
  label_color = "black",
  label_size = 4,
  bg_color = NULL,
  grid = TRUE,
  zero_line = TRUE,
  y_axis_title = NULL,
  x_axis_title = NULL,
  ...
)
```

Arguments

<code>x</code>	An object of class <code>sreg</code> .
<code>treatment_labels</code>	Optional vector of treatment labels to display on the y-axis. If <code>NULL</code> , default labels like "Treatment 1", "Treatment 2", etc., are used.
<code>title</code>	Optional plot title. Defaults to "Estimated ATEs with Confidence Intervals".

<code>bar_fill</code>	Optional fill color(s) for the confidence interval bars. Can be NULL (default viridis scale), a single color, or a vector of two colors for a gradient.
<code>point_shape</code>	Optional shape of the point used to mark the estimated ATE. Default is 23 (a diamond).
<code>point_size</code>	Optional size of the point marking the ATE.
<code>point_fill</code>	Optional fill color of the ATE point shape.
<code>point_stroke</code>	Optional stroke (border) thickness of the ATE point shape.
<code>point_color</code>	Optional outline color of the ATE point.
<code>label_color</code>	Optional color of the text label displaying the estimate and standard error.
<code>label_size</code>	Optional size of the text label displaying the estimate and standard error.
<code>bg_color</code>	Optional background color of the plot panel. If NULL, the default theme background is used.
<code>grid</code>	Optional logical flag. If TRUE (default), grid lines are shown; if FALSE, they are removed.
<code>zero_line</code>	Optional logical flag. If TRUE (default), a vertical dashed line at 0 is added for reference.
<code>y_axis_title</code>	Optional title of the y-axis. If NULL, no y-axis label is added.
<code>x_axis_title</code>	Optional title of the x-axis. If NULL, no x-axis label is added.
<code>...</code>	Additional arguments passed to other methods.

Value

Invisibly returns the ggplot object. Called for its side effects (i.e., generating a plot).

Examples

```
set.seed(22)
data <- sreg.rgen(
  n = 120, tau.vec = c(0.2, 0.5), n.strata = 4,
  cluster = FALSE
)
fit <- sreg(Y = data$Y, S = data$S, D = data$D)

plot(fit)

p <- plot(
  fit,
  treatment_labels = c("Program A", "Program B"),
  title = "Estimated treatment effects",
  x_axis_title = "ATE relative to control",
  bar_fill = c("#3B82F6", "#14B8A6")
)
class(p)
```

print.sreg	<i>Print sreg Objects</i>
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Description

Print the summary table of estimation results for sreg objects.

Usage

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

Arguments

x	An object of class sreg.
...	Additional arguments passed to other methods.

Value

No return value, called for side effects.

Examples

