**Description**

One of the assumptions required to use the `teffects` and `stteffects` estimators is the overlap assumption, which states that each individual has a positive probability of receiving each treatment level. `teffects overlap`, a postestimation command, plots the estimated densities of the probability of getting each treatment level. These plots can be used to check whether the overlap assumption is violated.

**Quick start**

Visually check whether the overlap assumption is violated

```
teffects overlap
```

As above, but use the Epanechnikov kernel function

```
teffects overlap, kernel(epanechnikov)
```

Plot probability of getting treatment 3 for subjects receiving treatments 2 or 3 of a multivalued treatment

```
teffects overlap, ptlevel(3) tlevels(2 3)
```

As above, and change legend labels to “Treated 2” and “Treated 3”

```
teffects overlap, ptlevel(3) tlevels(2 3) ///
    legend(label(1 "Treated 2") label(2 "Treated 3"))
```

**Menu**

Statistics > Treatment effects > Overlap plots
**Syntax**

```
teffects overlap [ , treat_options kden_options ]
```

**treat_options**

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**kden_options**

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**Options**

**Main**

```
ptlevel(treat_level) specifies that predicted probabilities be calculated for treatment level treat_level.
The default is ptlevel(first), where first is the first treatment level.
```
tlevels(treatments) specifies the observations for which to obtain predicted probabilities. By default, all treatment levels are used. Specify treatments as a space-delimited list.

For instance,

```
   . teffects overlap, ptlevel(1) tlevels(1 2)
```

says to predict the probability of getting treatment level 1 for those subjects who actually obtained treatment levels 1 or 2.

nolabel specifies that treatment level values and not value labels be used in legend and axis titles.

kernel(kernel) specifies the kernel function for use in calculating the kernel density estimates. The default kernel is the triangle kernel (triangle).

n(#) specifies the number of points at which the density estimate is to be evaluated. The default is e(N), the estimation sample size.

bwidth(#) specifies the half-width of the kernel, the width of the density window around each point. If bwidth() is not specified, the “optimal” width is calculated and used; see [R] kdensity. The optimal width is the width that would minimize the mean integrated squared error if the data were Gaussian and a Gaussian kernel were used, so it is not optimal in any global sense. In fact, for multimodal and highly skewed densities, this width is usually too wide and oversmooths the density (Silverman 1986).

at(var_x) specifies a variable that contains the values at which the density should be estimated. This option allows you to more easily obtain density estimates for different variables or different subsamples of a variable and then overlay the estimated densities for comparison.

Kernel plots

line#opts(cline_options) affect the rendition of the plotted kernel density estimates. See [G-3] cline_options.

Add plots

addplot(plot) provides a way to add other plots to the generated graph. See [G-3] addplot_option.

Y axis, X axis, Titles, Legend, Overall

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).

Remarks and examples

stata.com

teffects overlap plots the estimated densities of the probability of getting each treatment level after teffects.

These plots can be used to check whether the overlap assumption is violated. The overlap assumption is satisfied when there is a chance of seeing observations in both the control and the treatment groups at each combination of covariate values; see [TE] teffects intro or [TE] teffects intro advanced.

The overlap assumption is required by the estimators implemented in teffects. Intuitively, when the overlap assumption is violated, we cannot predict, or otherwise account for, the unobserved outcomes for some individuals.
There is evidence that the overlap assumption is violated when an estimated density has too much mass around 0 or 1; see Busso, DiNardo, and McCrary (2014). An implication of this point is that when the overlap assumption is violated, the estimated densities will have relatively little mass in the regions in which they overlap.

Example 1: Assumption not violated

Continuing with example 1 of [TE] `teffects ipw`, we estimate the average treatment effect of smoking on birthweight and then draw the overlap plot:

```
. use https://www.stata-press.com/data/r16/cattaneo2
. teffects ipw (bweight) (mbsmoke mmarried c.mage##c.mage fbaby medu, probit)
Iteration 0: EE criterion = 4.621e-21
Iteration 1: EE criterion = 7.358e-26

Treatment-effects estimation
Number of obs = 4,642
Estimator : inverse-probability weights
Outcome model : weighted mean
Treatment model : probit

| bweight | Robust Coef. | Std. Err. | z   | P>|z| | [95% Conf. Interval] |
|---------|--------------|-----------|-----|------|---------------------|
| ATE     |              |           |     |      |                     |
| mbsmoke (smoker vs nonsmoker) | -230.6886 | 25.81524 | -8.94 | 0.000 | [-281.2856, -180.0917] |
| POmean  |              |           |     |      |                     |
| mbsmoke nonsmoker | 3403.463 | 9.571369 | 355.59 | 0.000 | [3384.703, 3422.222] |
```
The graph displays the estimated density of the predicted probabilities that a nonsmoking mother is a nonsmoker and the estimated density of the predicted probabilities that a smoking mother is a nonsmoker.

