Title

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hdidregress postestimation — Postestimation tools for hdidregress and xthdidregress

Postestimation commands

The following postestimation commands are of special interest after `hdidregress` and `xthdidregress`:

Command	Description
`estat ptrends`	parallel-trends test
`estat atetplot`	plot the coefficients of ATET for each cohort
†`estat aggregation`	aggregate the ATETs to characterize the heterogeneity of treatment effects
*`estat sci`	multiplier bootstrap for simultaneous confidence intervals

†`estat aggregation` is not allowed after estimation with bootstrap or jackknife standard errors.

*`estat sci` may not be used after estimation using TWFE.

The following postestimation commands are also available:

Command	Description
`estat summarize`	summary statistics for the estimation sample
`estat vce`	variance–covariance matrix of the estimators (VCE)
`estimates`	cataloging estimation results
`etable`	table of estimation results
`lincom`	point estimates, standard errors, testing, and inference for linear combinations of coefficients
`nlcom`	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
`test`	Wald tests of simple and composite linear hypotheses
`testnl`	Wald tests of nonlinear hypotheses

estat

Description for estat

`estat ptrends` tests that all pretreatment periods are equal to zero.

`estat atetplot` plots the coefficients of ATET for each cohort across different periods.

`estat aggregation` aggregates the cohort-period ATETs to characterize the heterogeneity of treatment effects. Aggregation may be within cohorts, time periods, time exposed to treatment, or within cohort and time periods. You may display the output of `estat aggregation` simultaneously as a table and a graph. The default is the tabular output.

`estat sci` provides the simultaneous confidence intervals for ATETs using the multiplier bootstrap method proposed in Callaway and Sant'Anna (2021). It may not be used after estimation using the TWFE estimator.

Menu for estat

Statistics > Postestimation

Syntax for estat

Tests that all pretreatment periods are zero

```
estat ptrends
```

Plot coefficients for ATETs

```
estat atetplot [cohort_list] [, atetplot_options]
```

Aggregate ATETs

```
estat aggregation [, aggregation_options]
```

Simultaneous confidence intervals

```
estat sci [, level(#) sci_options]
```

cohort_list is a subset of all the cohorts when estimating the ATETs. By default, the *cohort_list* contains all the cohorts. *cohort_list* is not allowed when the TWFE estimator is combined with option `hettype(time)` or `hettype(cohort)`.

atetplot_options	Description
`level(#)`	set confidence level
*`sci`[`(`*_sci_options_*`)`]	use multiplier bootstrap to compute the simultaneous confidence intervals
Graph options	
Main	
`noci`	do not plot the confidence intervals
*`preteopts(`*_scatter_opts_*`)`	affect rendition of the pretreatment scatterplot
`postteopts(`*_scatter_opts_*`)`	affect rendition of the posttreatment scatterplot
[`no`]`zeroline`	suppress the y-axis reference line passing through zero
`zerolineopts(`*_refline_opts_*`)`	affect rendition of the y-axis reference line passing through zero
†[`no`]`cohortline`	suppress the x-axis reference line passing through the time when the treatment began for each cohort
†`cohortlineopts(`*_refline_opts_*`)`	affect rendition of the x-axis reference line passing through the time when the treatment began for each cohort
CI plot	
`ciopts(`*_area_opts_*`)`	affect rendition of the confidence interval
Y axis, X axis, Titles, Legend, Overall	
†`byopts(`*_byopts_*`)`	affect rendition of the graph by cohorts
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

*These options are not allowed for the TWFE estimators.

†These options are not allowed when the TWFE estimator is combined with option `hettype(time)` or `hettype(cohort)`.

aggregation_options	Description
`overall`	aggregate ATETs within cohorts and time periods; the default
`dynamic`[`(`*_event_list_*`)`]	aggregate ATETs within exposures to the treatment
`time`[`(`*_time_list_*`)`]	aggregate ATETs within time periods
`cohort`[`(`*_cohort_list_*`)`]	aggregate ATETs within cohorts
[`no`]`graph`	whether to suppress or display the aggregation plot; `nograph` is the default
`graph`[`(`*_graph_opts_*`)`]	affect rendition of the aggregation plot
`level(#)`	set confidence level
*`sci`[`(`*_sci_options_*`)`]	use multiplier bootstrap to compute the simultaneous confidence intervals

Only one of `overall`, `dynamic()`, `cohort()`, or `time()` is allowed.