```
set.seed(21)
data <- sreg.rgen(
  n = 80, tau.vec = c(0.2, 0.5), n.strata = 4,
  cluster = FALSE
)
fit <- sreg(
  Y = data$Y, S = data$S, D = data$D,
  X = data[c("x_1", "x_2")]
)
print(fit)
```

sreg	<i>Estimate Average Treatment Effects (ATEs) and Corresponding Standard Errors</i>
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Description

Estimate the ATE(s) and the corresponding standard error(s) for a (collection of) treatment(s) relative to a control.

Usage

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

Arguments

Y	a numeric $n \times 1$ vector/matrix/data.frame/tibble of the observed outcomes
S	a numeric $n \times 1$ vector/matrix/data.frame/tibble of strata indicators indexed by $\{1, 2, 3, \dots\}$; if NULL then the estimation is performed assuming no stratification
D	a numeric $n \times 1$ vector/matrix/data.frame/tibble of treatments indexed by $\{0, 1, 2, \dots\}$, where $D = 0$ denotes the control
G.id	a numeric $n \times 1$ vector/matrix/data.frame/tibble of cluster indicators; if NULL then estimation is performed assuming treatment is assigned at the individual level
Ng	a numeric $n \times 1$ vector/matrix/data.frame/tibble of cluster sizes; if NULL then Ng is assumed to be equal to the number of available observations in every cluster
X	a matrix/data.frame/tibble with columns representing the covariate values for every observation; if NULL then the estimator without linear adjustments is applied. (Note: sreg cannot use individual-level covariates for covariate adjustment in cluster-randomized experiments. Any individual-level covariates will be aggregated to their cluster-level averages)
HC1	a TRUE/FALSE logical argument indicating whether the small sample correction should be applied to the variance estimator
small.strata	a TRUE/FALSE logical argument indicating whether the estimators for small strata (i.e., strata with few units, such as matched pairs or n-tuples) should be used.
k	an optional positive integer specifying the number of units per small stratum, or the number of clusters per small stratum in cluster-randomized designs. When NULL, mixed designs retain the automatic detection rule for matched pairs and triplets. Supply k for general k-tuple mixed designs.

Details

Supplying G.id selects cluster-level assignment; otherwise, treatment is treated as assigned at the individual level. Setting small.strata = FALSE selects the large-strata procedure. With small.strata

= TRUE, a common observed stratum size selects the small-strata procedure, whereas varying stratum sizes select the mixed procedure. The optional `k` validates the common size in a uniform small-strata design and identifies the small-stratum size in a general mixed design.

Under cluster-level assignment, adjustment is performed using cluster-level covariates. Covariates supplied with one row per individual are replaced by their within-cluster means. The package computes the mean outcome among the available observations from each cluster and uses `Ng` as its represented cluster size. If `Ng = NULL`, the represented cluster size is set equal to the number of available observations in that cluster.

When covariates are supplied in a mixed design, they are used in both the small- and large-strata components. If the large-strata component cannot support the required treatment-by-stratum regressions, `sreg()` returns an error suggesting fewer covariates or `X = NULL`.

Value

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

- `tau.hat`: a numeric vector of ATE estimates, one for each active treatment arm relative to control
- `se.rob`: a numeric vector of estimated standard errors
- `t.stat`: a numeric vector of test statistics
- `p.value`: a numeric vector of corresponding *p*-values
- `CI.left`, `CI.right`: numeric vectors containing the lower and upper endpoints of the 95% asymptotic confidence intervals
- `as.CI`: the confidence-interval endpoints combined as `c(CI.left, CI.right)`
- `data`: the data used for estimation, including the outcome, strata, treatment, and any supplied cluster or covariate variables
- `lin.adj`: the covariates used for linear adjustment, or `NULL` when no adjustment is used
- `small.strata`: a logical value recording the requested strata procedure
- `HC1`: a logical value recording whether the HC1 finite-sample correction was applied
- `mixed.design`: present and `TRUE` for mixed designs
- `res.small`, `res.big`: for mixed designs, the fitted `sreg` objects for the small- and large-strata components

Depending on the selected design, the object may additionally contain the estimated adjustment coefficients in `ols.iter` or `beta.hat`.

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Examples

```
### Large strata with covariate adjustment
set.seed(1)
large_data <- sreg.rgen(
  n = 120, tau.vec = c(0.2, 0.5), n.strata = 4,
  cluster = FALSE
)
fit_large <- sreg(
  Y = large_data$Y, S = large_data$S, D = large_data$D,
  X = large_data[c("x_1", "x_2")]
)
fit_large$tau.hat
fit_large$se.rob

### Uniform triplets: k is observed and may be omitted from sreg()
set.seed(2)
small_data <- sreg.rgen(
  n = 60, tau.vec = c(0.2, 0.5), cluster = FALSE,
  small.strata = TRUE, k = 3, treat.sizes = c(1, 1, 1)
)
fit_small <- sreg(
  Y = small_data$Y, S = small_data$S, D = small_data$D,
  small.strata = TRUE
)
fit_small$tau.hat
```

```

### Mixed design with general k-tuples: specify k in sreg()
set.seed(3)
mixed_data <- sreg.rgen(
  n = 60, tau.vec = 0.5, cluster = FALSE,
  mixed.strata = TRUE, n.small = 40, k = 4,
  treat.sizes = c(2, 2), n.strata = 2
)
fit_mixed <- suppressWarnings(sreg(
  Y = mixed_data$Y, S = mixed_data$S, D = mixed_data$D,
  small.strata = TRUE, k = 4
))
fit_mixed$mixed.design

### Cluster-randomized design
set.seed(4)
cluster_data <- sreg.rgen(
  n = 24, tau.vec = 0.5, n.strata = 3, cluster = TRUE
)
fit_cluster <- sreg(
  Y = cluster_data$Y, S = cluster_data$S, D = cluster_data$D,
  G.id = cluster_data$G.id, Ng = cluster_data$Ng
)
fit_cluster$tau.hat

```

sreg.rgen

Generate a Pseudo-Random Sample under the Stratified Block Randomization Design

Description

The function generates the observed outcomes, treatment assignments, strata indicators, cluster indicators, cluster sizes, and covariates for estimating the treatment effect within the context of a stratified block randomization design under the covariate-adaptive randomization (CAR).

Usage

