

STATA TREATMENT-EFFECTS REFERENCE MANUAL: POTENTIAL OUTCOMES/COUNTERFACTUAL OUTCOMES RELEASE 16



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Cross-referencing the documentation

When reading this manual, you will find references to other Stata manuals, for example, [U] 27 Overview of Stata estimation commands; [R] regress; and [D] reshape. The first example is a reference to chapter 27, *Overview of Stata estimation commands*, in the *User's Guide*; the second is a reference to the regress entry in the *Base Reference Manual*; and the third is a reference to the reshape entry in the *Data Management Reference Manual*.

All the manuals in the Stata Documentation have a shorthand notation:

[GSM]	Getting Started with Stata for Mac
[GSU]	Getting Started with Stata for Unix
[GSW]	Getting Started with Stata for Windows
[U]	Stata User's Guide
[R]	Stata Base Reference Manual
[BAYES]	Stata Bayesian Analysis Reference Manual
[CM]	Stata Choice Models Reference Manual
[D]	Stata Data Management Reference Manual
[DSGE]	Stata Dynamic Stochastic General Equilibrium Models Reference Manual
[ERM]	Stata Extended Regression Models Reference Manual
[FMM]	Stata Finite Mixture Models Reference Manual
[FN]	Stata Functions Reference Manual
[G]	Stata Graphics Reference Manual
[IRT]	Stata Item Response Theory Reference Manual
[LASSO]	Stata Lasso Reference Manual
[XT]	Stata Longitudinal-Data/Panel-Data Reference Manual
[META]	Stata Meta-Analysis Reference Manual
[ME]	Stata Multilevel Mixed-Effects Reference Manual
[MI]	Stata Multiple-Imputation Reference Manual
[MV]	Stata Multivariate Statistics Reference Manual
[PSS]	Stata Power, Precision, and Sample-Size Reference Manual
[P]	Stata Programming Reference Manual
[RPT]	Stata Reporting Reference Manual
[SP]	Stata Spatial Autoregressive Models Reference Manual
[SEM]	Stata Structural Equation Modeling Reference Manual
[SVY]	Stata Survey Data Reference Manual
[ST]	Stata Survival Analysis Reference Manual
[TS]	Stata Time-Series Reference Manual
[TE]	Stata Treatment-Effects Reference Manual: Potential Outcomes/Counterfactual Outcomes
[I]	Stata Glossary and Index
[M]	Mata Reference Manual

[Intro — Introduction to treatment-effects manual

Description Reference Also see

Description

This manual documents commands for the analysis of treatment effects and is referred to as [TE] in cross-references.

After this entry, [TE] **Treatment effects** provides an overview of the treatment-effects estimation commands. The other parts of this manual are arranged alphabetically. If you are new to Stata's treatment-effects commands, we recommend that you read the following sections first:

- | | |
|--|---|
| [TE] teffects intro | Introduction to treatment effects for observational data |
| [TE] teffects intro advanced | Advanced introduction to treatment effects for observational data |
| [TE] teffects multivalued | Multivalued treatment effects |

If you are interested in survival analysis, we also recommend that you read the following section first:

- | | |
|---------------------------------------|--|
| [TE] stteffects intro | Introduction to treatment effects for observational survival-time data |
|---------------------------------------|--|

Stata is continually being updated, and Stata users are always writing new commands. To find out about the latest treatment-effects features, type **search treatment effects**.

Reference

Andresen, M. E. 2018. Exploring marginal treatment effects: Flexible estimation using Stata. *Stata Journal* 18: 118–158.

Also see

- [\[U\] 1.3 What's new](#)
- [\[R\] Intro —](#) Introduction to base reference manual

Description

This manual documents commands that use observational data to estimate the effect caused by getting one treatment instead of another. In observational data, treatment assignment is not controlled by those who collect the data; thus some common variables affect treatment assignment and treatment-specific outcomes. Observational data is sometimes called retrospective data or nonexperimental data, but to avoid confusion, we will always use the term “observational data”.

When all the variables that affect both treatment assignment and outcomes are observable, the outcomes are said to be conditionally independent of the treatment, and the **teffects** and **stteffects** estimators may be used.

When not all of these variables common to both treatment assignment and outcomes are observable, the outcomes are not conditionally independent of the treatment, and **eteffects**, **etpoisson**, or **etregress** may be used.

teffects and **stteffects** offer much flexibility in estimators and functional forms for the treatment-assignment models. **teffects** provides models for continuous, binary, count, fractional, and nonnegative outcome variables. **stteffects** provides many functional forms for survival-time outcomes. See [\[TE\] teffects intro](#), [\[TE\] teffects intro advanced](#), and [\[TE\] stteffects intro](#) for more information.

eteffects, **etpoisson**, and **etregress** offer less flexibility than **teffects** because more structure must be imposed when conditional independence is not assumed. **eteffects** is for continuous, binary, count, fractional, and nonnegative outcomes and uses a probit model for binary treatments; see [\[TE\] eteffects](#). **etpoisson** is for count outcomes and uses a normal distribution to model treatment assignment; see [\[TE\] etpoisson](#). **etregress** is for linear outcomes and uses a normal distribution to model treatment assignment; see [\[TE\] etregress](#).

Treatment effects

[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

Survival treatment effects

[TE] stteffects ipw	Survival-time inverse-probability weighting
[TE] stteffects ipwra	Survival-time inverse-probability-weighted regression adjustment
[TE] stteffects ra	Survival-time regression adjustment
[TE] stteffects wra	Survival-time weighted regression adjustment

Endogenous treatment effects

[TE] eteffects	Endogenous treatment-effects estimation
[TE] etpoisson	Poisson regression with endogenous treatment effects
[TE] etregress	Linear regression with endogenous treatment effects

Treatment effects with sample selection, endogenous covariates, and random effects

[ERM] egregress	Extended linear regression
[ERM] eintreg	Extended interval regression
[ERM] eprobit	Extended probit regression
[ERM] eoprobit	Extended ordered probit regression

Postestimation tools

[TE] tebalance	Check balance after teffects or stteffects estimation
[TE] tebalance box	Covariate balance box
[TE] tebalance density	Covariate balance density
[TE] tebalance overid	Test for covariate balance
[TE] tebalance summarize	Covariate-balance summary statistics
[TE] teffects overlap	Overlap plots
[TE] eteffects postestimation	Postestimation tools for eteffects
[TE] etpoisson postestimation	Postestimation tools for etpoisson
[TE] etregress postestimation	Postestimation tools for etregress
[TE] stteffects postestimation	Postestimation tools for stteffects

Also see

[U] 1.3 What's new	
[TE] teffects intro	— Introduction to treatment effects for observational data
[TE] teffects intro advanced	— Advanced introduction to treatment effects for observational data
[TE] teffects multivalued	— Multivalued treatment effects
[TE] stteffects intro	— Introduction to treatment effects for observational survival-time data
[TE] Glossary	

eteffects — Endogenous treatment-effects estimation[Description](#)[Options](#)[Acknowledgment](#)[Quick start](#)[Remarks and examples](#)[References](#)[Menu](#)[Stored results](#)[Also see](#)[Syntax](#)[Methods and formulas](#)

Description

`eteffects` estimates the average treatment effect (ATE), the average treatment effect on the treated (ATET), and the potential-outcome means (POMs) from observational data when treatment assignment is correlated with the potential outcomes. It allows for continuous, binary, count, fractional, and nonnegative outcomes and requires a binary treatment. To control for the endogeneity of the treatment assignment, the estimator includes residuals from the treatment model in the models for the potential outcomes, known as a control-function approach.

Quick start

ATE of binary treatment `treat` using a linear model for outcome `y1` on `x` and the residuals from a probit model for `treat` on `x` and `z`

```
eteffects (y1 x) (treat x z)
```

As above, but estimate ATET

```
eteffects (y1 x) (treat x z), atet
```

As above, but estimate POMs

```
eteffects (y1 x) (treat x z), pomeans
```

As above, and show parameters from auxiliary equations

```
eteffects (y1 x) (treat x z), pomeans aequations
```

ATE of `treat` using an exponential-mean model for `y1`

```
eteffects (y1 x, exponential) (treat x z)
```

Same as above, but for count outcome `y2`

```
eteffects (y2 x, exponential) (treat x z)
```

As above, but use a probit model for binary outcome `y3`

```
eteffects (y3 x, probit) (treat x z)
```

As above, but use a fractional probit model for `y4` ranging from 0 to 1

```
eteffects (y4 x, fractional) (treat x z)
```

Menu

Statistics > Treatment effects > Endogenous treatment > Control function estimator > Continuous outcomes

Statistics > Treatment effects > Endogenous treatment > Control function estimator > Binary outcomes

Statistics > Treatment effects > Endogenous treatment > Control function estimator > Count outcomes

Statistics > Treatment effects > Endogenous treatment > Control function estimator > Fractional outcomes

Statistics > Treatment effects > Endogenous treatment > Control function estimator > Nonnegative outcomes

Syntax

```
eteffects (ovar omvarlist [ , omodel noconstant ] )
          (tvar tmvarlist [ , noconstant ]) [if] [in] [weight] [ , stat options ]
```

ovar is the *depyar* of the outcome model.

omvarlist is the list of exogenous *indepvars* in the outcome model.

tvar is the binary treatment variable.

tmvarlist is the list of covariates that predict treatment assignment.

<i>omodel</i>	Description
---------------	-------------

Model

linear	linear outcome model; the default
fractional	fractional probit outcome model
probit	probit outcome model
exponential	exponential-mean outcome model

<i>stat</i>	Description
-------------	-------------

Model

ate	estimate average treatment effect in population; the default
atet	estimate average treatment effect on the treated
pomeans	estimate potential-outcome means

<i>options</i>	Description
----------------	-------------

Model

<u>noconstant</u>	suppress constant term
--------------------------	------------------------

SE/Robust

vce(<i>vcetype</i>)	<i>vcetype</i> may be robust , cluster <i>clustvar</i> , bootstrap , or jackknife
----------------------------	--

Reporting

level(#)	set confidence level; default is level(95)
aequations	display auxiliary-equation results
display_options	control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling

Maximization

maximize_options	control the maximization process; seldom used
-------------------------	---

Advanced

ps tolerance(#)	set tolerance for overlap assumption
osample(<i>newvar</i>)	generate <i>newvar</i> to mark observations that violate the overlap assumption
coeflegend	display legend instead of statistics

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omvarlist and *tmvarlist* may contain factor variables; see [U] 11.4.3 Factor variables.

bootstrap, *by*, *jackknife*, and *statsby* are allowed; see [U] 11.1.10 Prefix commands.