*This option is not allowed after the TWFE estimator.

sci_options	Description
`rseed(#)`	set random-number seed to #
`reps(#)`	perform # multiplier bootstrap replications; default is `reps(999)`

scatter_opts	Description
connect_options	change the look of lines or connecting method
marker_options	change the look of markers (color, size, etc.)

refline_opts	Description
`style(`*addedlinestyle*`)`	overall style of added line
[`no`]`extend`	extend line through plot region's margins
`lstyle(`*linestyle*`)`	overall style of line
`lpattern(`*linepatternstyle*`)`	line pattern (solid, dashed, etc.)
`lwidth(`*linewidthstyle*`)`	thickness of line
`lcolor(`*colorstyle*`)`	color and opacity of line

graph_opts	Description
Main	
`noci`	do not plot the confidence intervals
Marker options	
marker_options	change the look of markers (color, size, etc.)
Line options	
connect_options	change the look of lines or connecting method
CI plot	
`ciopts(`*area_options*`)`	affect rendition of the confidence interval
Y axis, X axis, Titles, Legend, Overall	
twoway_options	any options other than `by()` documented in [G-3] ***twoway_options***

Options for estat

Options for `estat` are presented under the following headings:

Options for estat atetplot
Options for estat aggregation
Options for estat sci

Options for estat atetplot

`level(#)` specifies the confidence level, as a percentage, for CIs. The default is `level(95)` or as set by `set level`; see **[U] 20.8 Specifying the width of confidence intervals**.

`sci` or `sci(`*sci_options*`)` plots the simultaneous confidence intervals (SCIs) using the multiplier bootstrap method proposed in Callaway and Sant'Anna (2021). SCIs simultaneously cover the true values of all the ATETs with a predefined probability level. By default, specifying `sci` implies using 999 bootstrap replications to construct the SCIs.

`sci(`*sci_options*`)` specifies the number of replications and the seed for the multiplier bootstrap when computing SCIs. *sci_options* may be `rseed(#)` or `reps(#)`. For the definition of these options, see *Options for estat sci*.

Option `sci` or `sci()` is not allowed after the TWFE estimator in `hdidregress` and `xthdidregress`. In addition, it is not allowed after estimation with bootstrap or jackknife standard errors for RA, IPW, and AIPW estimators.

By default, `estat atetplot` plots the pointwise CIs.

Main

`noci` removes plots of the CIs. The default is to plot the CIs.

`preteopts(`*scatter_opts*`)` affects the rendition of the scatterplot for pretreatment periods. This option is not allowed after the TWFE estimator in `hdidregress` and `xthdidregress`. *scatter_opts* may be the following:

connect_options specify how points on a graph are to be connected; [G-3] ***connect_options***.

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

`postteopts(`*scatter_opts*`)` affects the rendition of the scatterplot for posttreatment periods. *scatter_opts* may be the following:

connect_options specify how points on a graph are to be connected; [G-3] ***connect_options***.

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

`nozeroline` suppresses the y-axis reference line passing through zero. After estimation with `hdidregress` and the RA, IPW, or AIPW estimator, the default is to plot this reference line. After estimation with the TWFE estimator, the default is not to plot this reference line.

`zerolineopts(`*refline_opts*`)` affects the rendition of the reference line passing through zero. *refline_opts* may be the following:

`style(`*addedlinestyle*`)` specifies the overall style of the added line, which includes [`no`]`extend` and `lstyle(`*linestyle*`)` documented below. See [G-4] ***addedlinestyle***. The [`no`]`extend` and `lstyle()` options allow you to change the added line's attributes individually, but `style()` is the starting point.

