tesensitivity: A Stata Package for Assessing Sensitivity to the Unconfoundedness Assumption

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Introduction

A standard question in causal inference is to identify and estimate the effect of some treatment variable X on an outcome variable Y. A common assumption used to identify such effects is unconfoundedness, also known as selection on observables, conditional independence, ignorability, or exogenous selection. This assumption is not refutable, meaning that the data alone cannot tell us whether it is true. Nonetheless, researchers may wonder: How important is this assumption in their analyses? Put differently: How sensitive are results obtained under the unconfoundedness assumption?

Masten and Poirier (2018) provide a set of theoretical results used to answer this question. They define conditional partial independence as any assumption weaker than full conditional independence. They specifically consider a class of assumptions called conditional c-dependence. This class measures relaxations of conditional independence by a single parameter $c \in [0,1]$. When c=0, this corresponds to the conditional independence assumption. For any c>0, conditional independence only partially holds, and hence we cannot exactly learn the value of our treatment effect parameters, such as the average treatment effect (ATE). Instead, we only get bounds. Masten and Poirier (2018) characterize these bounds as a function of c. Small values of c give narrow bounds while larger values of c give wider bounds. Just how wide these bounds are, and hence how sensitive one's results are, depends on the data.

Specifically, define the following random variables:

- Y_x : the potential outcome for a given treatment $x \in \{0,1\}$
- X: the treatment
- W: a vector of covariates
- Y: the observed outcome

The observed outcome satisfies

$$Y = (1 - X)Y_0 + XY_1$$
.

Rather than observing the full data generating process, (Y_0, Y_1, X, Y) , we only observe (Y, X, W).

We say that X is conditionally c-dependent with Y_x given W if:

$$\sup_{y_x \in \text{supp}(Y_x|W=w)} |\mathbb{P}(X=1|Y_x=y_x, W=w) - \mathbb{P}(X=1|W=w)| \le c$$

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for all $w \in \text{supp}(W)$.

Under this assumption, the identified set for a treatment effect statistic will be a closed inteval, which depends on c and the distribution of (Y, X, W). The main purpose of the **tesensitivity** package is to calculate these intervals and show how the identified set for treatment effect statistics varies with the sensitivity parameter c.

In addition to estimating these bounds for a range of values of c, this pacakage also calculates a breakdown point relative to a conclusion about a treatment effect statistic. As discussed in Masten and Poirier (2020), the breakdown point is the maximum value of c under which the conclusion still holds. For example, if we consider the conclusion that the average treatment effect is positive, then the breakdown point is the minimum value of c such that 0 is included in the identified set.

The package also includes tools to visualize the analysis, interpret the scale of c-dependence, and compare results of multiple sensitivity analyses.

This vignette provides a tutorial for the package based on the empirical illustration in Masten, Poirier, and Zhang (2020).

Getting Started

We will illustrate usage of the package using data from LaLonde (1986) as reconstructed by Dehejia and Wahba (1999) and used in the empirical illustration in Masten, Poirier, and Zhang (2020).

The dataset is included with the package, and can be loaded using the sysuse command:

```
. sysuse lalonde1986, clear
```

These will be the variables used in the analysis:

- . local outcome "re78"
- . local treatment "treat"
- . local controls "married age black hispanic education re74 re75 re74pos re75pos"

The dataset includes all of the samples referenced in Masten, Poirier, and Zhang (2020). sample1 flags the experimental sample using the treatment and control groups from the National Supported Work (NSW) demonstration project. sample3 flags the sample using the NSW treatment group and a control group constructed from the PSID and trimmed to exclude workers with earnings above \$5,000 3 or 4 years before the program began. (sample2 is the same as sample3 but without trimming.)

For reference, we start by estimating the average treatment effect of these experimental and non-experimental samples using the teffects package.

For the experimental sample:

```
. teffects ipw ('outcome') ('treatment' 'controls') if sample1
Iteration 0:
               EE criterion = 1.061e-15
Iteration 1:
               EE criterion = 5.245e-23
Treatment-effects estimation
                                                 Number of obs
                                                                             445
               : inverse-probability weights
Outcome model : weighted mean
Treatment model: logit
                             Robust
        re78
                            Std. Err.
                                                            [95% Conf. Interval]
                    Coef.
                                            z
                                                 P>|z|
ATF.
       treat
   (1 vs 0)
                  1632.93
                             649.886
                                          2.51
                                                 0.012
                                                           359.1766
                                                                        2906.683
```

POmean						
treat						
0	4578.176	343.7891	13.32	0.000	3904.362	5251.99

For the trimmed observational sample:

Treatment-effects estimation Number of obs = 390

Estimator : inverse-probability weights

Outcome model : weighted mean

Treatment model: logit

re78	Coef.	Robust Std. Err.	z	P> z	[95% Conf.	Interval]
ATE						
treat (1 vs 0)	3336.676	769.1799	4.34	0.000	1829.112	4844.241
POmean						
treat						
0	2868.201	331.8332	8.64	0.000	2217.82	3518.582

Under the standard unconfoundedness assumption, the treatment effect is positive and statistically significant in both samples. Now we will use the **tesensitivity** package to analyze how sensitive these results are to this assumption.

The main subcommand of the tesensitivity package is cpi, i.e., conditional partial independence. This command estimates bounds on treatment effect statistics given a set of c-dependence values and calculates the breakdown point for the conclusion that the treatment effect statistic is above a given threshold.

