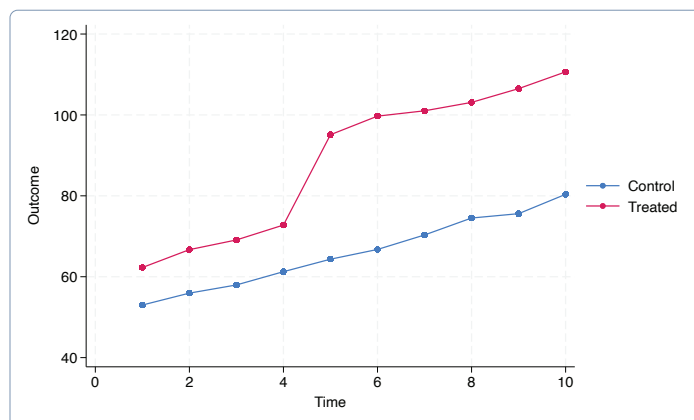


Difference in differences

Difference-in-differences (DID) estimation is one of the most popular methods for causal inference. Stata's **didregress** and **xtdidregress** commands fit DID and triple difference (DDD) models for repeated cross-sectional and panel data. DID and DDD models control for unobserved group and time fixed effects to consistently estimate the average treatment effect on the treated (ATET).

Key assumptions of the models can be tested and graphically displayed via the **estat trendplot**, **estat ptrends**, and **estat granger** commands.

For estimation of ATETs that vary across time and treatment cohorts, you can use the **hdidregress** and **xthdidregress** commands.



- DID and DDD models for ATET estimation
 - Repeated cross-sectional data
 - Panel data
- Donald and Lang's aggregation method
- Wild bootstrap p -values and confidence intervals
- Bell and McCaffrey's degrees-of-freedom adjustment for bias-corrected standard errors
- Mean-outcome and pretreatment parallel-trends graphical diagnostics
- Granger-type and pretreatment parallel-trends tests
- Heterogeneous DID models
- Bacon decomposition to assess treatment-effect heterogeneity

Fit a DID model and estimate ATET

We want to study the effect of a new hospital admissions procedure on patient satisfaction using monthly data on patients before and after the new procedure was implemented by some hospitals.

```
. didregress (satis) (procedure),
      group(hospital) time(month)
```

The ATET of **procedure** on satisfaction was 0.85, accounting for **hospital** and **month** fixed effects. The 95% confidence interval does not include 0.

If our data were panel, we would tell Stata using **xtset** and type

```
. xtdidregress (satis) (procedure),
      group(hospital) time(month)
```

Viewer - view did.smcl

view did.smcl

Dialog | Also see | Jump to

Difference-in-differences regression
Data type: Repeated cross-sectional
Number of obs = 7,368

(Std. err. adjusted for 46 clusters in hospital)

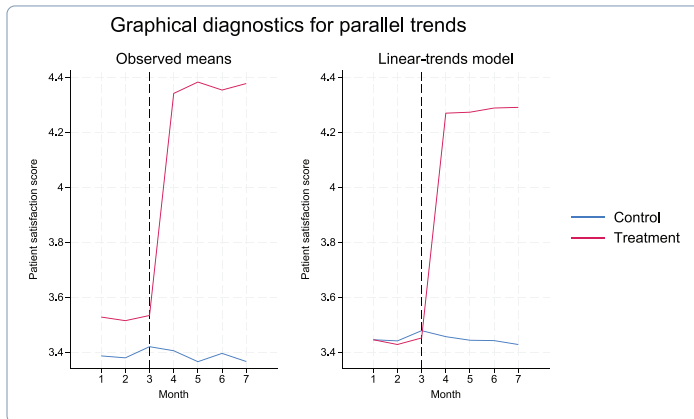
| | satis | Coefficient | Robust std. err. | t | P> t | [95% conf. interval] |
|--------------|-------|-------------|---------------------|-------|-------|----------------------|
| ATET | | | | | | |
| procedure | | .8479879 | .0321121 | 26.41 | 0.000 | .7833108 .912665 |
| (New vs Old) | | | | | | |

Note: ATET estimate adjusted for group effects and time effects.