You need not specify `style()` just because there is something that you want to change, and in fact, most people seldom specify the `style()` option. You specify `style()` when another style exists that is exactly what you desire or when another style would allow you to specify fewer changes to obtain what you want.

`extend` and `noextend` specify whether the line should extend through the plot region's margin and touch the axis; see [G-3] ***region_options***. Usually, `noextend` is the default, and `extend`

is the option, but that is determined by the overall `style()` and, of course, the scheme; see [G-4] **Schemes intro**.

`lstyle(`*linestyle*`)`, `lpattern(`*linepatternstyle*`)`, `lwidth(`*linewidthstyle*`)`, `lalign(`*linealignmentstyle*`)`, and `lcolor(`*colorstyle*`)` specify the look of the line; see [G-2] **graph twoway line**.

`nocohortline` suppresses the x-axis reference line passing through the time when the treatment began for each cohort. The default is to plot this reference line. This option is not allowed after the TWFE estimator.

`cohortlineopts(`*refline_opts*`)` affects the rendition of the reference line passing through the time when the treatment began for each cohort. This option is not allowed after the TWFE estimator. *refline_opts* may be the following:

`style(`*addedlinestyle*`)` specifies the overall style of the added line, which includes `[no]extend` and `lstyle(`*linestyle*`)` documented below. See [G-4] ***addedlinestyle***. The `[no]extend` and `lstyle()` options allow you to change the added line's attributes individually, but `style()` is the starting point.

You need not specify `style()` just because there is something that you want to change, and in fact, most people seldom specify the `style()` option. You specify `style()` when another style exists that is exactly what you desire or when another style would allow you to specify fewer changes to obtain what you want.

`extend` and `noextend` specify whether the line should extend through the plot region's margin and touch the axis; see [G-3] ***region_options***. Usually, `noextend` is the default, and `extend` is the option, but that is determined by the overall `style()` and, of course, the scheme; see [G-4] **Schemes intro**.

`lstyle(`*linestyle*`)`, `lpattern(`*linepatternstyle*`)`, `lwidth(`*linewidthstyle*`)`, `lalign(`*linealignmentstyle*`)`, and `lcolor(`*colorstyle*`)` specify the look of the line; see [G-2] **graph twoway line**.

CI plot

`ciopts(`*area_options*`)` affects the rendition of the CIs; see [G-3] ***area_options***.

Y axis, X axis, Titles, Legend, Overall

`byopts(`*byopts*`)` affects the rendition of the graph combined by cohorts. For *byopts*, see [G-3] ***by_option***. This option is not allowed after the TWFE estimator.

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

Options for estat aggregation

`overall` aggregates ATETs within all the cohorts and time periods; it is the default.

`dynamic` or `dynamic(`*event_list*`)` aggregates ATETs within exposure to the treatment. For example, two periods of exposure to the treatment means two periods after the treatment started. Specifying `dynamic` implies aggregating ATETs within all the estimable exposures to the treatment.

`dynamic(`*event_list*`)` aggregates ATETs within the exposure to the treatment specified by *event_list*. *event_list* is a numlist specifying length of exposures to the treatment.

`time` or `time(`*time_list*`)` aggregates ATETs within time periods. Specifying `time` implies aggregating ATETs within all the estimable time periods.

`time(`*time_list*`)` aggregates ATETs within the time specified by *time_list*. *time_list* is a numlist specifying time periods.

`cohort` or `cohort(`*cohort_list*`)` aggregates ATETs within cohort. Specifying `cohort` implies aggregating ATETs within all the estimable cohorts.

`cohort(`*cohort_list*`)` aggregates ATETs within the cohorts specified by *cohort_list*. *cohort_list* is a numlist specifying cohorts.

`nograph` and `graph` specifies whether to suppress or display the plot of aggregation of ATETs. `nograph` is the default.