First, we calculate bounds on the ATE. By default, the command calculates bounds for a uniform grid of 40 values of c, and the breakdown point for the conclusion that ATE >{} 0.

. tesensitivity cpi ('outcome' 'controls') ('treatment' 'controls') if sample1, ate

Treatment effects sensitivity

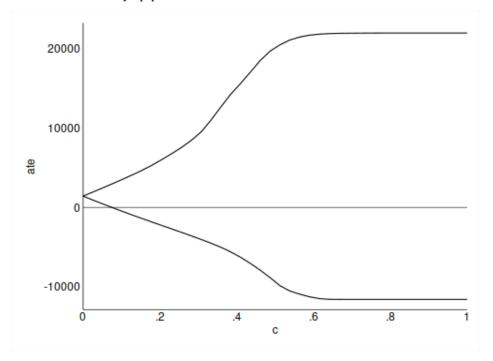
Analysis : cond. partial independence Number of obs = 445 Outcome model : linear quantile Breakdown = 0.075 Treatment model : logistic Conclusion = ate > 0

Outcome variable : re78

```
[ -5,026, 12,662]
0.359
0.385
        [-5,616,
                   14,257]
        [ -6,291,
                   15,611]
0.410
0.436
        [ -7,067, 17,048]
0.462
        [ -7,926, 18,514]
        [ -8,862, 19,680]
0.487
0.513
        [ -9,871,
                   20,477]
        [-10,532,
0.538
                   21,081]
0.564
        [-10,934,
                   21,454]
        [-11,265,
                   21,687]
0.590
        [-11,489,
                   21,811]
0.615
        [-11,582,
                   21,881]
0.641
0.667
        [-11,591,
                   21,915]
0.692
        [-11,594,
                   21,928]
        [-11,594,
                   21,937]
0.718
0.744
        [-11,594,
                   21,945]
0.769
        [-11,594,
                   21,950]
0.795
        [-11,594,
                   21,951]
0.821
        [-11,594,
                   21,951]
0.846
        [-11,594,
                   21,952]
0.872
        [-11,594,
                   21,952]
        [-11,594,
                   21,952]
0.897
0.923
        [-11,594,
                   21,952]
0.949
        [-11,594,
                   21,952]
0.974
        [-11,594,
                   21,952]
1.000
        [-11,594,
                   21,952]
```

We can see this graphically using the cpiplot subcommand, which can be called after tesensitivity cpi.

. tesensitivity cpiplot



By default, this command plots a horizontal line for the lower bound in the conclusion used for the breakdown point computation.

Interpreting the c-dependence parameter

In our ATE example, the bounds get very wide for moderately large values of c, but it isn't immediately clear what would be a reasonable assumption to maintain about the value of c. The cscale subcommand provides tools to interpret the scale of c-dependence.

The main tool provided in this subcommand is the leave-one-out analysis discussed in section 2 of Masten and Poirier (2018). Also see section 2 of Masten, Poirier, and Zhang (2020). This compares the propensity scores obtained when leaving out each covariate in the analysis compared to the propensity scores including all covariates. This provides a reference point for thinking about the level of c-dependence that might be caused by other omitted variables.

Since the deviation in propensity scores varies across the values of the covariate left out, this induces a distribution of deviations. The cscale subcommand provides options to calculate the supremum over this distribution and quantiles of the distribution for each covariate.

By default, tesensitivity cscale calculates the maximum and the 50th, 75th, and 90th percentiles of the distribution for each covariate.

. tesensitivity cscale

Treatment-effects sensitivity analysis

Analysis : leave one out prop. score diff. Number of obs = 445

Treatment model : logistic

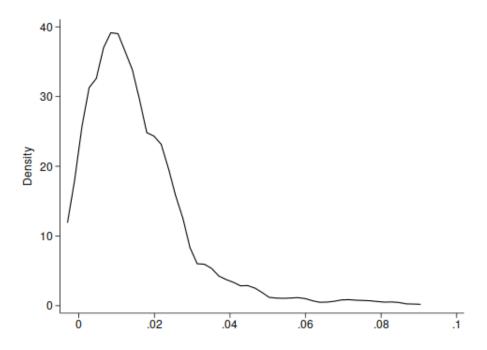
quantile	0.500	0.750	0.900	max
married	0.006	0.012	0.032	0.042
married	0.006	0.012	0.032	0.042
age	0.015	0.024	0.034	0.099
black	0.007	0.009	0.014	0.082
hispanic	0.007	0.017	0.099	0.124
education	0.012	0.022	0.031	0.087
re74	0.002	0.011	0.035	0.209
re75	0.001	0.004	0.008	0.053
re74pos	0.002	0.010	0.018	0.034
re75pos	0.013	0.017	0.062	0.082

Other quantiles can be calculated with the quantiles option.

Note that this command uses the specification of the last call to tesensitivity cpi. So it uses the covariates and the sample selection criteria given in the previous call.

We also can plot the density of propensity score deviations in the leave-one-out analysis. For example, for education, we have:

. tesensitivity cscale education, density



To see the bounds on the ATE at the maximum deviations for each covariate, use the creference option.