Weights are not allowed with the *bootstrap* prefix; see [R] bootstrap.

fweights, *iweights*, and *pweights* are allowed; see [U] 11.1.6 weight.

coeflegend does not appear in the dialog box.

See [U] 20 Estimation and postestimation commands for more capabilities of estimation commands.

Options

Model

noconstant; see [R] Estimation options.

stat is one of three statistics: *ate*, *atet*, or *pomeans*. *ate* is the default.

ate specifies that the average treatment effect be estimated.

atet specifies that the average treatment effect on the treated be estimated.

pomeans specifies that the potential-outcome means for each treatment level be estimated.

SE/Robust

vce(vcetype) specifies the type of standard error reported, which includes types that are robust to some kinds of misspecification (*robust*), that allow for intragroup correlation (*cluster clustvar*), and that use bootstrap or jackknife methods (*bootstrap*, *jackknife*); see [R] vce_option.

Reporting

level(#); see [R] Estimation options.

aequations specifies that the results for the outcome-model or the treatment-model parameters be displayed. By default, the results for these auxiliary parameters are not displayed.

display_options: *noci*, *nopvalues*, *noomitted*, *vsquish*, *noemptycells*, *baselevels*, *allbaselevels*, *nofvlabel*, *fvwrap(#)*, *fvrapon(style)*, *cformat(%fmt)*, *pformat(%fmt)*, *sformat(%fmt)*, and *nolstretch*; see [R] Estimation options.

Maximization

maximize_options: *iterate(#)*, *[no]log*, and *from(init_specs)*; see [R] Maximize. These options are seldom used.

init_specs is one of

matname [, *skip copy*]

[, # ...] , *copy*

Advanced

pstolerance(#) specifies the tolerance used to check the overlap assumption. The default value is *pstolerance(1e-5)*. *eteffects* will exit with an error if an observation has an estimated propensity score smaller than that specified by *pstolerance()*.

osample(newvar) specifies that indicator variable *newvar* be created to identify observations that violate the overlap assumption.

The following option is available with *eteffects* but is not shown in the dialog box:

coeflegend; see [R] Estimation options.

Remarks and examples

If you are unfamiliar with treatment-effects estimators for observational data or the `teffects` commands, we recommend that you look at [TE] **teffects intro**. For the intuition behind some of the concepts discussed below, we recommend that you read *Defining treatment effects* in [TE] **teffects intro advanced**.

The estimators implemented in `eteffects` extend the regression adjustment (RA) estimators implemented in `teffects ra` to allow for endogenous treatments, that is, when treatment assignment is not independent of outcomes. This endogeneity is a violation of the conditional mean independence assumption used by `teffects ra`, as discussed in *The potential-outcome model* in [TE] **teffects intro advanced**.

`eteffects` estimates the average treatment effect (ATE), the average treatment effect on the treated (ATET), and the potential-outcome means (POMs). It uses a linear, a probit, a fractional probit, or an exponential-mean model for the potential outcomes and a probit model for treatment assignment. After conditioning on the observable covariates, `eteffects` allows some remaining unobservable components to affect both treatment assignment and the potential outcomes. The treatment assignment process is endogenous because these unobservable components affect both treatment assignment and the potential outcomes.

To control for the endogeneity of the treatment assignment, `eteffects` uses a control-function approach. This method controls for endogeneity by including the residuals from the treatment-assignment model as a regressor in the models for the potential outcome. The implementation in `eteffects` follows Wooldridge (2010), who provides an excellent discussion of the control-function approach that addresses endogeneity problems in a treatment-effects context.

The control-function approach estimates the parameters of the conditional means of the potential outcomes. Sample averages of the conditional means are used to estimate the unconditional ATE, ATET, or POMs. This method is known as RA.

Taken collectively, the estimators implemented in `eteffects` are control-function RA estimators. See *Methods and formulas* below for details about the estimation procedure.

▷ Example 1: Linear outcome estimates for ATE

Suppose we want to know the effect of a mother smoking while pregnant on the birthweight of her infant. We use an extract from Cattaneo (2010) in which `bweight` records the baby's birthweight and `mbsmoke` is the variable (0 or 1) indicating whether a mother smoked while pregnant.

We may believe that birthweight (the potential outcome) is influenced by whether the mother had a prenatal exam in the first trimester, whether the mother is married, the mother's age, whether this is the first birth, and the education level of the father. We may also believe that the smoking decision (the treatment) is influenced by the mother's marital status, the education level of the mother, her age, whether she had a prenatal exam in the first trimester, and whether this baby is her first baby.

Thus we condition on different sets of covariates in the models for treatment assignment and the potential outcomes. In the probit model for smoking status (`mbsmoke`), we condition on marital status (`mmarried`), age (`mage`), mother's education level (`medu`), father's education level (`fedu`), and whether it was the mother's first baby (`fbaby`). We model birthweight (`bweight`) as a linear function of whether the mother had a first-trimester prenatal exam (`prenatal1`), `mmarried`, `mage`, and `fbaby`. We can estimate the ATE of smoking status using one of the `teffects` estimators if we believe that there are no unobservable components that affect both the decision to smoke while pregnant and the potential birthweights.

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If we believe there is some unobservable factor that affects both assignment to treatment and the potential outcome, we must select another estimator. For example, we do not observe a mother's health consciousness, which affects both the smoking decision and each potential birthweight through other behaviors such as intake of prenatal vitamins. Under these assumptions, the estimators in `eteffects` consistently estimate the ATE, but the estimators in [TE] `teffects` yield inconsistent estimates.

```
. use https://www.stata-press.com/data/r16/cattaneo2  
(Excerpt from Cattaneo (2010) Journal of Econometrics 155: 138–154)  
. teffects (bweight i.prenatal1 i.mmarried mage i.fbaby)  
> (mbsmoke i.mmarried mage i.fbaby medu fedu)  
Iteration 0: EE criterion = 4.704e-24  
Iteration 1: EE criterion = 1.223e-25  
Endogenous treatment-effects estimation Number of obs = 4,642  
Outcome model : linear  
Treatment model: probit
```

bweight	Coef.	Robust Std. Err.	z	P> z	[95% Conf. Interval]
ATE mbsmoke (smoker vs nonsmoker)	-455.9119	212.4393	-2.15	0.032	-872.2853 -39.53852
P0mean mbsmoke nonsmoker	3437.964	31.21145	110.15	0.000	3376.791 3499.138

When no mother smokes, the average birthweight is 3,438 grams. The average birthweight is 456 grams less when all mothers smoke than when no mother smokes.

We can compare these results with those obtained if we ignore the endogeneity of the smoking decision. Below we estimate the ATE using the inverse-probability-weighted regression-adjustment estimator in [TE] `teffects ipwra`.

```
. teffects ipwra (bweight i.prenatal1 i.mmarried mage i.fbaby)  
> (mbsmoke i.mmarried mage i.fbaby medu fedu)  
Iteration 0: EE criterion = 3.036e-22  
Iteration 1: EE criterion = 3.755e-26  
Treatment-effects estimation Number of obs = 4,642  
Estimator : IPW regression adjustment  
Outcome model : linear  
Treatment model: logit
```

bweight	Coef.	Robust Std. Err.	z	P> z	[95% Conf. Interval]
ATE mbsmoke (smoker vs nonsmoker)	-233.6835	25.07695	-9.32	0.000	-282.8335 -184.5336
P0mean mbsmoke nonsmoker	3403.191	9.529709	357.11	0.000	3384.513 3421.869

In magnitude, the estimated ATE is more than half the estimate that allows for endogenous treatment assignment. If there is endogeneity, disregarding it underestimates the effect of smoking on birthweight. We show how to test for endogeneity in [example 1](#) of [TE] **eteffects postestimation**.



▷ Example 2: Estimating the ATET

Continuing [example 1](#), we can use the `atet` option to estimate the ATET.

```
. eteeffects (bweight i.prenatal1 i.mmarried mage i.fbaby)
> (mbsmoke i.mmarried mage i.fbaby medu fedu), atet
Iteration 0: EE criterion = 4.688e-24
Iteration 1: EE criterion = 8.479e-26
Endogenous treatment-effects estimation      Number of obs      =      4,642
Outcome model : linear
Treatment model: probit
```

bweight	Coef.	Robust Std. Err.	z	P> z	[95% Conf. Interval]
ATET mbsmoke (smoker vs nonsmoker)	-409.8527	161.4816	-2.54	0.011	-726.3507 -93.35466
P0mean mbsmoke nonsmoker	3547.512	160.0595	22.16	0.000	3233.801 3861.223

In the population of mothers who smoke, the average infant birthweight would be 3,548 grams if none of these mothers smoked. For the mothers who smoke, the average infant birthweight is 410 grams less than if none of these mothers smoked.