`graph(`*graph_opts*`)` affects the rendition of the aggregation plot. *graph_opts* may be the following:

`noci` removes plots of the CIs. The default is to plot the CIs.

connect_options specify how points on a graph are to be connected; [G-3] ***connect_options***.

marker_options affect the rendition of markers drawn at the plotted points, including their shape, size, color, and outline; see [G-3] ***marker_options***.

`ciopts(`*area_options*`)` affects the rendition of the CIs; see [G-3] ***area_options***.

twoway_options are any of the options documented in [G-3] ***twoway_options***, excluding `by()`. These include options for titling the graph (see [G-3] ***title_options***) and for saving the graph to disk (see [G-3] ***saving_option***).

`level(#)` specifies the confidence level, as a percentage, for CIs. The default is `level(95)` or as set by `set level`; see **[U] 20.8 Specifying the width of confidence intervals**.

`sci` or `sci(`*sci_options*`)` plots the simultaneous confidence intervals (SCIs) using the multiplier bootstrap method proposed in Callaway and Sant'Anna (2021). SCIs simultaneously cover the true values of aggregations of ATETs with a predefined probability level. By default, specifying `sci` implies using 999 bootstrap replications to construct the SCIs.

`sci(`*sci_options*`)` specifies the number of replications and the seed for the multiplier bootstrap when computing SCIs. *sci_options* may be `rseed(#)` or `reps(#)`. For the definition of these options, see *Options for estat sci*.

Option `sci` or `sci()` is not allowed after the TWFE estimator in `hdidregress` and `xthdidregress`.

By default, `estat aggregation` plots the pointwise CIs if option `graph()` is specified.

Options for estat sci

`level(#)` specifies the confidence level, as a percentage, for CIs. The default is `level(95)` or as set by `set level`; see **[U] 20.8 Specifying the width of confidence intervals**.

`rseed(#)` sets the random-number seed. Specifying this option makes the results reproducible because the critical values are drawn from a bootstrap sample.

`reps(#)` specifies the number of bootstrap replications to get the critical values of the test. The default is `reps(999)`.

Remarks and examples

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For examples of the estat commands above, see [CAUSAL] **hdidregress** and [CAUSAL] **xthdidregress**. Both entries have examples that illustrate how the estimation and postestimation commands work together.

Stored results

estat ptrends stores the following in r():

Scalars

r(F)	F statistic
r(chi2)	χ^2
r(df)	test constraints degrees of freedom
r(p)	two-sided p-value
r(df_r)	residual degrees of freedom
r(drop)	1 if constraints were dropped, 0 otherwise

estat aggregation stores the following in r():

Scalars

r(reps)	number of replications

Macros

r(agg_type)	aggregation type

Matrices

r(b)	coefficient vector
r(V)	variance–covariance matrix of the estimators
r(table)	matrix containing test statistics and critical values

estat atetplot stores the following in r():

Macros

r(table)	matrix containing test statistics and critical values

estat sci stores the following in r():

Scalars

r(reps)	number of replications

Matrices

r(table)	matrix containing coefficients, bootstrap standard errors, and SCIs

Methods and formulas

Methods and formulas are presented under the following headings:

Test for all pretreatment period ATETs being zero
Aggregations for the RA, IPW, and AIPW estimators
Aggregations for the TWFE estimator
SCIs

Test for all pretreatment period ATETs being zero

estat ptrends tests that all pretreatment period ATETs are zero. This should be satisfied if both parallel trends and no anticipation of treatment hold for the pretreatment period.

For the RA, IPW, and AIPW estimators, `estat ptrends` is equivalent to a Wald test of all the pretreatment ATET estimates equaling zero. For methods and formulas on the Wald test, see *Methods and formulas* in [R] **test**.

Below, we will use the notation from *Methods and formulas* in [CAUSAL] **xthdidregress**. For the TWFE estimator, we fit the augmented model:

$$y_{it} = \eta + \sum_{g=q}^{T} G_{ig}\alpha_g + \sum_{s=q}^{T} f_s\gamma_s + \sum_{g=2}^{q-1}\sum_{s=g}^{q-1} d_{it}G_{ig}f_s\omega_{gs} + \sum_{g=q}^{T}\sum_{s=g}^{T} d_{it}G_{ig}f_s\delta_{gs} + \varepsilon_{it}$$

We then jointly test if the ω_{gs} terms are zero by using `test`.