. tesensitivity cpi (`outcome´ `controls´) (`treatment´ `controls´) if sample1, ate cref

 ${\tt Treatment\ effects\ sensitivity}$

Analysis : cond. partial independence Number of obs = 445 Outcome model : linear quantile Breakdown = 0.075 Treatment model : logistic Conclusion = ate > 0

Outcome variable : re78

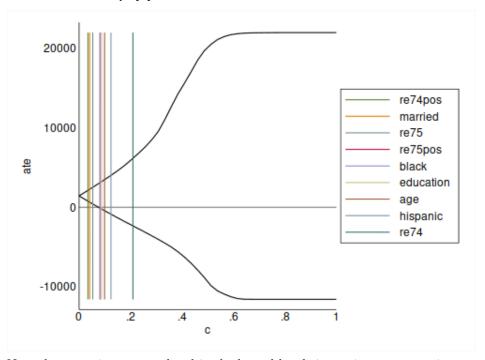
	С		ate
	0.000	[1,419,	1,419]
	0.026	[920,	1,930]
re74pos	0.034	[751,	2,109]
married	0.042	[616,	2,254]
	0.051	[433,	2,454]
re75	0.053	[398,	2,492]
	0.077	[-43,	2,986]
re75pos	0.082	[-128,	3,083]
black	0.082	[-134,	3,090]
education	0.087	[-234,	3,206]
age	0.099	[-448,	3,458]
	0.103	[-508,	3,529]
hispanic	0.124	[-888,	3,996]
	0.128	[-963,	4,091]
	0.154	[-1,411,	4,674]
	0.179	[-1,851,	5,313]
	0.205	[-2,282,	6,023]
re74	0.209	[-2,354,	6,146]
	0.231	[-2,714,	6,765]
	0.256	[-3,150,	7,554]
	0.282	[-3,594,	8,449]
	0.308	[-4,047,	9,513]
	0.333	[-4,520,	11,004]
	0.359	[-5,026,	12,662]
	0.385	[-5,616,	14,257]

```
0.410
        [ -6,291, 15,611]
0.436
        [-7,067,
                   17,048]
        [ -7,926,
0.462
                   18,514]
0.487
        [ -8,862,
                   19,680]
0.513
        [-9,871,
                   20,477]
        [-10,532,
                   21,081]
0.538
0.564
        [-10,934,
                   21,454]
0.590
        [-11,265,
                   21,687]
0.615
        [-11,489,
                   21,811]
                   21,881]
0.641
        [-11,582,
        [-11,591,
                   21,915]
0.667
        [-11,594,
0.692
                   21,928]
0.718
        [-11,594,
                   21,937]
0.744
        [-11,594,
                   21,945]
        [-11,594,
                   21,950]
0.769
        [-11,594,
0.795
                   21,951]
0.821
        [-11,594,
                   21,951]
        [-11,594,
                   21,952]
0.846
0.872
        [-11,594,
                   21,952]
0.897
        [-11,594,
                   21,952]
0.923
        [-11,594,
                   21,952]
        [-11,594,
0.949
                   21,952]
0.974
        [-11,594,
                   21,952]
1.000
        [-11,594,
                   21,952]
```

This table includes the values of c-dependence equal to the maximum propensity scores deviation for each of the covariates, which are displayed on the left of the table.

We can also plot these with a line for the maximum deviation of propensity scores for each covariate.

. tesensitivity cpiplot, creflines



Note that covariates are ordered in the legend by their maximum propensity score deviation.

Storing and comparing estimates

Results from calls to tesensitivity cpi are stored in e(), and are compatible with several built-in postestimation commands to store and combine results.

First, to see descriptive statistics of the variables used in a call to tesensitivity cpi, we can use the estat summarize command:

. estat summarize

Estimation sample tesensitivity Number of obs = 445 Variable Mean Std. Dev. Min Max re78 5300.764 6631.492 60307.93 treat .4157303 .4934022 0 1 .3747658 married .1685393 0 1 7.100282 25.37079 17 55 age .8337079 .3727617 black 0 1 hispanic .0876404 .2830895 0 1 education 10.19551 1.792119 3 16 2102.265 5363.582 0 39570.68 re74 1377.138 25142.24 re75 3150.961 re74pos .2674157 .4431092 0 1 ٥ .3505618 .4776829 1 re75pos

Note that a matrix of the covariates is also saved in e(covsupp).

We can also store results using estimates store and see the output from any stored results with replay.

- . qui tesensitivity cpi (`outcome´ `controls´) (`treatment´ `controls´) if sample1, ate
- . estimates store ate1
- . estimates replay ate1

Model ate1

Treatment effects sensitivity

Analysis : cond. partial independence Number of obs = 445 Outcome model : linear quantile Breakdown = 0.075 Treatment model : logistic Conclusion = ate > 0 Outcome variable : re78

ate С 0.000 [1,419, 1,419] 0.026 920, 1,930] 0.051 433, 2,454] 2,986] 0.077 -43, 0.103 -508, 3,529] 0.128 -963, 4,091] 0.154 [-1,411,4,6741 0.179 [-1,851,5,313] [-2,282,0.205 6,023] [-2,714,0.231 6,765] 0.256 [-3,150,7,554] 0.282 [-3,594,8,449] [-4,047,0.308 9,513] [-4,520, 11,004] 0.333 [-5,026,12,662] 0.359 0.385 [-5,616, 14,257] [-6,291, 15,611] 0.410 [-7,067, 17,048] 0.436

```
[ -7,926, 18,514]
0.462
0.487
        [ -8,862, 19,680]
        [ -9,871, 20,477]
0.513
0.538
       [-10,532, 21,081]
0.564
       [-10,934, 21,454]
       [-11,265, 21,687]
0.590
0.615
       [-11,489, 21,811]
        [-11,582, 21,881]
0.641
0.667
        [-11,591,
                  21,915]
        [-11,594, 21,928]
0.692
        [-11,594, 21,937]
0.718
0.744
        [-11,594, 21,945]
        [-11,594, 21,950]
0.769
0.795
        [-11,594, 21,951]
        [-11,594, 21,951]
0.821
        [-11,594,
                  21,952]
0.846
0.872
        [-11,594, 21,952]
        [-11,594, 21,952]
0.897
0.923
        [-11,594, 21,952]
0.949
        [-11,594, 21,952]
0.974
        [-11,594, 21,952]
        [-11,594, 21,952]
1.000
```

.