▷ Example 3: Exponential-mean outcomes

We estimate the ATE of living in an urban area on monthly earnings (`wage`), using a subset of the National Longitudinal Survey in 1980 found in [Wooldridge \(2010\)](#). We assume that once we condition on work experience (`exper`), whether education level attained is college or higher (`college`), and IQ (`iq`), individual wages follow an exponential mean. The variables used to predict residence in an urban area (`urban`) are `college` and whether the respondent's father attained a bachelor's degree or higher (`fcollege`).

```
. use https://www.stata-press.com/data/r16/nlsy80
. eteffects (wage exper iq i.college, exponential nocons)
> (urban i.college fcollege)
Iteration 0: EE criterion = 2.903e-25
Iteration 1: EE criterion = 2.903e-25 (backed up)
Endogenous treatment-effects estimation           Number of obs      =      935
Outcome model : exponential
Treatment model: probit
```

	wage	Robust				
		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ATE						
	urban (1 vs 0)	481.0465	31.74882	15.15	0.000	418.82 543.2731
P0mean						
	urban 0	233.8083	13.51028	17.31	0.000	207.3286 260.288

When everyone lives outside urban areas, wages are \$234 a month on average. Wages are \$481 a month greater, on average, when everyone lives in urban areas. □

Stored results

etoeffects stores the following in `e()`:

Scalars

<code>e(N)</code>	number of observations
<code>e(nj)</code>	number of observations for treatment level j
<code>e(k_eq)</code>	number of equations in <code>e(b)</code>
<code>e(k_levels)</code>	number of levels in treatment variable
<code>e(rank)</code>	rank of <code>e(V)</code>
<code>e(converged)</code>	1 if converged, 0 otherwise

Macros

<code>e(cmd)</code>	etoeffects
<code>e(cmdline)</code>	command as typed
<code>e(depvar)</code>	name of outcome variable
<code>e(tvar)</code>	name of treatment variable
<code>e(omodel)</code>	fractional, linear, probit, or exponential
<code>e(stat)</code>	statistic estimated, ate, atet, or pomeans
<code>e(wtype)</code>	weight type
<code>e(wexp)</code>	weight expression
<code>e(title)</code>	title in estimation output
<code>e(tlevels)</code>	levels of treatment variable
<code>e(vce)</code>	<i>vcetype</i> specified in <code>vce()</code>
<code>e(vcetype)</code>	title used to label Std. Err.
<code>e(properties)</code>	$b V$
<code>e(estat_cmd)</code>	program used to implement <code>estat</code>
<code>e(predict)</code>	program used to implement <code>predict</code>
<code>e(marginsnotok)</code>	predictions disallowed by <code>margins</code>
<code>e(asbalanced)</code>	factor variables <code>fvset</code> as <code>asbalanced</code>
<code>e(asobserved)</code>	factor variables <code>fvset</code> as <code>asobserved</code>

Matrices

<code>e(b)</code>	coefficient vector
<code>e(V)</code>	variance-covariance matrix of the estimators

Functions

<code>e(sample)</code>	marks estimation sample
------------------------	-------------------------

Methods and formulas

The treatment-effects models considered in `eteffects` are given by

$$y_{i0} = E(y_{i0}|\mathbf{x}_i) + \epsilon_{i0} \quad (1)$$

$$y_{i1} = E(y_{i1}|\mathbf{x}_i) + \epsilon_{i1} \quad (2)$$

$$t_i = E(t_i|\mathbf{z}_i) + \nu_i \quad (3)$$

$$y_i = t_i y_{i1} + (1 - t_i) y_{i0} \quad (4)$$

$$E(\epsilon_{ij}|\mathbf{x}_i, \mathbf{z}_i) = E(\epsilon_{ij}|\mathbf{z}_i) = E(\epsilon_{ij}|\mathbf{x}_i) = 0 \quad \text{for } j \in \{0, 1\} \quad (5)$$

$$E(\epsilon_{ij}|t) \neq 0 \quad \text{for } j \in \{0, 1\} \quad (6)$$

where the subscript i denotes individual level observations, y_{i1} is the potential outcome of receiving the treatment, y_{i0} is the potential outcome when the treatment is not received, t_i is the observed binary treatment, and y_i is the observed outcome. Each one of the potential outcomes is determined by its expected value conditional on a set of regressors \mathbf{x}_i and an unobserved random component ϵ_{ij} , for $j \in \{0, 1\}$. Similarly, the treatment is given by its expectation conditional on a set of regressors \mathbf{z}_i , which does not need to differ from \mathbf{x}_i , and an unobserved component ν_i .

Equations (1)–(5) describe the parametric treatment-effects models in [TE] `teffects`. Equation (6) adds endogeneity to the framework. It states that the unobservables in the potential-outcome equations are correlated to treatment status. For our birthweight example, this would happen if mothers who do not smoke are more health conscious than those who smoke and if we do not observe health awareness in our data. If we do not observe health awareness, the decision to smoke or not to smoke is not independent of the infant's birthweight.

Equations (3), (5), and (6) are the basis of the control-function estimator implemented by `eteffects`. Equation (5) states that the unobserved components in the potential outcome are independent of \mathbf{z}_i . Therefore, the correlation between t_i and the unobserved components must be equivalent to the correlation between ϵ_{ij} and ν_i . Another way of stating this is

from (3)

$$E(\epsilon_{ij}|t_i) = E(\epsilon_{ij}|E(t|\mathbf{z}_i) + \nu_i)$$

from (5)

$$= E(\epsilon_{ij}|\nu_i)$$

$$= \nu_i \beta_{2j}$$

We fit (3) using a probit estimator. We then obtain $\hat{\nu}_i$ as the difference between the treatment and our estimate of $E(t_i|\mathbf{z}_i)$ and use this statistic to compute an estimate of $E(y_{ij}|\mathbf{x}_i, \nu_i, t_i)$ for $j \in \{0, 1\}$. If the outcome is linear, for instance,

$$E(y_{ij}|\mathbf{x}_i, \nu_i, t_i = j) = \mathbf{x}'_i \beta_{1j} + \nu_i \beta_{2j} \quad \text{for } j \in \{0, 1\} \quad (7)$$

For the probit and exponential-mean cases, respectively, we have the following:

$$E(y_{ij} | \mathbf{x}_i, \nu_i, t_i = j) = \Phi(\mathbf{x}'_i \boldsymbol{\beta}_{1j} + \nu_i \boldsymbol{\beta}_{2j}) \quad (8)$$

$$E(y_{ij} | \mathbf{x}_i, \nu_i, t_i = j) = \exp(\mathbf{x}'_i \boldsymbol{\beta}_{1j} + \nu_i \boldsymbol{\beta}_{2j}) \quad (9)$$

The parameters of (3) and (7)–(9), and the ATE, ATET, and POMs are estimated using the generalized method of moments (GMM). The moment equations used in GMM are the sample analogs of $E\{\mathbf{w}'_i \epsilon_i(\theta)\} = 0$, where \mathbf{w}_i are the instruments, $\epsilon_i(\theta)$ are residuals, and θ are the parameters of the model (see [R] gmm). The moment conditions in the GMM estimation for the linear model are given by

$$\frac{1}{n} \sum_{i=1}^n \mathbf{x}'_i (y_i - \mathbf{x}'_i \hat{\boldsymbol{\beta}}_{1j} + \hat{\nu}_i \hat{\boldsymbol{\beta}}_{2j}) t_i = 0 \quad (10)$$

$$\frac{1}{n} \sum_{i=1}^n \mathbf{x}'_i (y_i - \mathbf{x}'_i \hat{\boldsymbol{\beta}}_{1j} + \hat{\nu}_i \hat{\boldsymbol{\beta}}_{2j})(1 - t_i) = 0 \quad (11)$$

$$\frac{1}{n} \sum_{i=1}^n \mathbf{z}'_i \left\{ t_i \frac{\phi(\mathbf{z}'_i \hat{\pi})}{\Phi(\mathbf{z}'_i \hat{\pi})} - (1 - t_i) \frac{\phi(\mathbf{z}'_i \hat{\pi})}{1 - \Phi(\mathbf{z}'_i \hat{\pi})} \right\} = 0 \quad (12)$$

$$\frac{1}{n} \sum_{i=1}^n \left\{ (\mathbf{x}'_i \hat{\boldsymbol{\beta}}_{10} + \hat{\nu}_i \hat{\boldsymbol{\beta}}_{20}) - \widehat{\text{POM0}} \right\} = 0 \quad (13)$$

$$\frac{1}{n} \sum_{i=1}^n \left\{ (\mathbf{x}'_i \hat{\boldsymbol{\beta}}_{11} + \hat{\nu}_i \hat{\boldsymbol{\beta}}_{21}) - \widehat{\text{POM0}} - \widehat{\text{ATE}} \right\} = 0 \quad (14)$$

where $\hat{\nu}_i = t_i - \Phi(\mathbf{z}'_i \hat{\pi})$, n is the number of observations, and $\hat{\boldsymbol{\beta}}_{11}, \hat{\boldsymbol{\beta}}_{10}, \hat{\boldsymbol{\beta}}_{21}, \hat{\boldsymbol{\beta}}_{20}, \hat{\pi}, \widehat{\text{ATE}}$, and $\widehat{\text{POM0}}$ are the parameters. If we want to estimate the ATET, we replace (14) with

$$\frac{1}{n} \sum_{i=1}^n \left\{ (\mathbf{x}'_i \hat{\boldsymbol{\beta}}_{11} + \hat{\nu}_i \hat{\boldsymbol{\beta}}_{21}) \frac{n}{n_t} - \widehat{\text{POM0}} \frac{n}{n_t} - \widehat{\text{ATET}} \right\} = 0 \quad (15)$$

and if we want to estimate the potential-outcome means, we replace (14) with

$$\frac{1}{n} \sum_{i=1}^n \left\{ (\mathbf{x}'_i \hat{\boldsymbol{\beta}}_{11} + \hat{\nu}_i \hat{\boldsymbol{\beta}}_{21}) - \widehat{\text{POM1}} \right\} = 0 \quad (16)$$

where $\widehat{\text{ATET}}$ and $\widehat{\text{POM1}}$ are the parameters of the model, and n_t is the number of treated units.