Aggregations for the RA, IPW, and AIPW estimators

Denote $\theta(g,t)$ as ATET(g,t). These are the parameters computed during estimation. Instead of looking at all of these parameters, we can aggregate them to explore heterogeneity in different dimensions. We denote θ as aggregations of ATETs. Regardless of whether we use cohort, time, or dynamic aggregation, we can always write θ as a weighted sum of $\theta(g,t)$ as follows

$$\theta = \sum_{g\in\mathbb{G}}\sum_{t=2}^{T} w(g,t)\theta(g,t)$$

where $\mathbb{G}$ is the set of all the possible cohort values and $w(g,t)$ is the cohort-time weights. The type of questions of interest determines the definitions of $w(g,t)$.

One popular question in DID with multiple time periods set up is to study the dynamics of treatment effects: how do the average treatment effects vary with the length of exposure to the treatment? In literature, it is also known as the event study. Let $e = t - g$ be the length of exposure to the treatment. We can summarize ATETs as

$$\theta_d(e) = \sum_{g\in\mathbb{G}} \mathbb{I}\{g + e \le T\}P\{G = g|G + e \le T\}\theta(g, g + e)$$

where $\mathbb{I}(\cdot)$ is an indicator function and G is a random categorical variable for a cohort. $\theta_d(e)$ is computed when the `dynamic` option is specified.

To account for the heterogeneous treatment effects across cohorts, we consider the following aggregation:

$$\theta_c(g) = \sum_{t=g}^{T} \theta(g,t)P(G = g|G = g, t \ge g)$$

$\theta_c(g)$ is computed when the `cohort` option is specified.

Time effects characterize treatment-effects heterogeneity across time. The average effect of participating in the treatment in a period t (among cohorts that are treated by time t) is

$$\theta_t(t) = \sum_{g\in\mathbb{G}} \mathbb{I}(t \ge g)P(G = g|G \le t)\theta(g,t)$$

$\theta_t(t)$ is computed when the `time` option is specified.

The overall aggregation is the average of all the identified posttreatment ATETs. It is defined as

$$\theta_o = \frac{1}{\kappa}\sum_{g\in\mathbb{G}}\sum_{t=2}^{T}\mathbb{I}(t \geq g)P(G=g|G\leq T)\theta(g,t)$$

where $\kappa = \sum_{g\in\mathbb{G}}\sum_{t=2}^{T}\mathbb{I}(t \geq g)P(G=g|G\leq T)$. θ_o is computed when the `overall` option is specified.

The variance–covariance matrix for the estimates of θ is computed using the influence function approach outlined in section 4.2 in Callaway and Sant'Anna (2021).

When the `sci` option is specified, the SCIs are computed using the multiplier bootstrap proposed in section 4.2 in Callaway and Sant'Anna (2021).

Aggregations for the TWFE estimator

Aggregation after TWFE uses `margins` after the Mundlak estimation of the model. Let `treat` denote the observation-level treatment, `cohort` denote the variable that contains treat-time cohorts, and `exposure` denote a variable that indicates the time exposed to treatment.

For `estat aggregation, overall`:

```
. margins r.treat, subpop(if treat==1) vce(unconditional)
```

For `estat aggregation, cohort`:

```
. margins, subpop(if treat==1) dydx(treat) over(cohort) vce(unconditional)
```

For `estat aggregation, time`:

```
. margins, subpop(if treat==1) dydx(treat) over(time) vce(unconditional)
```

For `estat aggregation, dynamic`:

```
. margins, subpop(if treat==1) dydx(treat) over(exposure) vce(unconditional)
```

SCIs

After the RA, IPW, and AIPW estimators, `estat sci` can provide the SCIs that are guaranteed to cover all the ATETs with a specified probability. `estat sci` computes the SCIs using the multiplier bootstrap approach outlined in section 4.1 in Callaway and Sant'Anna (2021).