We can also compare multiple sets of estimates. To illustrate, we'll compare the results from the experimental sample stored in ate1 with results from then observational, trimmed sample.

. tesensitivity cpi (`outcome' `controls') (`treatment' `controls') if sample3, ate

Treatment effects sensitivity

Analysis : cond. partial independence Number of obs = 390
Outcome model : linear quantile Breakdown = 0.020
Treatment model : logistic Conclusion = ate > 0

Outcome variable : re78

С	ate
0.000 0.026 0.051 0.077 0.103 0.128 0.154 0.179 0.205 0.231 0.256 0.282 0.308 0.333 0.359 0.385 0.410 0.436 0.462 0.487	ate [2,865, 2,865] [-663, 11,806] [-2,879, 15,385] [-4,389, 17,794] [-5,356, 19,300] [-6,121, 20,318] [-6,764, 21,055] [-7,296, 21,687] [-7,746, 22,256] [-8,232, 22,747] [-8,678, 23,234] [-9,092, 23,642] [-9,485, 23,984] [-9,798, 24,278] [-10,127, 24,599] [-10,438, 24,905] [-10,438, 24,905] [-10,993, 25,478] [-11,247, 25,734] [-11,463, 25,929] [-11,692, 26,126]
0.538 0.564 0.590 0.615 0.641	[-11,935, 26,314] [-12,120, 26,469] [-12,327, 26,655] [-12,465, 26,788] [-12,602, 26,900] [-12,711, 27,007]

```
0.692 | [-12,834, 27,071]

0.718 | [-12,936, 27,130]

0.744 | [-13,044, 27,189]

0.769 | [-13,114, 27,241]

0.795 | [-13,175, 27,275]

0.821 | [-13,242, 27,302]

0.846 | [-13,316, 27,326]

0.872 | [-13,345, 27,348]

0.897 | [-13,358, 27,368]

0.923 | [-13,367, 27,383]

0.949 | [-13,374, 27,392]

0.974 | [-13,376, 27,397]

1.000 | [-13,376, 27,399]
```

. estimates store ate3

The tesensitivity cpitable command provides a simple way to compare results:

. tesensitivity cpitable ate1 ate3

Treatment effects sensitivity

Analysis : conditional partial independence, multiple results

С		ate1		ate3
0.000	[1,419,	1,419]	[2,865,	2,865]
0.026	[920,	1,930]	[-663,	11,806]
0.051	[433,	2,454]	[-2,879,	15,385]
0.077	[-43,	2,986]	[-4,389,	17,794]
0.103	[-508,	3,529]	[-5,356,	19,300]
0.128	[-963,	4,091]	[-6,121,	20,318]
0.154	[-1,411,	4,674]	[-6,764,	21,055]
0.179	[-1,851,	5,313]	[-7,296,	21,687]
0.205	[-2,282,	6,023]	[-7,746,	22,256]
0.231	[-2,714,	6,765]	[-8,232,	22,747]
0.256	[-3,150,	7,554]	[-8,678,	23,234]
0.282	[-3,594,	8,449]	[-9,092,	23,642]
0.308	[-4,047,	9,513]	[-9,485,	23,984]
0.333	[-4,520,	11,004]	[-9,798,	24,278]
0.359	[-5,026,	12,662]	[-10,127,	24,599]
0.385	[-5,616,	14,257]	[-10,438,	24,905]
0.410	[-6,291,	15,611]	[-10,752,	25,231]
0.436	[-7,067,	17,048]	[-10,993,	25,478]
0.462	[-7,926,	18,514]	[-11,247,	25,734]
0.487	[-8,862,	19,680]	[-11,463,	25,929]
0.513	[-9,871,	20,477]	[-11,692,	26,126]
0.538	[-10,532,	21,081]	[-11,935,	26,314]
0.564	[-10,934,	21,454]	[-12,120,	26,469]
0.590	[-11,265,	21,687]	[-12,327,	26,655]
0.615	[-11,489,	21,811]	[-12,465,	26,788]
0.641	[-11,582,	21,881]	[-12,602,	26,900]
0.667	[-11,591,	21,915]	[-12,711,	27,007]
0.692	[-11,594,	21,928]	[-12,834,	27,071]
0.718	[-11,594,	21,937]	[-12,936,	27,130]
0.744	[-11,594,	21,945]	[-13,044,	27,189]
0.769	[-11,594,	21,950]	[-13,114,	27,241]
0.795	[-11,594,	21,951]	[-13,175,	27,275]
0.821	[-11,594,	21,951]	[-13,242,	27,302]
0.846	[-11,594,	21,952]	[-13,316,	27,326]
0.872	[-11,594,	21,952]	[-13,345,	27,348]
0.897	[-11,594,	21,952]	[-13,358,	27,368]
0.923	[-11,594,	21,952]	[-13,367,	27,383]
0.949	[-11,594,	21,952]	[-13,374,	27,392]
0.974	[-11,594,	21,952]	[-13,376,	27,397]
1.000	[-11,594,	21,952]	[-13,376,	27,399]