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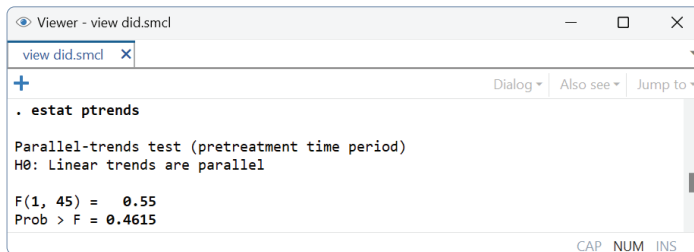
Graphical diagnostics

Our DID model assumes that the trends of **satis** for the control and treatment groups are parallel prior to the implementation of the new procedure. We can obtain a diagnostic of this assumption using **estat trendplot**.



Test for pretreatment parallel trends

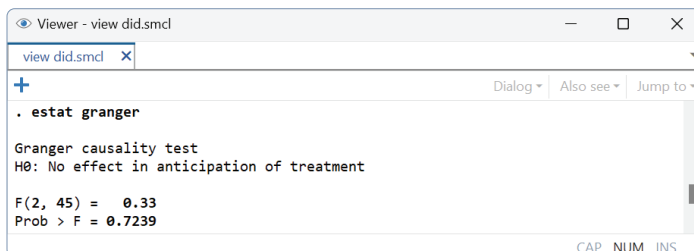
We can complement our graphical diagnostic with a formal statistical test using **estat ptrends**.



Thus, the null hypothesis of pretreatment parallel trends is not rejected.

Granger causality test

Our DID model also assumes that the treatment and control groups do not change their behavior in anticipation of the treatment. To test this hypothesis, we can implement a Granger causality test using **estat granger**.



The null hypothesis of no behavior change in anticipation of treatment is not rejected.

A graphical diagnostic is also available using **estat grangerplot**.

Compute appropriate standard errors

It is common to have few groups. In these scenarios, cluster-robust standard errors are unreliable. For such cases, we can use alternative methods to compute standard errors.

We can use HC2 bias-adjusted clustered standard errors by adding the **vce(hc2)** option.

```
. didregress (satis) (procedure),  
              group(hospital) time(month) vce(hc2)
```

We can use Donald and Lang's aggregation method by using the **aggregate(dlang)** option.

```
. didregress (satis) (procedure),  
              group(hospital) time(month)  
              aggregate(dlang)
```

Wild cluster bootstrap *p*-values and confidence intervals are also available. As with all bootstrap methods, we need to set a seed to make results replicable.

```
. didregress (satis) (procedure),  
              group(hospital) time(month)  
              wildbootstrap(rseed(123))
```

DDD models

To fit a DDD model, just add another variable to the **group()** option, and define the new treated observations.

```
. didregress (satis) (new_treated),  
              group(hospital another_group)  
              time(month)
```

Testing for treatment heterogeneity when treatment time varies

If units are treated at different times, the ATET might change for each treatment cohort. If so, DID estimates are inconsistent.

We can inspect ATET heterogeneity after **didregress** and **xtdidregress** using Bacon decomposition by typing

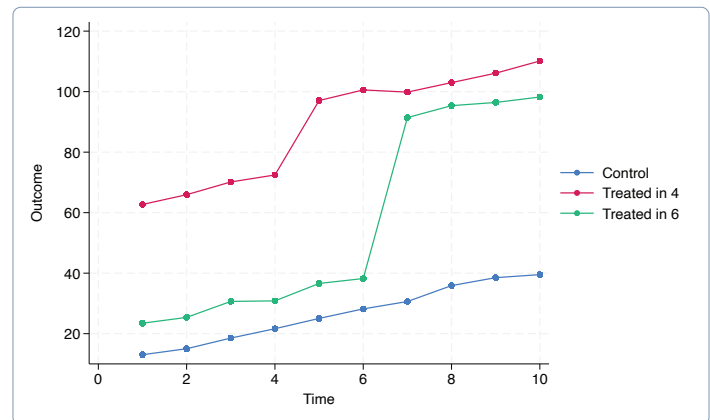
```
. estat bdecomp
```

And we can display the results in a graph by typing

```
. estat bdecomp, graph
```

Heterogeneous DID

Heterogeneous DID estimates ATETs when treatment effects change over time and are different across cohorts. Use the **hddidregress** and **xthddidregress** commands to estimate ATETs for each cohort and time period with repeated cross-sectional data and panel data.



