**teffects postestimation — Postestimation tools for teffects**

The following postestimation command is of special interest after **teffects**:

Command | Description
---|---
**teffects overlap** | overlap plots

The following standard 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
**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
**predict** | predictions, residuals, influence statistics, and other diagnostic measures predictnl point estimates, standard errors, testing, and inference for generalized predictions
**test** | Wald tests of simple and composite linear hypotheses
**testnl** | Wald tests of nonlinear hypotheses

**Syntax**

Syntaxes are presented under the following headings:

- Syntax for predict after aipw and ipwra
- Syntax for predict after ipw
- Syntax for predict after nnmatch and psmatch
- Syntax for predict after ra

**Syntax for predict after aipw and ipwra**

```
predict [type] { stub* | newvar | newvarlist } [if] [in] [, statistic tlevel(treat_level) ]
predict [type] { stub* | newvarlist } [if] [in], scores
```
### statistic Description

<table>
<thead>
<tr>
<th>Statistic</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>te</code></td>
<td>treatment effect; the default</td>
</tr>
<tr>
<td><code>cm</code></td>
<td>conditional mean at treatment level</td>
</tr>
<tr>
<td><code>ps</code></td>
<td>propensity score</td>
</tr>
<tr>
<td><code>xb</code></td>
<td>linear prediction</td>
</tr>
<tr>
<td><code>psxb</code></td>
<td>linear prediction for propensity score</td>
</tr>
<tr>
<td><code>lnsigma</code></td>
<td>log square root of conditional latent variance (for outcome model <code>hetprobit()</code>) at treatment level</td>
</tr>
<tr>
<td><code>pslnsigma</code></td>
<td>log square root of latent variance (for treatment model <code>hetprobit()</code>) for propensity score</td>
</tr>
</tbody>
</table>

If you do not specify `tlevel()` and only specify one new variable, `te` and `psxb` assume `tlevel()` specifies the first noncontrol treatment level.

If you do not specify `tlevel()` and only specify one new variable, `cm`, `ps`, `xb`, and `lnsigma` assume `tlevel()` specifies the first treatment level.

You specify one or \( t \) new variables with `cm`, `ps`, `xb`, and `lnsigma`, where \( t \) is the number of treatment levels.

You specify one or \( t-1 \) new variables with `te`, `psxb`, and `pslnsigma`.

#### Syntax for predict after ipw

```stata
predict [type] {stub* | newvar | newvarlist} [if] [in] [, statistic tlevel(treat_level)]
```

```stata
predict [type] {stub* | newvarlist} [if] [in], scores
```

#### Syntax for predict after nnmatch and psmatch

```stata
predict [type] {stub* | newvarlist} [, statistic tlevel(treat_level)]
```
statistic | Description
--|--
treatment effect; the default
potential outcome
nearest-neighbor distance
propensity score (psmatch only)
log square root of latent variance (for treatment model `hetprobit()`)

These statistics are available for the estimation sample only and require the estimation option `generate(stub)`. This is because of the nonparametric nature of the matching estimator.

If you do not specify `tlevel()` and only specify one new variable, `po` and `ps` assume `tlevel()` specifies the first treatment level.

You specify one new variable with `te` and `lnsigma`.

You specify one or two new variables with `po` and `ps`.

### Syntax for predict after ra

```
predict [type] { stub* | newvar | newvarlist } [if] [in]
  [, statistic tlevel(treat_level) ]

predict [type] { stub* | newvarlist } [if] [in] [, scores]
```

### Options

Options are presented under the following headings:

- **Options for predict after aipw and ipwra**
- **Options for predict after ipw**
- **Options for predict after nnmatch and psmatch**
- **Options for predict after ra**
Options for predict after aipw and ipwra

**Main**

te, the default, calculates the treatment effect for each noncontrol treatment level or the treatment level specified in `tlevel()`. If you specify the `tlevel()` option, you need to specify only one new variable; otherwise, you must specify a new variable for each treatment level (except the control level).

cmean calculates the conditional mean for each treatment level or the treatment level specified in `tlevel()`. If you specify the `tlevel()` option, you need to specify only one new variable; otherwise, you must specify a new variable for each treatment level.

ps calculates the propensity score of each treatment level or the treatment level specified in `tlevel()`. If you specify the `tlevel()` option, you need to specify only one new variable; otherwise, you must specify a new variable for each treatment level.