For the exponential-mean outcome model, we replace $\mathbf{x}'_i \hat{\beta}_{1j} + \hat{\nu}_i \hat{\beta}_{2j}$ with $\exp(\mathbf{x}'_i \hat{\beta}_{1j} + \hat{\nu}_i \hat{\beta}_{2j})$ to obtain the residual equations in (10)–(16). For the probit outcome model, we replace (10) and (11) with the following:

$$\frac{1}{n} \sum_{i=1}^n t_i \mathbf{x}'_i \left\{ y_i \frac{\phi(\mathbf{x}'_i \hat{\beta}_{1j} + \hat{\nu}_i \hat{\beta}_{2j})}{\Phi(\mathbf{x}'_i \hat{\beta}_{1j} + \hat{\nu}_i \hat{\beta}_{2j})} - (1 - y_i) \frac{\phi(\mathbf{x}'_i \hat{\beta}_{1j} + \hat{\nu}_i \hat{\beta}_{2j})}{1 - \Phi(\mathbf{x}'_i \hat{\beta}_{1j} + \hat{\nu}_i \hat{\beta}_{2j})} \right\} = 0$$

$$\frac{1}{n} \sum_{i=1}^n (1 - t_i) \mathbf{x}'_i \left\{ y_i \frac{\phi(\mathbf{x}'_i \hat{\beta}_{1j} + \hat{\nu}_i \hat{\beta}_{2j})}{\Phi(\mathbf{x}'_i \hat{\beta}_{1j} + \hat{\nu}_i \hat{\beta}_{2j})} - (1 - y_i) \frac{\phi(\mathbf{x}'_i \hat{\beta}_{1j} + \hat{\nu}_i \hat{\beta}_{2j})}{1 - \Phi(\mathbf{x}'_i \hat{\beta}_{1j} + \hat{\nu}_i \hat{\beta}_{2j})} \right\} = 0$$

For the remaining equations, $\mathbf{x}'_i \hat{\beta}_{1j} + \hat{\nu}_i \hat{\beta}_{2j}$ is replaced with $\Phi(\mathbf{x}'_i \hat{\beta}_{1j} + \hat{\nu}_i \hat{\beta}_{2j})$. The fractional probit model uses the same moment conditions as the probit model.

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Also see

- [TE] **eteffects postestimation** — Postestimation tools for eteeffects
- [TE] **etregress** — Linear regression with endogenous treatment effects
- [TE] **teffects** — Treatment-effects estimation for observational data
- [R] **gmm** — Generalized method of moments estimation
- [R] **probit** — Probit regression
- [R] **regress** — Linear regression
- [U] **20 Estimation and postestimation commands**

eteffects postestimation — Postestimation tools for eteffects

Postestimation commands predict estat Remarks and examples Also see

Postestimation commands

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

Command	Description
---------	-------------

estat endogenous perform tests of endogeneity

The following standard postestimation commands are available after **eteffects**:

Command	Description
---------	-------------

estat summarize	summary statistics for the estimation sample
estat vce	variance–covariance matrix of the estimators (VCE)
estimates	cataloging estimation results
hausman	Hausman’s specification test
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

predict

Description for predict

predict creates a new variable containing predictions such as treatment effects, conditional means, propensity scores, and linear predictions.

Menu for predict

Statistics > Postestimation

Syntax for predict

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

statistic	Description
<hr/>	
Main	
<code>te</code>	treatment effect; the default
<code>cmean</code>	conditional mean at treatment level
<code>ps</code>	propensity score
<code>xb</code>	linear prediction
<code>psxb</code>	linear prediction for propensity score
<code>xbtot</code>	linear prediction, using residuals from treatment model
<code>scores</code>	parameter-level or equation-level scores

Specify one new variable with `te`; specify one or two new variables with `cmean`, `ps`, and `xb`.

Options for predict

Main

`te`, the default, calculates the treatment effect.

`cmean` calculates the conditional mean for the control group. To also obtain the conditional mean for the treatment group, specify two variables. If you want the conditional mean for only the treatment group, specify the `tlevel` option.

`ps` calculates the probability of being in the control group. To also obtain the probability of being in the treatment group, specify two variables. If you want the probability of being in the treatment group only, specify the `tlevel` option.

`xb` calculates the linear prediction for the control group. To also obtain the linear prediction for the treatment group, specify two variables. If you want the linear prediction for only the treatment group, specify the `tlevel` option.

`psxb` calculates the linear prediction for the propensity score.

`xbtot` calculates the linear prediction for the control group, including the residuals from the treatment model as regressors. To also obtain the linear prediction for the treatment group, specify two variables. If you want the linear prediction, including the residuals from the treatment model as regressors, only for the treatment group, specify the `tlevel` option.

`tlevel` specifies that the statistic be calculated for the treatment group; the default is to calculate the statistic for the control group.

`scores` calculates the score variables. For `eteffects`, this is the same as the residuals in the moment conditions used by the generalized method of moments (see [R] `gmm`). For the average treatment effect, the average treatment effect on the treated, and the potential-outcome means, parameter-level scores are computed. For the auxiliary equations, equation-level scores are computed.

estat

Description for estat

estat endogenous performs a Wald test to determine whether the estimated correlations between the treatment-assignment and potential-outcome models are different from zero. The null hypothesis is that the correlations are jointly zero. Rejection of the null hypothesis suggests endogeneity.

Menu for estat

Statistics > Postestimation

Syntax for estat

estat endogenous

Remarks and examples

▷ Example 1: Testing for endogeneity

In example 3 of [TE] **eteffects**, endogeneity could arise if unobservable factors that determine wages are correlated with the decision to live in an urban area. If there is no endogeneity, we would prefer to use one of the **teffects** estimators because they will give us the more efficient standard errors. The control-function approach used by **eteffects** allows us to test for endogeneity.

The control-function approach estimates the correlation between the unobservables of the treatment-assignment and potential-outcome models. If there is no correlation between the unobservables, then there is no endogeneity. We test for correlation, and thus for endogeneity, by typing

```
. use https://www.stata-press.com/data/r16/nlsy80  
. eteffects (wage exper iq i.college, exponential nocons)  
> (urban i.college fcollege)  
    (output omitted)  
. estat endogenous  
Test of endogeneity  
Ho: treatment and outcome unobservables are uncorrelated  
    chi2( 2) = 275.36  
    Prob > chi2 = 0.0000
```

We reject the null hypothesis of no endogeneity. This suggests that unobservable factors that determine wages mediate the decision to live in an urban area.



□ Technical note

The estimated correlations between the unobservables of the treatment-assignment and potential-outcome models are auxiliary parameters. They appear under the headings **TEOM0** and **TEOM1**, which refer to treatment residuals (TE) for outcome model 0 (OM0) and outcome model 1 (OM1), when the option **aequations** is specified.

For the model in [example 3](#) of [TE] **eteffects** with the `aequations` option, the results are the following:

		Robust		Number of obs = 935		
	wage	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ATE						
urban						
(1 vs 0)	481.0465	31.74882	15.15	0.000	418.82	543.2731
P0mean						
urban						
0	233.8083	13.51028	17.31	0.000	207.3286	260.288
TME1						
college						
1	.195811	.1012119	1.93	0.053	-.0025607	.3941827
fcollege						
_cons	.1069748	.0992075	1.08	0.281	-.0874683	.3014179
_cons	.498012	.056408	8.83	0.000	.3874543	.6085698
OME0						
exper						
iq	.0193244	.0085633	2.26	0.024	.0025405	.0361082
iq	.0099473	.0036949	2.69	0.007	.0027053	.0171892
college						
1	-.3718598	.2678636	-1.39	0.165	-.8968629	.1531433
OME1						
exper						
iq	.0238566	.017597	1.36	0.175	-.0106329	.058346
iq	.0148581	.0113311	1.31	0.190	-.0073505	.0370667
college						
1	1.236947	.6401383	1.93	0.053	-.0177013	2.491595
TEOM0						
_cons	-7.771932	.6406251	-12.13	0.000	-9.027534	-6.51633
TEOM1						
_cons	16.7739	4.777519	3.51	0.000	7.410131	26.13766

Among other things, we can use these correlations to test the joint significance of the coefficients on the residuals from the treatment-assignment models. This is equivalent to the endogeneity test in [example 1](#). We type

```
. test [TEOM0]_cons [TEOM1]_cons
( 1) [TEOM0]_cons = 0
( 2) [TEOM1]_cons = 0
      chi2( 2) = 275.36
      Prob > chi2 = 0.0000
```



Also see

[TE] **eteffects** — Endogenous treatment-effects estimation

[U] **20 Estimation and postestimation commands**

etpoisson — Poisson regression with endogenous treatment effects

Description	Quick start	Menu	Syntax
Options	Remarks and examples	Stored results	Methods and formulas
References	Also see		

Description

`etpoisson` estimates the parameters of a Poisson regression model in which one of the regressors is an endogenous binary treatment. Both the average treatment effect and the average treatment effect on the treated can be estimated with `etpoisson`.

Quick start

Poisson model of `y` on `x` and endogenous binary treatment `treat` modeled by `x` and `w`

```
etpoisson y x, treat(treat = x w)
```

With robust standard errors

```
etpoisson y x, treat(treat = x w) vce(robust)
```

Average treatment effect after `etpoisson` with the required `vce(robust)` option

```
margins r.treat, vce(unconditional)
```

As above, but calculate average treatment effect on the treated

```
margins, vce(unconditional) predict(cte) subpop(if treat==1)
```

Menu

Statistics > Treatment effects > Endogenous treatment > Maximum likelihood estimator > Count outcomes

Syntax

etpoisson *depvar* [*indepvars*] [*if*] [*in*] [*weight*] ,
treat(*depvar_t* = *indepvar_t* [, noconstant offset(*varname_o*)]) [*options*]

<i>options</i>	Description
Model	
* <u><i>treat()</i></u>	equation for treatment effects
<u><i>noconstant</i></u>	suppress constant term
<u><i>exposure</i>(<i>varname_e</i>)</u>	include $\ln(varname_e)$ in model with coefficient constrained to 1
<u><i>offset</i>(<i>varname_o</i>)</u>	include <i>varname_o</i> in model with coefficient constrained to 1
<u><i>constraints</i>(<i>constraints</i>)</u>	apply specified linear constraints
SE/Robust	
<u>vce</u> (<i>vcetype</i>)	<i>vcetype</i> may be <i>oim</i> , <u>robust</u> , <u>cluster</u> <i>clustvar</i> , <i>opg</i> , <u>bootstrap</u> , or <u>jackknife</u>
Reporting	
<u><i>level</i>(#)</u>	set confidence level; default is <i>level</i> (95)
<u><i>irr</i></u>	report incidence-rate ratios
<u><i>nocnsreport</i></u>	do not display constraints
<u><i>display_options</i></u>	control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling
Integration	
<u><i>intpoints</i>(#)</u>	use # Gauss–Hermite quadrature points; default is <i>intpoints</i> (24)
Maximization	
<u><i>maximize_options</i></u>	control the maximization process; seldom used
<u><i>collinear</i></u>	keep collinear variables
<u><i>coeflegend</i></u>	display legend instead of statistics

**treat()* is required.

The full specification is *treat*(*depvar_t* = *indepvar_t* [, noconstant offset(*varname_o*)]).

indepvars and *indepvar_t* may contain factor variables; see [\[U\] 11.4.3 Factor variables](#).

depvar, *depvar_t*, *indepvars*, and *indepvar_t* may contain time-series operators; see [\[U\] 11.4.4 Time-series varlists](#).

bootstrap, *by*, *jackknife*, *rolling*, *statsby*, and *svy* are allowed; see [\[U\] 11.1.10 Prefix commands](#).