Neither plot indicates too much probability mass near 0 or 1, and the two estimated densities have most of their respective masses in regions in which they overlap each other. Thus there is no evidence that the overlap assumption is violated.

Example 2: Assumption violated

This example produces an overlap plot that indicates a failure of the overlap assumption. We will use simulated data, so we know that the assumption is not true.

In our simulated dataset, some of the 1,000 adult males were given drug XY1 for high blood pressure and others were not. A scatterplot of systolic blood pressure (systolic) and weight (weight) reveals that heavier men were given the treatment. (The scatterplots corresponding to the treatment group are colored red, while the scatterplots corresponding to the control group are colored blue.)
. use https://www.stata-press.com/data/r16/systolic2
(Systolic blood pressure)
. twoway (scatter systolic weight if xy1==1, mcolor(red))
> (scatter systolic weight if xy1==0, mcolor(blue)),
> legend(label(1 "Treated") label(2 "Untreated"))

There are no observations in the treated group for small weights, and there are no observations in
the control group for large weights. There is clear evidence that the overlap assumption is violated.

Drawing an overlaid scatterplot is a straightforward way to check the overlap assumption in this
example because there is only one covariate. This method is not available when there is more than
one covariate. The predicted probability is a one-dimensional measure that captures the relevant
multivariate information.

Below we estimate the parameters needed to calculate the predicted probabilities. The
pstolerance(1e-8) option is specified to ensure that estimation is performed as long as the
predicted probabilities are at least as large as 1e–8.

. teffects ipw (systolic) (xy1 weight), pstolerance(1e-8)
Iteration 0: EE criterion = 9.523e-18
Iteration 1: EE criterion = 3.489e-28
Treatment-effects estimation Number of obs = 1,000
Estimator : inverse-probability weights
Outcome model : weighted mean
Treatment model: logit

|                  | Coef.  | Std. Err. | z   | P>|z|   |  [95% Conf. Interval] |
|------------------|--------|-----------|-----|-------|-----------------------|
| systolic         |        |           |     |       |                       |
| ATE xyl          | -16.23679 | 2.191703  | -7.41 | 0.000 | -20.53245 -11.94114 |
| (Treated vs Untreated) |       |           |     |       |                       |
| POmean xyl       | 127.9094  | .7004533  | 182.61 | 0.000 | 126.5365 129.2822    |
| Untreated        |        |           |     |       |                       |
Now we can obtain the overlap plot.

```
. teffects overlap
```

![Overlap plot](image)

The estimated density of the predicted probabilities that a treated individual is not assigned to XY1 treatment has most of its mass near 0. The estimated density of the predicted probabilities that an untreated individual is not assigned to XY1 treatment has most of its mass near 1. Note that the two have very little mass in the region in which they overlap. There is clear evidence that the overlap assumption is violated.

### Stored results

`teffects overlap` stores the following in `r()`:

**Scalars**

- `r(bwidthj)` kernel bandwidth for treatment level `j`
- `r(nj)` number of points at which the estimate was evaluated for treatment level `j`
- `r(scalej)` density bin width for treatment level `j`

**Macros**

- `r(kernel)` name of kernel

### References


Also see

[TE] stteffects — Treatment-effects estimation for observational survival-time data
[TE] stteffects ipw — Survival-time inverse-probability weighting
[TE] stteffects ipwra — Survival-time inverse-probability-weighted regression adjustment
[TE] tteffects — Treatment-effects estimation for observational data
[TE] tteffects aipw — Augmented inverse-probability weighting
[TE] tteffects ipw — Inverse-probability weighting
[TE] tteffects ipwra — Inverse-probability-weighted regression adjustment
[TE] tteffects nnmatch — Nearest-neighbor matching
[TE] tteffects psmatch — Propensity-score matching
[TE] tteffects ra — Regression adjustment