- Estimation of the ATET for each cohort and period
 - Repeated cross-sectional data
 - Panel data
- Aggregation of ATETs over the following
 - Cohort
 - Period
 - Exposure to treatment
- Plots and tests of treatment-effect heterogeneity
- Simultaneous confidence intervals
- Four estimators
 - Regression adjustment (RA)
 - Inverse-probability weighting (IPW)
 - Augmented inverse-probability weighting (AIPW)
 - Two-way fixed-effects regression (TWFE)
- Test of pretreatment parallel trends

Fit a model with heterogeneous treatment effects

We would like to know whether a school district program, Healthy Habits, has an effect on students' body mass index (BMI). Our data are at the school district level and include information on whether a school participates in the program and the BMI of students. We have repeated samples of students from 40 school districts from 2014 to 2020.

We use the **aipw** estimator to model both the outcome and the treatment. We use the number of parks in the district to model treatment and the mother's education to model the outcome.

```
. hddidregress aipw (bmi medu) (hhabit parksd)  
      group(schools) time(year)
```

The AIPW estimator is doubly robust, meaning that even when the treatment model or the outcome model (but not both) is misspecified, the estimates are still consistent.

Treatment-effect heterogeneity is evident in the results. ATET estimates vary across cohort and time combinations.

Viewer - view hetdid.smcl

view hetdid.smcl

Heterogeneous treatment-effects regression Number of obs = 14,896
Estimator: Augmented IPW
Treatment level: schools
Control group: Never treated

(Std. err. adjusted for 40 clusters in schools)

| Cohort | ATET | Robust std. err. | z | P> z | [95% conf. interval] |
|--------|-----------|---------------------|--------|-------|----------------------|
| 2015 | | | | | |
| year | | | | | |
| 2014 | .4383554 | .6317095 | 0.69 | 0.488 | -.7997724 1.676483 |
| 2015 | -1.148953 | .4106347 | -2.80 | 0.005 | -1.953783 -.3441241 |
| 2016 | -2.442539 | .389955 | -6.26 | 0.000 | -3.206837 -1.678242 |
| 2017 | -2.47216 | .2469231 | -10.01 | 0.000 | -2.956121 -1.9882 |
| 2018 | -2.61101 | .6811369 | -3.83 | 0.000 | -3.946014 -1.276006 |
| 2019 | -3.853724 | .3430176 | -11.23 | 0.000 | -4.526026 -3.181422 |
| 2020 | -.4349252 | .6658255 | -0.65 | 0.514 | -1.739919 .8700687 |
| 2017 | | | | | |
| year | | | | | |
| 2014 | .5847558 | .2734447 | 2.14 | 0.032 | .048814 1.120698 |
| 2015 | -1.327894 | .4119237 | -3.22 | 0.001 | -2.13525 -.5205384 |
| 2016 | .6134559 | .4378406 | 1.40 | 0.161 | -.244696 1.471608 |
| 2017 | -1.655656 | .4547377 | -3.64 | 0.000 | -2.546926 -.7643869 |
| 2018 | -3.063113 | .5123237 | -5.98 | 0.000 | -4.067249 -2.058977 |
| 2019 | -2.95452 | .4682755 | -6.31 | 0.000 | -3.872324 -2.036717 |
| 2020 | .1679379 | .6764323 | 0.25 | 0.804 | -1.157845 1.493721 |
| 2019 | | | | | |
| year | | | | | |
| 2014 | -1.582866 | .5090601 | -3.11 | 0.002 | -2.580605 -.5851261 |
| 2015 | 1.189118 | .4966923 | 2.39 | 0.017 | .2156191 2.162617 |
| 2016 | -.3868035 | .4540723 | -0.85 | 0.394 | -1.276769 .5031617 |
| 2017 | .342599 | .4860828 | 0.70 | 0.481 | -.6101058 1.295304 |
| 2018 | .0661505 | .6188046 | 0.11 | 0.915 | -1.146684 1.278985 |
| 2019 | -3.733731 | .3690283 | -10.12 | 0.000 | -4.457013 -3.010448 |
| 2020 | -1.275938 | .6071755 | -2.10 | 0.036 | -2.46598 -.0858956 |

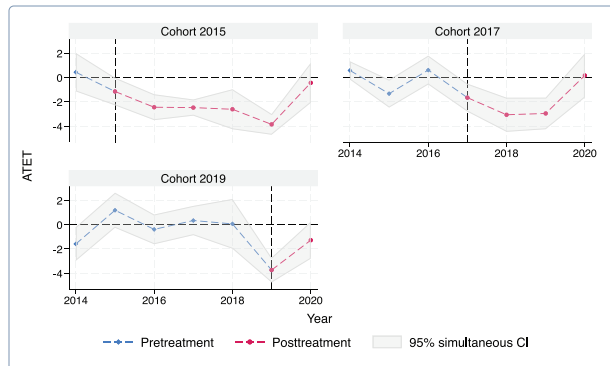
Note: ATET computed using covariates.