Weights are not allowed with the *bootstrap* prefix; see [\[R\] bootstrap](#).

aweights are not allowed with the *jackknife* prefix; see [\[R\] jackknife](#).

vce() and weights are not allowed with the *svy* prefix; see [\[SVY\] svy](#).

fweights, *aweights*, *iweights*, and *pweights* are allowed; see [\[U\] 11.1.6 weight](#).

collinear and *coeflegend* do not appear in the dialog box.

See [\[U\] 20 Estimation and postestimation commands](#) for more capabilities of estimation commands.

Options

Model

`treat(depvart = indepvarst [, noconstant offset(varnameo)])` specifies the variables and options for the treatment equation. It is an integral part of specifying a treatment-effects model and is required.

The indicator of treatment, `depvart`, should be coded as 0 or 1.

`noconstant`, `exposure(varnamee)`, `offset(varnameo)`, `constraints(constraints)`; see [R] [Estimation options](#).

SE/Robust

`vce(vcetype)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory (oim, opg), that are robust to some kinds of misspecification (robust), that allow for intragroup correlation (`cluster clustvar`), and that use bootstrap or jackknife methods (bootstrap, jackknife); see [R] [vce_option](#).

Reporting

`level(#)`; see [R] [Estimation options](#).

`irr` reports estimated coefficients transformed to incidence-rate ratios, that is, e^{β_i} rather than β_i . Standard errors and confidence intervals are similarly transformed. This option affects how results are displayed, not how they are estimated or stored. `irr` may be specified at estimation or when replaying previously estimated results.

`nocnsreport`; see [R] [Estimation options](#).

`display_options`: `noci`, `nopvalues`, `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `nofvlabel`, `fwwrap(#)`, `fvwrapon(style)`, `cformat(%fmt)`, `pformat(%fmt)`, `sformat(%fmt)`, and `nolstretch`; see [R] [Estimation options](#).

Integration

`intpoints(#)` specifies the number of integration points to use for integration by quadrature. The default is `intpoints(24)`; the maximum is `intpoints(128)`. Increasing this value improves the accuracy but also increases computation time. Computation time is roughly proportional to its value.

Maximization

`maximize_options`: `difficult`, `technique(algorithm_spec)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `nrtolerance(#)`, `nonrtolerance`, and `from(init_specs)`; see [R] [Maximize](#). These options are seldom used.

Setting the optimization type to `technique(bhhh)` resets the default `vcetype` to `vce(opg)`.

The following options are available with `etpoisson` but are not shown in the dialog box:
`collinear`, `coeflegend`; see [R] [Estimation options](#).

Remarks and examples

Remarks are presented under the following headings:

[Overview](#)

[Basic example](#)

[Average treatment effect \(ATE\)](#)

[Average treatment effect on the treated \(ATET\)](#)

Overview

`etpoisson` estimates the parameters of a Poisson regression model that includes an endogenous binary-treatment variable. The dependent variable must be a Poisson distributed count. The parameters estimated by `etpoisson` can be used to estimate the average treatment effect (ATE) and average treatment effect on the treated (ATET).

We call the model fit by `etpoisson` an endogenous treatment-regression model, although it is also known as an endogenous binary-variable model or as an endogenous dummy-variable model. The endogenous treatment-regression model fit by `etpoisson` is a specific endogenous treatment-effects model; it uses a nonlinear model for the outcome and a constrained normal distribution to model the deviation from the conditional independence assumption imposed by the estimators implemented by `teffects`; see [TE] [teffects intro](#). In treatment-effects jargon, the endogenous binary-variable model fit by `etpoisson` is a nonlinear potential-outcome model that allows for a specific correlation structure between the unobservables that affect the treatment and the unobservables that affect the potential outcomes. See [TE] [etregress](#) for an estimator that allows for a linear-outcome model and a similar model for the endogeneity of the treatment.

More formally, we have an equation for outcome y_j and an equation for treatment t_j :

$$E(y_j | \mathbf{x}_j, t_j, \epsilon_j) = \exp(\mathbf{x}_j \boldsymbol{\beta} + \delta t_j + \epsilon_j)$$
$$t_j = \begin{cases} 1, & \mathbf{w}_j \boldsymbol{\gamma} + u_j > 0 \\ 0, & \text{otherwise} \end{cases}$$

The \mathbf{x}_j are the covariates used to model the outcome, \mathbf{w}_j are the covariates used to model treatment assignment, and error terms ϵ_j and u_j are bivariate normal with mean 0 and covariance matrix

$$\begin{bmatrix} \sigma^2 & \sigma\rho \\ \sigma\rho & 1 \end{bmatrix}$$

The covariates \mathbf{x}_j and \mathbf{w}_j are unrelated to the error terms; in other words, they are exogenous. Note that y_j may be a count or continuous and nonnegative in this specification.

Terza (1998) describes the maximum likelihood estimator used in `etpoisson`. Terza (1998) categorized the model fit by `etpoisson` as an endogenous-switching model. These models involve a binary switch that is endogenous for the outcome. Calculation of the maximum likelihood estimate involves numeric approximation of integrals via Gauss–Hermite quadrature. This is computationally intensive, but the computational costs are reasonable on modern computers.

Basic example

▷ Example 1

In this example, we observe a simulated random sample of 5,000 households. The outcome of interest is the number of trips taken by members of the household in the 24-hour period immediately prior to the interview time.

We have fictional household level data on the following variables: number of trips taken in the past 24 hours (`trips`), distance to the central business district from the household (`cbd`), distance from the household to a public transit node (`ptn`), an indicator of whether there is a full-time worker in the household (`worker`), an indicator of whether the examined period is on a weekend (`weekend`), the ratio of the household income to the median income of the census tract (`realinc`), and an indicator of car ownership (`owncar`). We suspect that unobservables that affect the number of trips also affect the household's propensity to own a car.

We use `etpoisson` to estimate the parameters of a Poisson regression model for the number of trips with car ownership as an endogenous treatment. In subsequent examples, we will use `margins` (see [R] `margins`) to estimate the ATE and the ATET of car ownership on the number of trips taken by the household. In the `etpoisson` command below, we specify the `vce(robust)` option because we need to specify `vce(unconditional)` when we use `margins` later.

```
. use https://www.stata-press.com/data/r16/trip1
(Household trips, car ownership)

. etpoisson trips cbd ptn worker weekend,
> treat(owncar = cbd ptn worker realinc) vce(robust)

Iteration 0: log pseudolikelihood = -14845.147 (not concave)
Iteration 1: log pseudolikelihood = -14562.997 (not concave)
Iteration 2: log pseudolikelihood = -13655.592 (not concave)
Iteration 3: log pseudolikelihood = -12847.219 (not concave)
Iteration 4: log pseudolikelihood = -12566.037
Iteration 5: log pseudolikelihood = -12440.974
Iteration 6: log pseudolikelihood = -12413.485
Iteration 7: log pseudolikelihood = -12412.699
Iteration 8: log pseudolikelihood = -12412.696
Iteration 9: log pseudolikelihood = -12412.696

Poisson regression with endogenous treatment      Number of obs      =      5,000
(24 quadrature points)                          Wald chi2(5)       =     397.94
Log pseudolikelihood = -12412.696               Prob > chi2        =     0.0000
```

	Robust					
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
trips	cbd	-.0100919	.0020071	-5.03	0.000	-.0140258 -.006158
	ptn	-.0204038	.0020289	-10.06	0.000	-.0243805 -.0164272
	worker	.692301	.0548559	12.62	0.000	.5847854 .7998166
	weekend	.0930517	.0345538	2.69	0.007	.0253585 .160745
	1.owncar	.5264713	.1124157	4.68	0.000	.3061406 .746802
	_cons	-.2340772	.0810812	-2.89	0.004	-.3929934 -.0751609
owncar	cbd	.007218	.00239	3.02	0.003	.0025337 .0119023
	ptn	.0084769	.0024518	3.46	0.001	.0036714 .0132824
	worker	.543643	.0504267	10.78	0.000	.4448085 .6424774
	realinc	.176479	.0108746	16.23	0.000	.1551652 .1977928
	_cons	-.4611246	.0592161	-7.79	0.000	-.5771859 -.3450633
/athrho	/lnsigma	.5741169	.0957832	5.99	0.000	.3863852 .7618486
		-.2182037	.0256281	-8.51	0.000	-.2684338 -.1679735
	rho	.5183763	.0700449			.3682398 .6421645
	sigma	.8039617	.020604			.764576 .8453762

Wald test of indep. eqns. (rho = 0): chi2(1) = 35.93 Prob > chi2 = 0.0000

The Wald test in the header is highly significant, indicating a good model fit. All the covariates are statistically significant, and the Wald test in the footer indicates that we can reject the null hypothesis of no correlation between the treatment errors and the outcome errors.

We can interpret the coefficient on 1.owncar as the logarithm of the ratio of the treatment potential-outcome mean to the control potential-outcome mean. The treatment variable did not interact with any of the outcome covariates, so the effect of each regressor is the same in the two regimes and will cancel from the ratio of potential-outcome means. This means the ratio is equivalent to the exponentiated coefficient on 1.owncar. After discussing the other parameters, we will use lincom to obtain this ratio. See [R] lincom for more information.