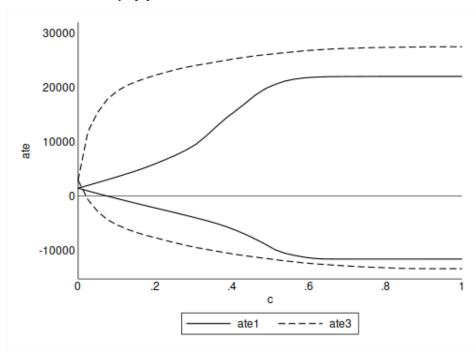
Analysis : breakdown point, multiple

conclusion ate1 ate3

stat > 0 0.075 0.020

We can also see this graphically by passing multiple results to tesensitiviy cpiplot

. tesensitivity cpiplot ate1 ate3



Other treatment effect statistics

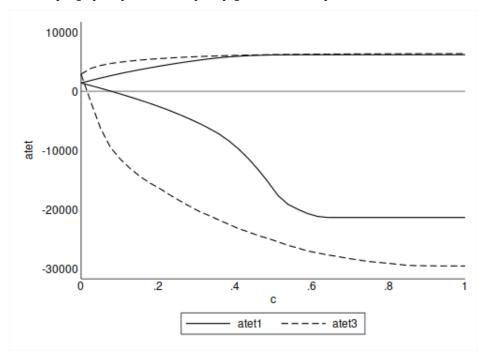
The tesensitivity package includes support for five treatment effect statistics:

- 1. Average treatment effect (ATE)
- 2. Average treatment effect on the treated (ATET)
- 3. Quantile treatment effect (QTE)
- 4. Conditional average treatment effect (CATE)
- 5. Conditional quantile treatment effect (CQTE)

Like the ATE, bounds on the ATET can be calculated without further options. To illustrate, let's compare the sensitivity of ATET in the two samples graphically.

- . qui tesensitivity cpi (`outcome' `controls') (`treatment' `controls') if sample1, atet
- . qui estimates store atet1
- . qui tesensitivity cpi (`outcome´ `controls´) (`treatment´ `controls´) if sample3, atet
- . ${\tt qui}$ estimates store atet3
- . tesensitivity cpiplot atet1 atet3

. qui graph export ATET_compare.png, width(500) replace



For QTE, we also have to specify the quantile using the quantiles option. The median is used by default. Let's compare the QTE at the median to the ATE for the experimental sample:

- . qui tesensitivity cpi (`outcome´ `controls´) (`treatment´ `controls´) if sample1, qte
- . qui estimates store qte1_50
- . tesensitivity cpitable ate1 qte1_50

Treatment effects sensitivity

Analysis : conditional partial independence, multiple results

c		ate1		qte1_50
0.000 0.026 0.051 0.077 0.103 0.128 0.154 0.179 0.205 0.231 0.256 0.282	[1,419, [920, [433, [-43, [-508, [-963, [-1,411, [-1,851, [-2,282, [-2,714, [-3,150, [-3,594, [-4,047,	1,419] 1,930] 2,454] 2,986] 3,529] 4,091] 4,674] 5,313] 6,023] 6,765] 7,554] 8,449] 9,513]	[988, [321, [-541, [-1,051, [-1,989, [-3,036, [-3,497, [-4,082, [-4,824, [-5,209, [-6,073, [-6,910, [-7,171,	988] 2,009] 2,857] 3,835] 4,724] 6,029] 6,755] 7,877] 8,882] 9,643] 9,973] 10,784] 11,177]
0.333 0.359 0.385 0.410 0.436 0.462 0.487 0.513	[-4,520, [-5,026, [-5,616, [-6,291, [-7,067, [-7,926, [-8,862, [-9,871, [-10,532,	11,004] 12,662] 14,257] 15,611] 17,048] 18,514] 19,680] 20,477] 21,081]	[-7,345, [-7,643, [-8,271, [-8,795, [-9,379, [-9,737, [-10,211, [-10,313, [-60,308,	12,558] 60,308] 60,308] 60,308] 60,308] 60,308] 60,308] 60,308]

```
0.564
        [-10,934,
                   21,454]
                              [-60,308,
                                          60,308]
0.590
        [-11,265,
                   21,687]
                              [-60,308,
                                          60,308]
        [-11,489,
                   21,811]
                              [-60,308,
                                          60,308]
0.615
        [-11,582,
                   21,881]
                              [-60,308,
                                          60,308]
0.641
0.667
        [-11,591,
                   21,915]
                              [-60,308,
                                          60,308]
        [-11,594,
0.692
                   21,928]
                               [-60,308,
                                          60,308]
0.718
        [-11,594,
                   21,937]
                              [-60,308,
                                          60,308]
0.744
        [-11,594,
                   21,945]
                              [-60,308,
                                          60,308]
0.769
        [-11,594,
                   21,950]
                               [-60,308,
                                          60,308]
0.795
        [-11,594,
                   21,951]
                               [-60,308,
                                          60,308]
                                          60,308]
        [-11,594,
                   21,951]
                              [-60,308,
0.821
0.846
        [-11,594,
                   21,952]
                              [-60,308,
                                          60,308]
0.872
        [-11,594,
                   21,952]
                              [-60,308,
                                          60,308]
                   21,952]
        [-11,594,
                              [-60,308,
                                          60,308]
0.897
                   21,952]
                              [-60,308,
        [-11,594,
                                          60,308]
0.923
0.949
        [-11,594,
                   21,952]
                               [-60,308,
                                          60,308]
0.974
        [-11,594,
                   21,952]
                               [-60,308,
                                          60,308]
1.000
        [-11,594,
                   21,952]
                              [-60,308,
                                          60,308]
```