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Visualizing ATETs for each cohort

It is difficult to see the trends in ATETs just by looking at all the ATETs estimates. We can use **estat atetplot** to visualize the time profile of ATETs for each cohort. We specify the **sci** option to show the simultaneous confidence bands that cover the true values of ATETs across all the cohorts and times with the predefined probability level.

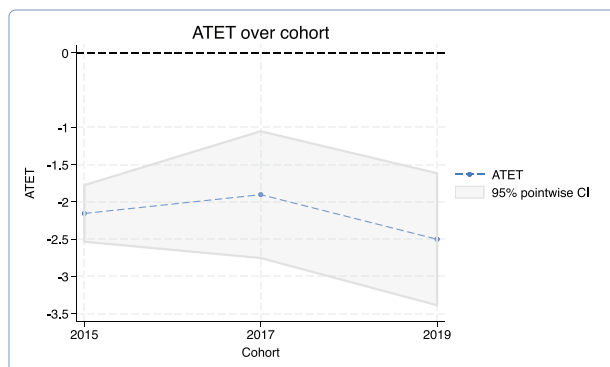
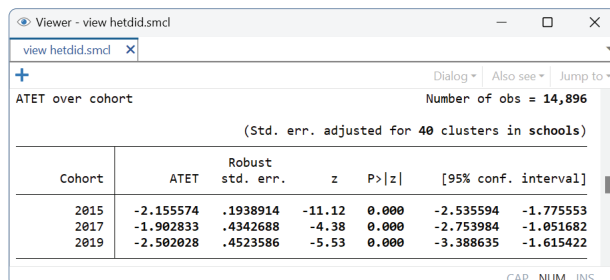
• **estat atetplot, sci**



Aggregating ATETs

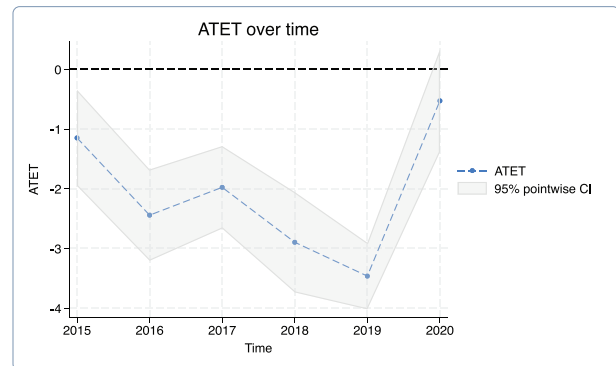
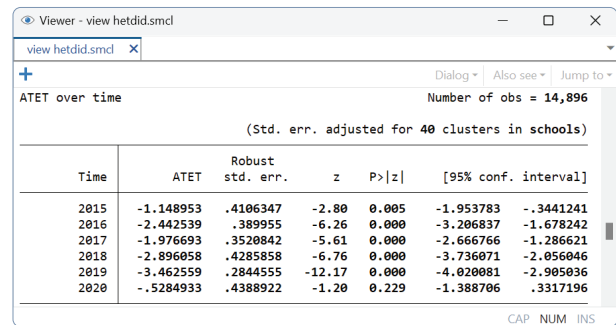
After fitting the model, we can use **estat aggregation** to aggregate the ATETs within cohort, time, or exposure to treatment. For example, we use **estat aggregation, cohort** to summarize the ATETs within each cohort.

• **estat aggregation, cohort graph**



If we want to summarize ATETs within time, we specify the **time** option with **estat aggregation**.

• **estat aggregation, time graph**



Finally, if we want to summarize ATETs within different lengths of exposure to treatment, we specify the **dynamic** option.

• **estat aggregation, dynamic graph**