The estimated correlation between the treatment-assignment errors and the outcome errors is 0.518, indicating that unobservables that increase the number of trips tend to occur with unobservables that increase the chance of car ownership.

The results for the two ancillary parameters require explanation. `etpoisson` estimates the inverse hyperbolic tangent of ρ ,

$$\operatorname{atanh} \rho = \frac{1}{2} \ln \left(\frac{1 + \rho}{1 - \rho} \right)$$

and $\ln\sigma$ rather than ρ and σ . For numerical stability during optimization, `etpoisson` does not directly estimate ρ and σ .

Now we use `lincom` and the `eform` option to estimate the exponentiated coefficient for `1.owncar`. This corresponds to the ratio of the treatment regime potential-outcome mean to the control regime potential-outcome mean.

```
. lincom [trips]_b[1.owncar], eform
( 1) [trips]1.owncar = 0
```

	exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]
(1)	1.692948	.1903139	4.68	0.000	1.358173 2.110241

The potential-outcome mean for the treatment regime is 1.69 times the potential-outcome mean for the control regime. So the average number of trips in the treatment regime is over one and a half times the average number of trips in the control regime.

By interacting the treatment, `owncar`, with the other regressors, we could estimate different coefficients for the regressors in the treatment and control regimes. In the current model, there are no treatment interactions, so the coefficients are the same in each regime.



Average treatment effect (ATE)

The parameter estimates from `etpoisson` can be used by `margins` to estimate the ATE, the average difference of the treatment and control potential outcomes.

▷ Example 2

Continuing with [example 1](#), we use `margins` to estimate the ATE of car ownership on the number of trips taken in a 24-hour period.

We can estimate the ATE of car ownership by using the potential-outcome means obtained through the `predict`, `pomean` command and the `margins` command; see [Methods and formulas](#) below and [\[TE\] etpoisson postestimation](#) for more details about the use of `predict` after `etpoisson`.

The `r.` notation indicates that the potential-outcome means for treatment and control will be contrasted. We specify the `contrast(nowald)` option to suppress the Wald tests that `margins` displays by default for contrasts.

<code>. margins r.owncar, vce(unconditional) contrast(nowald)</code>				
Contrasts of predictive margins			Number of obs	= 5,000
Expression	: Potential-outcome mean, <code>predict()</code>			
	Unconditional			
	Contrast	Std. Err.	[95% Conf. Interval]	
owncar (1 vs 0)	1.058914	.1922909	.6820309 1.435797	

The estimated ATE of car ownership on the number of trips taken is 1.06. The average household will take 1.06 more trips when it owns a car.



Average treatment effect on the treated (ATET)

The parameter estimates from **etpoisson** can be used by **margins** to estimate the ATET, the average difference of the treatment and control potential outcomes in the treated population.

▷ Example 3

Continuing with the [previous example](#), we use **margins** to estimate the ATET of car ownership on the number of trips taken in a 24-hour period.

We can estimate the ATET of car ownership by using the conditional treatment effect (conditional on exogenous covariates and treatment level) obtained through the **predict**, **cte** command and the **margins** command; see [Methods and formulas](#) below and [\[TE\] etpoisson postestimation](#) for more details about the use of **predict** after **etpoisson**.

We estimate the ATET with **margins**. We specify **cte** in the **predict()** option. Estimation is restricted to the treated subpopulation by specifying **owncar** in the **subpop()** option.

. margins, predict(cte) vce(unconditional) subpop(owncar)									
Predictive margins		Number of obs = 5,000							
		Subpop. no. obs = 3,504							
Expression : Conditional treatment effect, predict(cte)									
	Unconditional								
	Margin	Std. Err.	z	P> z	[95% Conf. Interval]				
_cons	1.251971	.2059201	6.08	0.000	.8483747 1.655567				

The estimated ATET of car ownership on the number of trips taken is 1.25. Thus the average household in the treated population will take 1.25 more trips than it would if it did not own a car. This number is higher than the ATE. In this model, the ATE and ATET will only coincide when there is no correlation between the treatment errors and outcome errors and the exogenous covariates **x** have the same distribution in the general population and treated subpopulation. See [Methods and formulas](#) for more details.



Stored results

`etpoisson` stores the following in `e()`:

Scalars

<code>e(N)</code>	number of observations
<code>e(k)</code>	number of parameters
<code>e(k_eq)</code>	number of equations in <code>e(b)</code>
<code>e(k_eq_model)</code>	number of equations in overall model test
<code>e(k_aux)</code>	number of auxiliary parameters
<code>e(k_dv)</code>	number of dependent variables
<code>e(df_m)</code>	model degrees of freedom
<code>e(l1)</code>	log likelihood
<code>e(N_clust)</code>	number of clusters
<code>e(chi2)</code>	χ^2
<code>e(chi2_c)</code>	χ^2 for comparison, $\rho=0$ test
<code>e(n_quad)</code>	number of quadrature points
<code>e(p)</code>	<i>p</i> -value for model test
<code>e(p_c)</code>	<i>p</i> -value for comparison test
<code>e(rank)</code>	rank of <code>e(V)</code>
<code>e(ic)</code>	number of iterations
<code>e(rc)</code>	return code
<code>e(converged)</code>	1 if converged, 0 otherwise

Macros

<code>e(cmd)</code>	<code>etpoisson</code>
<code>e(cmdline)</code>	command as typed
<code>e(depvar)</code>	name of dependent variable
<code>e(wtype)</code>	weight type
<code>e(wexp)</code>	weight expression
<code>e(title)</code>	title in estimation output
<code>e(title2)</code>	secondary title in estimation output
<code>e(clustvar)</code>	name of cluster variable
<code>e(offset1)</code>	offset for regression equation
<code>e(offset2)</code>	offset for treatment equation
<code>e(chi2type)</code>	Wald; type of model χ^2 test
<code>e(chi2_ct)</code>	Wald; type of comparison χ^2 test
<code>e(vce)</code>	<i>vcetype</i> specified in <code>vce()</code>
<code>e(vcetype)</code>	title used to label Std. Err.
<code>e(opt)</code>	type of optimization
<code>e(which)</code>	max or min; whether optimizer is to perform maximization or minimization
<code>e(ml_method)</code>	type of <code>ml</code> method
<code>e(user)</code>	name of likelihood-evaluator program
<code>e(technique)</code>	maximization technique
<code>e(properties)</code>	b V
<code>e(predict)</code>	program used to implement <code>predict</code>
<code>e(marginsok)</code>	predictions allowed by <code>margins</code>
<code>e(asbalanced)</code>	factor variables <code>fvset</code> as <code>asbalanced</code>
<code>e(asobserved)</code>	factor variables <code>fvset</code> as <code>asobserved</code>

Matrices

<code>e(b)</code>	coefficient vector
<code>e(Cns)</code>	constraints matrix
<code>e(ilog)</code>	iteration log (up to 20 iterations)
<code>e(gradient)</code>	gradient vector
<code>e(V)</code>	variance-covariance matrix of the estimators
<code>e(V_modelbased)</code>	model-based variance

Functions

<code>e(sample)</code>	marks estimation sample
------------------------	-------------------------

Methods and formulas

Terza (1998) derives the maximum likelihood estimator implemented here. We provide some details of the derivation and then explain how the model is nested in a more general potential-outcomes model. Then the ATE and ATET are derived.

Let \mathbf{x}_j be the covariates used to model the outcome, and let \mathbf{w}_j be the covariates used to model treatment assignment. Define $\mathbf{z}_j = (\mathbf{w}_j, \mathbf{x}_j)$. The vector \mathbf{z}_j contains all the exogenous covariates in the model. When offsets o_j^β are used in the outcome variable equation, the following formulas apply with $\mathbf{x}_j\beta$ changed to $\mathbf{x}_j\beta + o_j^\beta$. Similarly, when offsets o_j^γ are used in the endogenous treatment equation, the following formulas apply with $\mathbf{w}_j\gamma$ changed to $\mathbf{w}_j\gamma + o_j^\gamma$. If offsets are used in either equation, they are included in the vector of exogenous covariates \mathbf{z}_j .

For treatment t_j , \mathbf{z}_j , and ϵ_j , outcome y_j of this model has conditional mean

$$E(y_j|\mathbf{x}_j, t_j, \epsilon_j) = \exp(\mathbf{x}_j\beta + \delta t_j + \epsilon_j) \quad (1)$$

The probability density function of y_j for this model, conditioned on treatment t_j , \mathbf{z}_j , and ϵ_j , is given by

$$f(y_j|\mathbf{z}_j, t_j, \epsilon_j) = \frac{\exp\{-\exp(\mathbf{x}_j\beta + \delta t_j + \epsilon_j)\} \{\exp(\mathbf{x}_j\beta + \delta t_j + \epsilon_j)\}^{y_j}}{y_j!}$$

The treatment t_j is determined by

$$t_j = \begin{cases} 1, & \text{if } \mathbf{w}_j\gamma + u_j > 0 \\ 0, & \text{otherwise} \end{cases}$$

The error terms ϵ_j and u_j are bivariate normal with mean zero and covariance matrix

$$\begin{bmatrix} \sigma^2 & \sigma\rho \\ \sigma\rho & 1 \end{bmatrix}$$

Conditional on ϵ_j , u_j is normal with mean $\epsilon_j\rho/\sigma$ and variance $(1 - \rho^2)$; thus we obtain the following conditional probability density for t_j :

$$\Pr(t_j|\mathbf{z}_j, \epsilon_j) = t_j \Phi \left\{ \frac{\mathbf{w}_j\gamma + (\rho/\sigma)\epsilon_j}{\sqrt{1 - \rho^2}} \right\} + (1 - t_j) \left[1 - \Phi \left\{ \frac{\mathbf{w}_j\gamma + (\rho/\sigma)\epsilon_j}{\sqrt{1 - \rho^2}} \right\} \right]$$

Φ denotes the standard normal cumulative distribution function. This leads to the following joint density of y_j , t_j , and ϵ_j :

$$f(y_j, t_j, \epsilon_j|\mathbf{z}_j) = f(y_j|\mathbf{z}_j, t_j, \epsilon_j) P(t_j|\mathbf{z}_j, \epsilon_j) f(\epsilon_j)$$