Unlike the traditional bootstrap, the multiplier bootstrap resamples the influence functions (which are already computed in the estimation step). Thus, the multiplier bootstrap is much faster than the traditional bootstrap because there is no need to recompute the estimators.

The influence function is a linear representation of the estimator. Let $\widehat{\theta}(g,t)$ be the RA, IPW, and AIPW estimators, and denote $\theta(g,t)$ the true ATET for cohort g at time t. Then the linear representation of these estimators can be written as

$$\widehat{\theta}(g,t) - \theta(g,t) = \frac{1}{n}\sum_{i=1}^{n}\psi_{g,t}(\mathbf{w}_i) + o_p(1)$$

where $\psi_{g,t}()$ is the influence function, n is the sample size of the estimation sample for $\widehat{\theta}(g,t)$, $\mathbf{w}_i$ are the data, and $o_p(1)$ is a term that vanishes to zero in probability as n grows. For a more detailed discussion on influence functions, see section 4.1 in Callaway and Sant'Anna (2021).

Denote $\widehat{\boldsymbol{\theta}}$ as estimates of all the ATETs, and let $\widehat{\Psi}$ be estimates of the influence functions for $\widehat{\boldsymbol{\theta}}$. Let $\widehat{\boldsymbol{\theta}}^b$ be the bth bootstrap draw, which is defined as

$$\widehat{\boldsymbol{\theta}}^b = \widehat{\boldsymbol{\theta}} + \frac{1}{n}\sum_{i=1}^{n} V_i \cdot \widehat{\Psi}_i$$

where $\{V_i\}$ is a Bernoulli draw with $P(V = 1-\eta) = \eta/\sqrt{5}$, $P(V = \eta) = 1 - \eta/\sqrt{5}$ and $\eta = (\sqrt{5}+1)/2$. Then the SCIs can be computed in the following steps:

1. Draw B samples of $\{V_i\}_{i=1,\ldots,n}$, and compute $\widehat{\boldsymbol{\theta}}^b$ using each sample.
2. Compute the bootstrap diagonal of $\Sigma^{1/2}$ as

$$\widehat{\Sigma}^{1/2}_{g,t} = \frac{q_{0.75}(g,t) - q_{0.25}(g,t)}{z_{0.75} - z_{0.25}}$$

   where $q_p(g,t)$ is the pth sample quantile of $\widehat{R}^b_{g,t} = \sqrt{n}\left\{\widehat{\theta}^b(g,t) - \widehat{\theta}(g,t)\right\}$ in B draws and z_p is the pth sample quantile of standard normal distribution.
3. For each bootstrap draw, compute the t test^b as

$$t \text{ test}^b = \max_{(g,t)} |\widehat{R}^b_{g,t}| \widehat{\Sigma}^{-1/2}_{g,t}$$

4. Compute the critical values $\widehat{c}_{1-\alpha/2}$ as the $1-\alpha/2$ quantile of the B draws of t test^b.
5. Construct the simultaneous bootstrap confidence intervals for $\widehat{\theta}(g,t)$ as

$$\widehat{C}(g,t) = \left\{\widehat{\theta}(g,t) - \widehat{c}_{1-\alpha/2}\widehat{\Sigma}^{1/2}_{g,t}/\sqrt{n}, \quad \widehat{\theta}(g,t) + \widehat{c}_{1-\alpha/2}\widehat{\Sigma}^{1/2}_{g,t}/\sqrt{n}\right\}$$

Reference

Callaway, B., and P. H. C. Sant'Anna. 2021. Difference-in-differences with multiple time periods. *Journal of Econometrics* 225: 200–230. https://doi.org/10.1016/j.jeconom.2020.12.001.

Also see

[CAUSAL] **hdidregress** — Heterogeneous difference in differences

[CAUSAL] **xthdidregress** — Heterogeneous difference in differences for panel data

[CAUSAL] **DID intro** — Introduction to difference-in-differences estimation

[U] 20 Estimation and postestimation commands