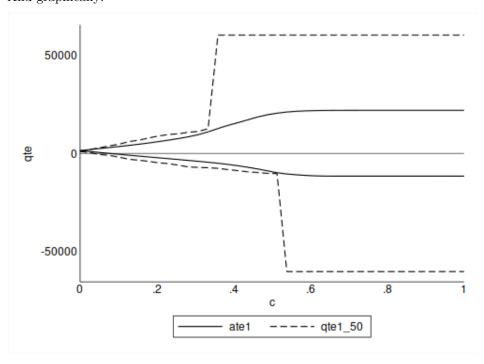
Analysis : br

: breakdown point, multiple

conclusion	ate1	qte1_50
stat > 0	0.075	0.038

. tesensitivity cpiplot ate1 qte1_50

And graphically:



The two conditional statistics, CATE and CQTE, are evaluated at a single point in the support of the covariates. By default the mean of each covariate is used. The median option can be selected to use median values instead.

There are two ways to specify a custom covariate value: it can be specified directly using the covariates option, or quantiles of the covariates can be specified using the qcovariates option.

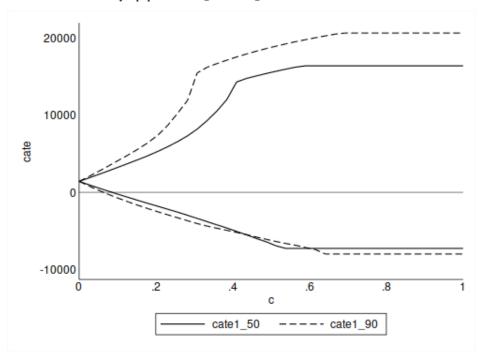
Both options can accept input in three forms:

- 1. a list of values separated with spaces.
- 2. a 1 x K unlabeled matrix.
- 3. a 1 x S $(S \leq K)$ matrix with column names corresponding to variable names.

If formats 1 or 2 are used, values must be provided for all covariates and they must be in the same order as they were in the call to tesensitivity cpi. If format 3 is used, it is not necessary to specify the support for all covariates. Covariates not included will be evaluated at the mean by default or at the median if the median option is selected. If format 3 is used, it is also possible to use both the covariates and qcovariates options for different covariates.

In this example, we'll compare the CATE for married people at the median income to the CATE for unmarried people at the 90th percentile of earnings in 1974. For both analyses, all other covariates are set at their median values.

```
. matrix cov = (1)
. matrix colnames cov = married
. qui tesensitivity cpi (`outcome´ `controls´) (`treatment´ `controls´) ///
>    if sample1, cate median cov(cov)
. qui estimates store cate1_50
.
. matrix cov[1,1] = 0
. matrix qcov = (.9)
. matrix colnames qcov = re74
. qui tesensitivity cpi (`outcome´ `controls´) (`treatment´ `controls´) ///
>    if sample1, cate median qcov(qcov) cov(cov)
. qui estimates store cate1_90
.
. tesensitivity cpiplot cate1_50 cate1_90
```

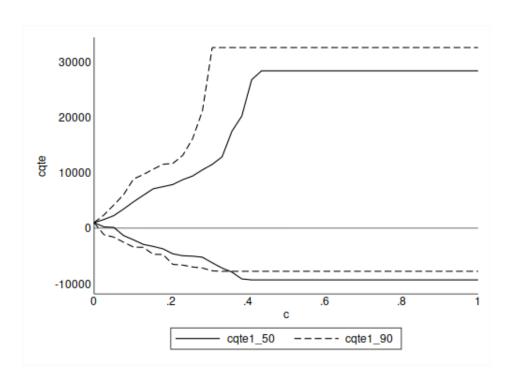


We can see what the values of the covariates in this specification where by using the stored result e(covsupp)

```
. estimates restore cate1_50
(results cate1_50 are active now)
. matrix list e(covsupp)
e(covsupp)[1,10]
      married
                              black
                                      hispanic education
                                                                  re74
                                                                             re75
                                                                                     re74pos
r1
            1
                      24
                                  1
                                              0
                                                        10
                                                                                0
      re75pos
                  _const
r1
. estimates restore cate1_90
(results cate1_90 are active now)
. matrix list e(covsupp)
e(covsupp)[1,10]
      married
                               black
                                       hispanic education
                                                                             re75
                                                                                     re74pos
                     age
r1
            0
                      24
                                   1
                                              0
                                                        10 7914.1309
                                                                                0
                                                                                           0
      re75pos
                  _const
r1
```