The density of y_j and t_j , conditioned on \mathbf{z}_j , is obtained by integrating the above with respect to ϵ_j . Recall that ϵ_j is normal with mean 0 and variance σ^2 .

$$f(y_j, t_j|\mathbf{z}_j) = \int_{-\infty}^{\infty} f(y_j|\mathbf{z}_j, t_j, \epsilon_j) P(t_j|\mathbf{z}_j, \epsilon_j) \frac{1}{\sigma\sqrt{2\pi}} \exp \left\{ -\left(\frac{\epsilon_j}{\sigma\sqrt{2}} \right)^2 \right\} d\epsilon_j$$

$f(y_j, t_j | \mathbf{z}_j)$ cannot be evaluated in a closed form. We change the variable of integration from ϵ_j to $\eta_j = \epsilon_j / (\sigma\sqrt{2})$, which yields

$$f(y_j, t_j | \mathbf{z}_j) = \frac{1}{\sqrt{\pi}} \int_{-\infty}^{\infty} f(y_j | \mathbf{z}_j, t_j, \sqrt{2}\sigma\eta_j) P(t_j | \mathbf{z}_j, \sqrt{2}\sigma\eta_j) \exp(-\eta_j^2) d\eta_j$$

We approximate this integral by Gauss–Hermite quadrature. Observing a sample of t_j , y_j , and \mathbf{z}_j , we calculate the log likelihood as the following:

$$\ln L = \sum_{j=1}^n w_j \ln \{f(y_j, t_j | \mathbf{z}_j)\}$$

The w_j terms denote optional weights.

In the maximum likelihood estimation, σ and ρ are not directly estimated. Directly estimated are $\ln \sigma$ and $\text{atanh } \rho$:

$$\text{atanh } \rho = \frac{1}{2} \ln \left(\frac{1 + \rho}{1 - \rho} \right)$$

Now we present formulas for the ATE and ATET. First, we nest the endogenous-treatment Poisson regression model in a potential-outcome model. A potential-outcome model specifies what each individual would obtain in each treatment level.

A potential-outcome model that nests the endogenous-treatment Poisson regression fit by etpoisson is

$$\begin{aligned} E(y_{0j} | \mathbf{x}_j, \epsilon_j) &= \exp(\mathbf{x}_j \boldsymbol{\beta}_0 + \epsilon_{0j}) \\ E(y_{1j} | \mathbf{x}_j, \epsilon_j) &= \exp(\mathbf{x}_j \boldsymbol{\beta}_1 + \epsilon_{1j}) \\ t_j &= \begin{cases} 1, & \text{if } \mathbf{w}_j \gamma + u_j > 0 \\ 0, & \text{otherwise} \end{cases} \end{aligned}$$

where y_{0j} is the outcome that person j obtains if person j selects treatment 0, and y_{1j} is the outcome that person j obtains if person j selects treatment 1. This formulation allows differing coefficients for the control ($\boldsymbol{\beta}_0$) and treatment ($\boldsymbol{\beta}_1$) regimes. The constant intercept for the control group is β_{00} . The constant intercept for the treatment group is $\beta_{11} = \beta_{00} + \delta$, where δ is the coefficient for treatment t_j in the outcome (1). The remaining notation was defined above.

We may allow other coefficients to differ across regimes in the outcome (1) by adding interactions between the treatment t_j and covariates \mathbf{x}_j to the model. To be concise, we use two coefficient vectors $\boldsymbol{\beta}_0$ and $\boldsymbol{\beta}_1$ here rather than a single coefficient vector with interactions between the treatment t_j and covariates \mathbf{x}_j . The two formulations are equivalent.

We never observe both y_{0j} and y_{1j} , only one or the other. We observe

$$y_j = t_j y_{1j} + (1 - t_j) y_{0j}$$

The vector of error terms $(\epsilon_{0j}, \epsilon_{1j}, u_j)'$ comes from a mean zero trivariate normal distribution with covariance matrix

$$\begin{bmatrix} \sigma^2 & \theta & \sigma\rho \\ \theta & \sigma^2 & \sigma\rho \\ \sigma\rho & \sigma\rho & 1 \end{bmatrix}$$

The parameters σ and ρ were discussed earlier. The parameter θ is the covariance between the two potential outcomes. We cannot estimate θ because we have no observations in which an individual is observed in both potential outcomes. Fortunately, θ is not required for the calculations that we present.

The ATE is the difference in means of the potential outcomes. The mean of each potential outcome accounts for each individual's contribution, regardless of whether that individual selects that treatment level.

The conditional means of the potential outcomes y_{tj} , $t \in (0, 1)$ for exogenous covariates \mathbf{z}_j are

$$E(y_{tj} | \mathbf{z}_j) = \exp\left(\mathbf{x}_j \boldsymbol{\beta}_t + \frac{\sigma^2}{2}\right)$$

We can see that when the coefficients are the same across the regimes, the ratio of potential-outcome means will be equal to $\exp(\delta)$; this is true of the conditional and marginal potential-outcome means.

The difference in potential-outcome means or treatment effect at exogenous covariates \mathbf{z}_j is

$$E(y_{1j} - y_{0j} | \mathbf{z}_j) = \{\exp(\mathbf{x}_j \boldsymbol{\beta}_1) - \exp(\mathbf{x}_j \boldsymbol{\beta}_0)\} \exp\left(\frac{\sigma^2}{2}\right)$$

By the law of iterated expectations, the ATE is

$$\begin{aligned} E(y_{1j} - y_{0j}) &= E\{E(y_{1j} - y_{0j} | \mathbf{z}_j)\} \\ &= E\left[\{\exp(\mathbf{x}_j \boldsymbol{\beta}_1) - \exp(\mathbf{x}_j \boldsymbol{\beta}_0)\} \exp\left(\frac{\sigma^2}{2}\right)\right] \end{aligned}$$

This expectation can be estimated as a predictive margin.

Now we will derive an expression for the ATET.

The conditional means of the potential outcomes y_{tj} , $t \in (0, 1)$ for exogenous covariates \mathbf{z}_j and treatment t_j are

$$E(y_{tj} | \mathbf{z}_j, t_j) = \exp\left(\mathbf{x}_j \boldsymbol{\beta}_t + \frac{\sigma^2}{2}\right) \left\{ \frac{\Phi(\rho\sigma + \mathbf{w}_j \boldsymbol{\gamma})}{\Phi(\mathbf{w}_j \boldsymbol{\gamma})} \right\}^{t_j} \left\{ \frac{1 - \Phi(\rho\sigma + \mathbf{w}_j \boldsymbol{\gamma})}{1 - \Phi(\mathbf{w}_j \boldsymbol{\gamma})} \right\}^{1-t_j}$$

Rather than the conditional potential-outcome means, the conditional mean of the observed outcome may be of interest. The conditional mean of the observed outcome y_j for endogenous treatment indicator t_j and exogenous covariates \mathbf{z}_j is given by

$$\begin{aligned} E(y_j | \mathbf{z}_j, t_j) &= t_j \exp\left(\mathbf{x}_j \boldsymbol{\beta}_1 + \frac{\sigma^2}{2}\right) \frac{\Phi(\rho\sigma + \mathbf{w}_j \boldsymbol{\gamma})}{\Phi(\mathbf{w}_j \boldsymbol{\gamma})} \\ &\quad + (1 - t_j) \exp\left(\mathbf{x}_j \boldsymbol{\beta}_0 + \frac{\sigma^2}{2}\right) \frac{1 - \Phi(\rho\sigma + \mathbf{w}_j \boldsymbol{\gamma})}{1 - \Phi(\mathbf{w}_j \boldsymbol{\gamma})} \end{aligned}$$

The treatment effect at exogenous covariates \mathbf{z}_j and treatment t_j is

$$E(y_{1j} - y_{0j} | \mathbf{z}_j, t_j) = \\ \left\{ \exp(\mathbf{x}_j \beta_1) - \exp(\mathbf{x}_j \beta_0) \right\} \exp\left(\frac{\sigma^2}{2}\right) \left\{ \frac{\Phi(\rho\sigma + \mathbf{w}'_j \gamma)}{\Phi(\mathbf{w}'_j \gamma)} \right\}^{t_j} \left\{ \frac{1 - \Phi(\rho\sigma + \mathbf{w}'_j \gamma)}{1 - \Phi(\mathbf{w}'_j \gamma)} \right\}^{1-t_j}$$

By the law of iterated expectations, the ATET is

$$E(y_{1j} - y_{0j} | t_j = 1) = E\{E(y_{1j} - y_{0j} | \mathbf{z}_j, t_j = 1) | t_j = 1\} \\ = E\left[\left\{ \exp(\mathbf{x}_j \beta_1) - \exp(\mathbf{x}_j \beta_0) \right\} \exp\left(\frac{\sigma^2}{2}\right) \frac{\Phi(\rho\sigma + \mathbf{w}'_j \gamma)}{\Phi(\mathbf{w}'_j \gamma)} \middle| t_j = 1\right]$$

This can be estimated as a predictive margin on the treated subpopulation.

We note that when $\rho = 0$, the correction factor involving Φ will disappear from the ATET. Then the ATE and ATET will be equivalent if the distribution of \mathbf{x}_j under the treated population is identical to the distribution over the entire population.

The probability of y_j conditional on t_j and \mathbf{z}_j is

$$\Pr(y_j = n | \mathbf{z}_j, t_j) = \frac{f(y_j = n, t_j | \mathbf{z}_j)}{\Phi(\mathbf{w}'_j \gamma)^{t_j} \Phi(-\mathbf{w}'_j \gamma)^{1-t_j}}$$

As discussed earlier, we approximate $f(y_j, t_j | \mathbf{z}_j)$ using Gauss–Hermite quadrature.

References

- Cerulli, G. 2015. *Econometric Evaluation of Socio-Economic Programs: Theory and Applications*. Berlin: Springer.
 Terza, J. V. 1998. Estimating count data models with endogenous switching: Sample selection and endogenous treatment effects. *Journal of Econometrics* 84: 129–154.