```

sreg.rgen(
  n,
  Nmax = 50,
  n.strata = 10,
  tau.vec = c(0),
  gamma.vec = c(0.4, 0.2, 1),
  cluster = TRUE,
  is.cov = TRUE,
  small.strata = FALSE,
  k = 3,
  treat.sizes = c(1, 1, 1),
  mixed.strata = FALSE,
  n.small = NULL,

```

```

allocation.probs = NULL,
stratum.effects = NULL,
treatment.effects.by.stratum = NULL
)

```

Arguments

<code>n</code>	the total number of units when <code>cluster = FALSE</code> , or the total number of clusters when <code>cluster = TRUE</code>
<code>Nmax</code>	a maximum size of generated clusters (maximum number of observations in a cluster)
<code>n.strata</code>	an integer specifying the number of strata
<code>tau.vec</code>	a numeric $1 \times \mathcal{A} $ vector of treatment effects, where $ \mathcal{A} $ represents the number of treatments
<code>gamma.vec</code>	a numeric 1×3 vector of parameters corresponding to covariates
<code>cluster</code>	a TRUE/FALSE argument indicating whether the data-generating process should use cluster-level or individual-level treatment assignment
<code>is.cov</code>	a TRUE/FALSE argument indicating whether the data-generating process should include covariates
<code>small.strata</code>	a TRUE/FALSE argument indicating whether the data-generating process should use a small-strata design (e.g., matched pairs, n-tuples)
<code>k</code>	an integer specifying the number of units per stratum when <code>small.strata = TRUE</code>
<code>treat.sizes</code>	a numeric $1 \times (\mathcal{A} + 1)$ vector specifying the number of units assigned to each treatment within a stratum; the first element corresponds to control units ($D = 0$), the second to the first treatment ($D = 1$), and so on. When omitted for a mixed design, the k positions are allocated across arms as evenly as possible
<code>mixed.strata</code>	a TRUE/FALSE argument indicating whether to generate both small and large strata. When TRUE, <code>small.strata</code> is ignored, <code>n.small</code> units (or clusters when <code>cluster = TRUE</code>) are generated in strata of size k , and the remaining units or clusters are generated in <code>n.strata</code> large strata
<code>n.small</code>	the number of units (or clusters when <code>cluster = TRUE</code>) assigned to the small-strata component when <code>mixed.strata = TRUE</code> . It must be divisible by k ; if NULL, the largest multiple of k not exceeding half of n is used
<code>allocation.probs</code>	an optional <code>n.strata</code> by $(\text{length}(\text{tau.vec}) + 1)$ matrix of stratum-specific treatment probabilities for large-strata individual-level designs. Columns correspond to control and the active treatment arms and every row must sum to one. If NULL, equal treatment probabilities are used in every stratum
<code>stratum.effects</code>	an optional numeric vector of length <code>n.strata</code> added to every potential outcome in the corresponding stratum for large-strata individual-level designs
<code>treatment.effects.by.stratum</code>	an optional <code>n.strata</code> by $\text{length}(\text{tau.vec})$ matrix whose entries give the stratum-specific mean effects of the active treatments relative to control for large-strata individual-level designs. If NULL, <code>tau.vec</code> is used in every stratum

Value

A data.frame with one row per generated individual. Under individual-level assignment it contains n rows; under cluster-level assignment, n is the number of generated clusters and the number of rows equals the total number of individuals generated across those clusters. The returned columns are:

- Y : the observed outcome
- S : the stratum indicator
- D : the treatment indicator indexed by $\{0, 1, 2, \dots\}$, where $D = 0$ denotes control
- $G.id$: the cluster indicator, included when `cluster = TRUE`
- Ng : the generated cluster size, included when `cluster = TRUE`
- x_1, x_2 : generated covariate columns, included when `is.cov = TRUE`

Examples

```
### Large-strata individual-level design
set.seed(11)
large_data <- sreg.rgen(
  n = 80, tau.vec = 0.5, n.strata = 4, cluster = FALSE
)

### Uniform matched pairs
set.seed(12)
pair_data <- sreg.rgen(
  n = 40, tau.vec = 0.5, cluster = FALSE,
  small.strata = TRUE, k = 2, treat.sizes = c(1, 1)
)

### Mixed design with 4-tuples and large strata
set.seed(13)
mixed_data <- sreg.rgen(
  n = 60, tau.vec = 0.5, cluster = FALSE,
  mixed.strata = TRUE, n.small = 40, k = 4,
  treat.sizes = c(2, 2), n.strata = 2
)
sort(table(mixed_data$S))

### For cluster assignment, n counts clusters rather than observations
set.seed(14)
cluster_data <- sreg.rgen(
  n = 20, tau.vec = 0.5, n.strata = 2, cluster = TRUE
)
length(unique(cluster_data$G.id))
```

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