

Package: xsynthdid (via r-universe)

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Type Package

Title Simple function to adjust for covariates in synthdid

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Description Simple function to adjust for covariates in synthdid. See vignete for details.

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Depends synthdid, fixest, dplyr

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Repository <https://skranz.r-universe.dev>

RemoteUrl <https://github.com/skranz/xsynthdid>

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adjust.outcome.for.x *Adjust outcome for using synthdid with additional covariates x*

Description

Implements a way to adjust the outcome variable for additional covariates x . The adjusted outcome can be used for a synthdid estimate that accounts for the covariates. More precisely, you can use the name of the new adjusted outcome (by default "y.adj") as argument outcome in your call to panel.matrices that prepares the data for synthdid_estimate. See the Vignete for an example.

Usage

```
adjust.outcome.for.x(
  panel,
  unit = 1,
  time = 2,
  outcome = 3,
  treatment = 4,
  x,
  x.rows = NULL,
  add.mean = FALSE
)
```

Arguments

panel	A data frame with columns consisting of units, time, outcome, and treatment indicator. It should be a balanced panel and not contain any NA.
unit	The column number/name corresponding to the unit identifier. Default is 1.
time	The column number/name corresponding to the time identifier. Default is 2.
outcome	The column number/name corresponding to the outcome identifier. Default is 3.
treatment	The column number/name corresponding to the treatment status. Default is 4.
x	The column numbers/names of all additional control variables
x.rows	To estimate the effect of x on y , we use by default all rows in which no treatment takes places. The argument x.rows allows to specify these rows manually. E.g. you could only take all rows before the first treatment starts (i.e. compared to the default exclude the rows of the control group during the treatment period).
add.mean	Shall the average of the effect of x on the outcome over all observatios be added to the outcome? If TRUE, the mean of the adjusted outcome is the same as the mean of the original outcome. Default is FALSE.

Value

The computed adjusted values for y . They can be used as outcome column in a subsequent call to panel.matrices in order to then estimate synthdid adjusted for the control variables that where specified here in x .

xsdid.mc	<i>Useful for monte-Carlo study about different variants of Synth-DID and DID</i>
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Description

For details look at the code. For an illustration see the vignette.

Usage

```
xsdid.mc(  
  N = 100,  
  T = 200,  
  tau = 50,  
  beta.tt = 50,  
  beta.x = 50,  
  beta.xc = 0,  
  beta.treat = 50,  
  x.tt.load = 0,  
  xc.x.load = 0,  
  x.treat.load.mean = 3/4,  
  x.contr.load.mean = 1/4,  
  x.load.alpha.beta = 2,  
  xc.treat.load.mean = 3/4,  
  xc.contr.load.mean = 1/4,  
  xc.load.alpha.beta = 2,  
  ar = 0.97,  
  ar.tt = ar,  
  ar.x = ar,  
  ar.xc = ar,  
  return.data = FALSE  
)
```

xsdid_estimate	<i>A shortcut function to directly perform SDID estimation with covariates from a panel data set</i>
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Description

Calls `adjust.outcome.for.y`, `panel.matrices` and then `synthdid_estimate`. Has similar syntax to `xsdid_se_bootstrap`.

Usage

```
xsdid_estimate(
  panel,
  unit = 1,
  time = 2,
  outcome = 3,
  treatment = 4,
  x,
  x.rows = NULL
)
```

Arguments

panel	A data frame with columns consisting of units, time, outcome, and treatment indicator. It should be a balanced panel and not contain any NA.
unit	The column number/name corresponding to the unit identifier. Default is 1.
time	The column number/name corresponding to the time identifier. Default is 2.
outcome	The column number/name corresponding to the outcome identifier. Default is 3.
treatment	The column number/name corresponding to the treatment status. Default is 4.
x	The column numbers/names of all additional control variables
x.rows	To estimate the effect of x on y, we use by default all rows in which no treatment takes places. The argument x.rows allows to specify these rows manually. E.g. you could only take all rows before the first treatment starts (i.e. compared to the default exclude the rows of the control group during the treatment period).

Value

The resulting object from the call to `synthdid_estimate`.

Examples

```
## Not run:
dat = xsdid.mc(N=20, T=20, return.data = TRUE)
xsdid_estimate(dat, unit="i", time = "t", outcome = "y", treatment = "treat_exp", x = "x")
xsdid_se_bootstrap(dat, unit="i", time = "t", outcome = "y", treatment = "treat_exp", x = "x", B=100)$se

## End(Not run)
```

xsdid_se_bootstrap	<i>Compute bootstrap standard errors for SDID with time varying covariates</i>
--------------------	--

Description

Each clustered bootstrap sample is a sample of units with replacement. It is guaranteed that at least 2 treatment group and at least 2 control group units are selected. (Ideally at least 1 of each should suffice but just a single observation in a group can lead to downstream errors when calling `synthdid_estimate`. This issue needs to be explored further)

Usage

```
xsdid_se_bootstrap(
  panel,
  unit = 1,
  time = 2,
  outcome = 3,
  treatment = 4,
  x,
  B = 100,
  num.cores = 1
)
```

Arguments

<code>panel</code>	A data frame with columns consisting of units, time, outcome, and treatment indicator. It should be a balanced panel and not contain any NA.
<code>unit</code>	The column number/name corresponding to the unit identifier. Default is 1.
<code>time</code>	The column number/name corresponding to the time identifier. Default is 2.
<code>outcome</code>	The column number/name corresponding to the outcome identifier. Default is 3.
<code>treatment</code>	The column number/name corresponding to the treatment status. Default is 4.
<code>x</code>	The column numbers/names of all additional control variables
<code>B</code>	number of bootstrap samples (Default 100).
<code>num.cores</code>	if larger than 1 use the parallel package to perform the bootstrap estimation on multiple cores. (More than 1 core does not work on Windows.)

Details

In each bootstrap sample, we use the function `adjust.outcome.for.x` to adjust for the covariates.

Value

As list with 2 elements: - `se` is the estimated standard error of the treatment effect τ . - `boot.tau` is a vector containing the estimated treatment effects τ for each bootstrap replication.

Examples

```
## Not run:
dat = xsdid.mc(N=20, T=20, return.data = TRUE)
xsdid_estimate(dat, unit="i", time = "t", outcome = "y", treatment = "treat_exp", x = "x")
xsdid_se_bootstrap(dat, unit="i", time = "t", outcome = "y", treatment = "treat_exp", x = "x", B=100)$se
```

```
## End(Not run)
```

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