And we can consider consider the same analysis for the conditional quantile treatment effect for the 50th percentile.

```
. matrix cov = (1)
. matrix colnames cov = married
. qui tesensitivity cpi (`outcome´ `controls´) (`treatment´ `controls´) ///
>    if sample1, cqte median cov(cov)
. qui estimates store cqte1_50
.
. matrix cov[1,1] = 0
. matrix qcov = (.9)
. matrix colnames qcov = re74
. qui tesensitivity cpi (`outcome´ `controls´) (`treatment´ `controls´) ///
>    if sample1, cqte median qcov(qcov) cov(cov)
. qui estimates store cqte1_90
.
. tesensitivity cpiplot cqte1_50 cqte1_90
```



Binary outcome variables

In all of the previous analysis, we have assumed that the outcome variable has continuous support. For binary outcomes, only the ATE is currently supported. To illustrate, we'll look at the outcome of having positive earnings (i.e., re78 > 0).

```
. gen re78pos = re78 > 0
```

. tesensitivity cpi (re78pos `controls´) (`treatment´ `controls´) if sample1, ate

Treatment effects sensitivity

Analysis : cond. partial independence Number of obs = 445 Outcome model : logistic Breakdown = 0.059 Treatment model : logistic Conclusion = ate > 0 Outcome variable : re78pos

С ate 0.000 [0.1121, 0.1121] 0.1431] 0.026 [0.0654, 0.051 [0.0162, 0.1741] 0.077 [-0.0346, 0.2057] 0.103 [-0.0909, 0.2378] [-0.1490, 0.2666] 0.128 [-0.1886, 0.154 0.2928] 0.179 [-0.2249,0.3174] 0.3405] 0.205 [-0.2562, 0.231 0.3628] [-0.2824, 0.256 [-0.3067, 0.3845] 0.282 [-0.3283, 0.4052] [-0.3483, 0.4243] 0.308 [-0.3670, 0.4420] 0.333 [-0.3833, 0.4579] 0.359 0.385 [-0.3983, 0.4717] 0.410 [-0.4120, 0.4838] 0.436 [-0.4255, 0.4945]

```
0.462
        [-0.4370, 0.5025]
0.487
        [-0.4464, 0.5080]
        [-0.4545, 0.5121]
0.513
        [-0.4613, 0.5152]
0.538
0.564
        [-0.4668, 0.5175]
        [-0.4711, 0.5192]
0.590
0.615
        [-0.4744, 0.5203]
0.641
        [-0.4763, 0.5208]
0.667
        [-0.4773, 0.5211]
        [-0.4778, 0.5211]
0.692
        [-0.4782, 0.5212]
0.718
        [-0.4785, 0.5212]
0.744
0.769
        [-0.4787, 0.5212]
0.795
        [-0.4787, 0.5212]
        [-0.4787, 0.5213]
0.821
        [-0.4787, 0.5213]
[-0.4787, 0.5213]
0.846
0.872
        [-0.4787, 0.5213]
0.897
0.923
        [-0.4787, 0.5213]
0.949
        [-0.4787, 0.5213]
0.974
        [-0.4787, 0.5213]
        [-0.4787, 0.5213]
1.000
```

Displaying progress updates

0.462

0.487

[-0.4370, 0.5025] [-0.4464, 0.5080]

The computation of some statistics, particularly ate, atet, and qte can take some time. To see progress updates, use the verbose option. This produces output as follows:

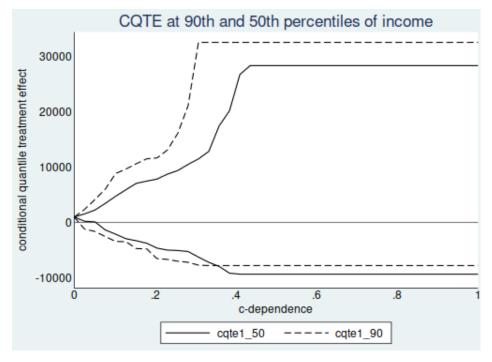
```
. tesensitivity cpi (re78pos `controls´) (`treatment´ `controls´) if sample1, ate verbose
calculating ate (41)
1 2 3 4 5
calculating breakdown point...
Treatment effects sensitivity
            : cond. partial independence Number of obs =
                                                                       445
Analysis
Outcome model
               : logistic
                                            Breakdown
                                                                     0.059
Treatment model : logistic
                                                                   ate > 0
                                            Conclusion
Outcome variable : re78pos
                                  ate
                   [ 0.1121, 0.1121]
            0.000
            0.026
                   [ 0.0654, 0.1431]
            0.051
                   [ 0.0162, 0.1741]
            0.077
                   [-0.0346, 0.2057]
                   [-0.0909, 0.2378]
            0.103
            0.128
                   [-0.1490, 0.2666]
                   [-0.1886, 0.2928]
            0.154
            0.179
                   [-0.2249, 0.3174]
            0.205
                   [-0.2562, 0.3405]
                   [-0.2824, 0.3628]
            0.231
            0.256
                   [-0.3067, 0.3845]
            0.282
                   [-0.3283, 0.4052]
            0.308
                   [-0.3483, 0.4243]
            0.333
                   [-0.3670, 0.4420]
                   [-0.3833, 0.4579]
            0.359
            0.385
                   [-0.3983, 0.4717]
            0.410
                   [-0.4120, 0.4838]
            0.436
                   [-0.4255, 0.4945]
```

```
0.513
        [-0.4545, 0.5121]
0.538
        [-0.4613,
                  0.5152]
        [-0.4668, 0.5175]
0.564
        [-0.4711, 0.5192]
0.590
0.615
        [-0.4744, 0.5203]
        [-0.4763, 0.5208]
0.641
0.667
        [-0.4773, 0.5211]
0.692
        [-0.4778,
                   0.5211]
0.718
        [-0.4782,
                   0.5212]
                   0.5212]
0.744
        [-0.4785,
                  0.5212]
0.769
        [-0.4787,
0.795
        [-0.4787, 0.5212]
0.821
        [-0.4787, 0.5213]
0.846
        [-0.4787, 0.5213]
        [-0.4787, 0.5213]
0.872
        [-0.4787,
0.897
                  0.5213]
0.923
        [-0.4787, 0.5213]
        [-0.4787, 0.5213]
0.949
0.974
        [-0.4787, 0.5213]
1.000
        [-0.4787, 0.5213]
```