xb calculates the linear prediction at each treatment level or the treatment level specified in `tlevel()`. If you specify the `tlevel()` option, you need to specify only one new variable; otherwise, you must specify a new variable for each treatment level.

psxb calculates the linear prediction for the propensity score at each noncontrol level of the treatment or the treatment level specified in `tlevel()`. If you specify the `tlevel()` option, you need to specify only one new variable; otherwise, you must specify a new variable for each treatment level (except the control level).

lnsigma calculates the log square root of the conditional latent variance for each treatment level or the treatment level specified in `tlevel()`. This option is valid when outcome model `hetprobit()` was used. If you specify the `tlevel()` option, you need to specify only one new variable; otherwise, you must specify a new variable for each treatment level.

pslnsigma calculates the log square root of the latent variance for the propensity score. This option is only valid when treatment model `hetprobit()` was used. Specify only one new variable.

tlevel(treat_level) specifies the treatment level for prediction.

scores calculates the score variables. Parameter-level scores are computed for the treatment mean and average treatment-effect equations. Equation-level scores are computed for the propensity-score equations.

The $j$th new variable will contain the scores for the $j$th parameter in the coefficient table if $j \leq t$, where $t$ is the number of treatment levels. Otherwise, it will contain the scores for fitted equation $j - t$ following the first $t$ parameters in the coefficient table.

Options for predict after ipw

**Main**

ps, the default, calculates the propensity score of each treatment level or the treatment level specified in `tlevel()`. If you specify the `tlevel()` option, you need to specify only one new variable; otherwise, you must specify a new variable for each treatment level.

xb calculates the linear prediction for the propensity score at each noncontrol level of the treatment or the treatment level specified in `tlevel()`. If you specify the `tlevel()` option, you need to specify only one new variable; otherwise, you must specify a new variable for each treatment level (except the control level).

lnsigma calculates the log square root of the latent variance. This option is only valid when treatment model `hetprobit()` was used. Specify only one new variable.
tlevel(treat_level) specifies the treatment level for prediction.

scores calculates the score variables. Parameter-level scores are computed for the treatment mean and average treatment-effect equations. Equation-level scores are computed for the propensity-score equations.

The \( j \)th new variable will contain the scores for the \( j \)th parameter in the coefficient table if \( j \leq t \), where \( t \) is the number of treatment levels. Otherwise, it will contain the scores for fitted equation \( j - t \) following the first \( t \) parameters in the coefficient table.

Options for predict after nnmatch and psmatch

- **Main**
  - **te**, the default, calculates the treatment effect.
  - **po** calculates the predicted potential outcomes for each observation and treatment level or the treatment level specified in tlevel(). If you specify the tlevel() option, you need to specify only one new variable; otherwise, you must specify new variables for the control and treated groups.
  - **distance** calculates the distances of the nearest neighbors for each observation. The number of variables generated is equal to the maximum number of nearest-neighbor matches. This is equal to the number of index variables generated by the estimation option generate(stub). You may use the stub* syntax to set the distance variable prefix: stub1, stub2, ....
  - **ps** calculates the propensity score of each treatment level or the propensity score of the treatment level specified in tlevel(). If you specify the tlevel() option, you need to specify only one new variable; otherwise, you must specify new variables for the control and treated groups.
  - **lnsigma** calculates the log square root of the latent variance. This option is only valid when treatment model hetprobit() was used. Specify only one new variable.

Options for predict after ra

- **Main**
  - **te**, the default, calculates the treatment effect for each noncontrol treatment level or the treatment level specified in tlevel(). If you specify the tlevel() option, you need to specify only one new variable; otherwise, you must specify a new variable for each treatment level (except the control level).
  - **cmean** calculates the conditional mean for each treatment level or the treatment level specified in tlevel(). If you specify the tlevel() option, you need to specify only one new variable; otherwise, you must specify a new variable for each treatment level.
  - **xb** calculates the linear prediction at each treatment level or the treatment level specified in tlevel(). If you specify the tlevel() option, you need to specify only one new variable; otherwise, you must specify a new variable for each treatment level.
  - **lnsigma** calculates the log square root of the conditional latent variance for each treatment level or the treatment level specified in tlevel(). This option is valid when outcome model hetprobit() was used. If you specify the tlevel() option, you need to specify only one new variable; otherwise, you must specify a new variable for each treatment level.

wlevel(treat_level) specifies the treatment level for prediction.
scores calculates the score variables. Parameter-level scores are computed for the treatment mean and average treatment-effect equations. Equation-level scores are computed for the regression equations.