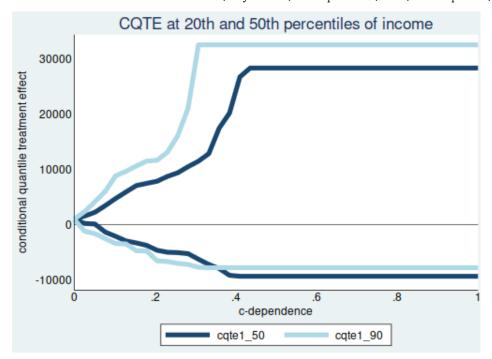
Controlling the formatting of plots

The formatting of graphs produced by tesensitivity cpiplot can be specified by the user.

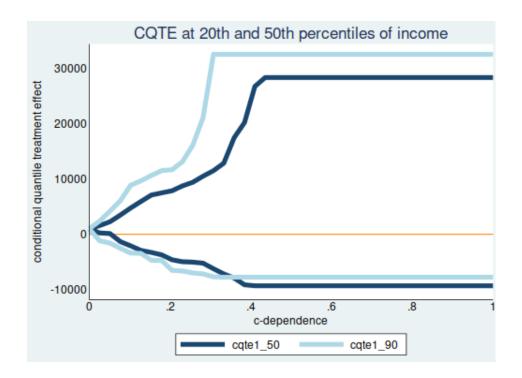
To change the overall formatting of the figure, any of the twoway_options to Stata's graph twoway command can be passed to tesensitivity cpiplot. Let's change some of the titles, background colors, and margins of the CQTE comparison in the previous section.



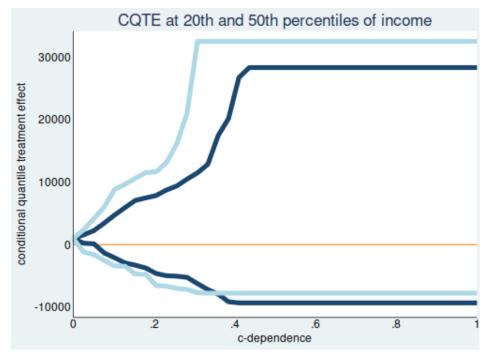
By default, the bound lines are black and line patterns are used to mark the different estimates included in the plot. This can be customized using the boundpatterns and boundcolors options. If only one color or pattern is specified, then this is applied to bound lines for all estimates Any other options to Stata's graph twoway line command can be passed to tesensitivity cpiplot in the boundoptions options. These are applied to the bounds lines for all estimates. In the following example, we use colors rather than patterns to indicate the different estimates and change the width of the lines to be thicker.



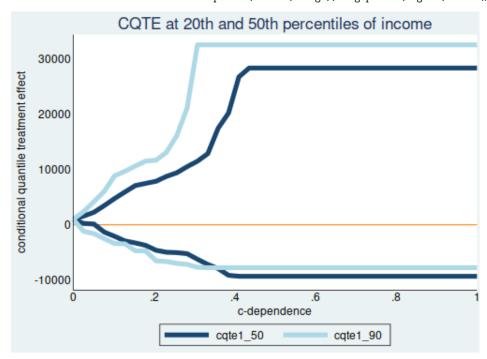
Finally, by default the plot includes a horizontal line at the conclusion for the breakdown point. This can be removed with the nobreakdown option and the formatting can be controlled with the breakdownoptions option. Any suboptions of the added_line_options options to Stata's yline option can be included here. In the following example, we change the color of the breakdown line.



To suppress the legend, simply use the nolegend option



Alternatively, any *legend_option* to Stata's legend option can be specified in legoptions except for order and label which are handled automatically:



References

Dehejia, Rajeev, and Sadek Wahba. 1999. "Causal Effects in Nonexperimental Studies: Reevaluating the Evaluation of Training Programs." *Journal of the American Statistical Association* 94 (448): 1053–62.

LaLonde, Robert. 1986. "Evaluating the Econometric Evaluations of Training Programs with Experimental Data." The American Economic Review 76 (4). American Economic Association: 604–20.

Masten, Matthew, and Alexandre Poirier. 2018. "Identification of Treatment Effects Under Conditional Partial Independence." *Econometrica* 86 (1): 317–51.

——. 2020. "Inference on Breakdown Frontiers." Quantitative Economics 11 (1): 41–111.

Masten, Matthew, Alexandre Poirier, and Linqi Zhang. 2020. "Assessing Sensitivity to Unconfoundedness: Estimation and Inference." arXiv:2012.15716.