The \( j \)th new variable will contain the scores for the \( j \)th parameter in the coefficient table if \( j \leq t \), where \( t \) is the number of treatment levels. Otherwise, it will contain the scores for fitted equation \( j - t \) following the first \( t \) parameters in the coefficient table.

### Remarks and examples

Checking model specification is the most frequent reason for postestimation computation after `teffects`. `teffects overlap` provides a graphical method for checking the overlap assumption; see [TE] `teffects overlap`. Summarizing the estimated probabilities provides another check. Recall that the reciprocals of these estimated probabilities are used as weights by some of the estimators. If the estimated probabilities are too small, the weights blow up.

We estimate the ATE of maternal smoking on infant birthweight by inverse-probability weighting; see example 1 of [TE] `teffects ipw` for background.

```stata
. use http://www.stata-press.com/data/r13/cattaneo2
. teffects ipw (bweight) (mbsmoke mmarried c.mage##c.mage fbaby medu, probit)
Iteration 0:   EE criterion =  4.622e-21
Iteration 1:   EE criterion =  8.070e-26
Treatment-effects estimation       Number of obs  =   4642
Estimator : inverse-probability weights
Outcome model : weighted mean
Treatment model: probit

<table>
<thead>
<tr>
<th></th>
<th>Robust</th>
<th></th>
<th></th>
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</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Coef.</td>
<td>Std. Err.</td>
<td>z</td>
<td>P&gt;</td>
<td>z</td>
</tr>
<tr>
<td>ATE</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>mbsmoke</td>
<td>(smoker vs nonsmoker)</td>
<td>-230.6886</td>
<td>25.81524</td>
<td>-8.94</td>
<td>0.000</td>
</tr>
<tr>
<td>POmean</td>
<td>mbsmoke</td>
<td>3403.463</td>
<td>9.571369</td>
<td>355.59</td>
<td>0.000</td>
</tr>
<tr>
<td></td>
<td>nonsmoker</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
```

Note: The table shows the estimated coefficients, standard errors, z-values, p-values, and 95% confidence intervals for the ATE and POmean of maternal smoking on infant birthweight.
Below we compute and summarize the estimated treatment probabilities.

```
. predict pr1
   (option ps assumed; propensity score)
. summarize pr1 if mbsmoke==1, detail
   propensity score, mbsmoke=nonsmoker

Percentiles   Smallest
1%    .2991634    .2196947
5%    .5441550    .2258079
10%   .5973879    .2258079     Obs    864
25%   .6377725    .2409025     Sum of Wgt. 864
50%   .7601717     Mean .7456264
75%   .8453946    .9533503     Largest Std. Dev. .1276102
90%   .8943686    .9561444     Variance .0162844
95%   .9096801    .9610222     Skewness -.7701643
99%   .9367017    .9665684     Kurtosis 3.858214
```

The smallest values do not imply very large weights.

Below we compute and summarize the estimated probabilities of not getting the treatment.

```
. generate pr0 = 1 -pr1
. summarize pr0 if mbsmoke==0, detail
   pr0

Percentiles   Smallest
1%    .0351884    .0074551
5%    .0578012    .0079309
10%   .0674359    .0106305     Obs    3778
25%   .0950869    .0106305     Sum of Wgt. 3778
50%   .1372589     Mean .1698913
75%   .2211142    .7547572     Largest Std. Dev. .1059434
90%   .3242757    .7741922     Variance .011224
95%   .3883457    .7803053     Skewness 1.514456
99%   .5015371    .7816764     Kurtosis 6.151114
```

Although there are two small probabilities, overall the small values do not imply large weights.

Also see

[TE] teffects overlap — Overlap plots
[TE] teffects aipw — Augmented inverse-probability weighting
[TE] teffects ipw — Inverse-probability weighting
[TE] teffects ipwra — Inverse-probability-weighted regression adjustment
[TE] teffects nnmatch — Nearest-neighbor matching
[TE] teffects psmatch — Propensity-score matching
[TE] teffects ra — Regression adjustment
[U] 20 Estimation and postestimation commands