Also see

- [TE] **etpoisson postestimation** — Postestimation tools for etpoisson
- [TE] **etregress** — Linear regression with endogenous treatment effects
- [R] **heckpoisson** — Poisson regression with sample selection
- [R] **ivpoisson** — Poisson model with continuous endogenous covariates
- [R] **ivprobit** — Probit model with continuous endogenous covariates
- [R] **ivregress** — Single-equation instrumental-variables regression
- [R] **ivtobit** — Tobit model with continuous endogenous covariates
- [R] **poisson** — Poisson regression
- [SVY] **svy estimation** — Estimation commands for survey data
- [U] **20 Estimation and postestimation commands**

etpoisson postestimation — Postestimation tools for etpoisson

[Postestimation commands](#)
[Remarks and examples](#)

[predict](#)
[Methods and formulas](#)

[margins](#)
[Also see](#)

Postestimation commands

The following standard postestimation commands are available after `etpoisson`:

Command	Description
<code>contrast</code>	contrasts and ANOVA-style joint tests of estimates
<code>estat ic</code>	Akaike's and Schwarz's Bayesian information criteria (AIC and BIC)
<code>estat summarize</code>	summary statistics for the estimation sample
<code>estat vce</code>	variance–covariance matrix of the estimators (VCE)
<code>estat (svy)</code>	postestimation statistics for survey data
<code>estimates</code>	cataloging estimation results
* <code>hausman</code>	Hausman's specification test
<code>lincom</code>	point estimates, standard errors, testing, and inference for linear combinations of coefficients
* <code>lrtest</code>	likelihood-ratio test
<code>margins</code>	marginal means, predictive margins, marginal effects, and average marginal effects
<code>marginsplot</code>	graph the results from <code>margins</code> (profile plots, interaction plots, etc.)
<code>nlcom</code>	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
<code>predict</code>	predictions, probabilities, and treatment effects
<code>predictnl</code>	point estimates, standard errors, testing, and inference for generalized predictions
<code>pwcompare</code>	pairwise comparisons of estimates
<code>suest</code>	seemingly unrelated estimation
<code>test</code>	Wald tests of simple and composite linear hypotheses
<code>testnl</code>	Wald tests of nonlinear hypotheses

* `hausman` and `lrtest` are not appropriate with `svy` estimation results.

predict

Description for predict

`predict` creates a new variable containing predictions such as counts, conditional treatment effects, probabilities, and linear predictions.

Menu for predict

Statistics > Postestimation

Syntax for predict

```
predict [type] newvar [if] [in] [, statistic nooffset]
```

```
predict [type] { stub* | newvarreg newvartreat newvarathrho newvarlnsigma }
[if] [in], scores
```

<i>statistic</i>	Description
<hr/>	
Main	
<u>pomean</u>	potential-outcome mean (the predicted count); the default
<u>omean</u>	observed-outcome mean (the predicted count)
<u>cte</u>	conditional treatment effect at treatment level
<u>pr(<i>n</i>)</u>	probability $\Pr(y_j = n)$
<u>pr(<i>a,b</i>)</u>	probability $\Pr(a \leq y_j \leq b)$
<u>xb</u>	linear prediction
<u>xbtreat</u>	linear prediction for treatment equation

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

Options for predict

Main

pomean, the default, calculates the potential-outcome mean.

omean calculates the observed-outcome mean.

cte calculates the treatment effect, the difference of potential-outcome means, conditioned on treatment level.

pr(*n*) calculates the probability $\Pr(y_j = n)$, where *n* is a nonnegative integer that may be specified as a number or a variable.

pr(*a*,*b*) calculates the probability $\Pr(a \leq y_j \leq b)$, where *a* and *b* are nonnegative integers that may be specified as numbers or variables;

b missing ($b \geq .$) means $+\infty$;

pr(20,.) calculates $\Pr(y_j \geq 20)$;

pr(20,*b*) calculates $\Pr(y_j \geq 20)$ in observations for which $b \geq .$ and calculates $\Pr(20 \leq y_j \leq b)$ elsewhere.

pr(.,*b*) produces a syntax error. A missing value in an observation of the variable *a* causes a missing value in that observation for **pr**(*a*,*b*).

xb calculates the linear prediction for the dependent count variable, which is $\mathbf{x}_j\beta$ if neither **offset()** nor **exposure()** was specified; $\mathbf{x}_j\beta + \text{offset}_j^\beta$ if **offset()** was specified; or $\mathbf{x}_j\beta + \ln(\text{exposure}_j)$ if **exposure()** was specified.

xbtreat calculates the linear prediction for the endogenous treatment equation, which is $\mathbf{w}_j\gamma$ if **offset()** was not specified in **treat()** and $\mathbf{w}_j\gamma + \text{offset}_j^\alpha$ if **offset()** was specified in **treat()**.

nooffset is relevant only if you specified **offset()** or **exposure()** when you fit the model. It modifies the calculations made by **predict** so that they ignore the offset or exposure variable. **nooffset** removes the offset from calculations involving both the **treat()** equation and the dependent count variable.

scores calculates equation-level score variables.

The first new variable will contain $\partial \ln L / \partial (\mathbf{x}_j\beta)$.

The second new variable will contain $\partial \ln L / \partial (\mathbf{w}_j\gamma)$.

The third new variable will contain $\partial \ln L / \partial \text{atanh } \rho$.

The fourth new variable will contain $\partial \ln L / \partial \ln \sigma$.

margins

Description for margins

`margins` estimates margins of response for counts, conditional treatment effects, probabilities, and linear predictions.

Menu for margins

Statistics > Postestimation

Syntax for margins

```
margins [marginlist] [, options]
margins [marginlist], predict(statistic ...) [predict(statistic ...) ...] [options]
```

statistic	Description
<code>pomean</code>	potential-outcome mean (the predicted count); the default
<code>omean</code>	observed-outcome mean (the predicted count)
<code>cte</code>	conditional treatment effect at treatment level
<code>pr(<i>n</i>)</code>	probability $\Pr(y_j = n)$
<code>pr(<i>a</i>,<i>b</i>)</code>	probability $\Pr(a \leq y_j \leq b)$
<code>xb</code>	linear prediction
<code>xbtreat</code>	linear prediction for treatment equation

Statistics not allowed with `margins` are functions of stochastic quantities other than `e(b)`.

For the full syntax, see [\[R\] margins](#).

Remarks and examples

The average treatment effect (ATE) and the average treatment effect on the treated (ATET) are the parameters most frequently estimated by postestimation techniques after `etpoisson`.

You can use the `margins` command (see [\[R\] margins](#)) after `etpoisson` to estimate the ATE or ATET. See [example 2 of \[TE\] etpoisson](#) for an example of ATE estimation. See [example 3 of \[TE\] etpoisson](#) for an example of ATET estimation.

See [example 1 of \[TE\] etpoisson](#) for an example using `lincom` after `etpoisson`.

Methods and formulas

See [Methods and formulas of \[TE\] etpoisson](#) for details.

Also see

[\[TE\] etpoisson](#) — Poisson regression with endogenous treatment effects

[\[U\] 20 Estimation and postestimation commands](#)

etregress — Linear regression with endogenous treatment effects

Description	Quick start
Menu	Syntax
Options for maximum likelihood estimates	Options for two-step consistent estimates
Options for control-function estimates	Remarks and examples
Stored results	Methods and formulas
References	Also see

Description

etregress estimates an average treatment effect (ATE) and the other parameters of a linear regression model augmented with an endogenous binary-treatment variable. Estimation is by full maximum likelihood, a two-step consistent estimator, or a control-function estimator.

In addition to the ATE, **etregress** can be used to estimate the average treatment effect on the treated (ATET) when the outcome may not be conditionally independent of the treatment.

Quick start

ATE and ATET from a linear regression model of *y* on *x* and endogenous binary treatment *treat* modeled by *x* and *w*

```
etregress y x, treat(treat = x w)
```

As above, but use a control-function estimator

```
etregress y x, treat(treat = x w) cfunction
```

With robust standard errors

```
etregress y x, treat(treat = x w) vce(robust)
```

Add the interaction between *treat* and continuous covariate *x* using **factor variables**

```
etregress y x i.treat#c.x, treat(treat = x w) vce(robust)
```

ATE after **etregress** with the required *vce(robust)* option and endogenous treatment interaction terms

```
margins r.treat, vce(unconditional)
```

As above, but calculate ATET

```
margins, vce(unconditional) predict(cte) subpop(if treat==1)
```

Menu

Statistics > Treatment effects > Endogenous treatment > Maximum likelihood estimator > Continuous outcomes

Syntax

Basic syntax

```
etregress depvar [indepvars], treat(depvart = indepvarst) [twostep|cfunction]
```

Full syntax for maximum likelihood estimates only

```
etregress depvar [indepvars] [if] [in] [weight] ,  
treat(depvart = indepvarst [, noconstant]) [etregress_ml_options]
```

Full syntax for two-step consistent estimates only

```
etregress depvar [indepvars] [if] [in] ,  
treat(depvart = indepvarst [, noconstant]) twostep [etregress_ts_options]
```

Full syntax for control-function estimates only

```
etregress depvar [indepvars] [if] [in] ,  
treat(depvart = indepvarst [, noconstant]) cfunction [etregress_cf_options]
```

<i>etregress_ml_options</i>	Description
Model	
* treat()	equation for treatment effects
<u>noconstant</u>	suppress constant term
<u>poutcomes</u>	use potential-outcome model with separate treatment and control group variance and correlation parameters
<u>constraints</u> (<i>constraints</i>)	apply specified linear constraints
SE/Robust	
vce(<i>vcetype</i>)	<i>vcetype</i> may be <u>oim</u> , <u>robust</u> , <u>cluster</u> <i>clustvar</i> , <u>opg</u> , <u>bootstrap</u> , or <u>jackknife</u>
Reporting	
<u>level</u> (#)	set confidence level; default is <u>level</u> (95)
<u>first</u>	report first-step probit estimates
<u>hazard</u> (<i>newvar</i>)	create <i>newvar</i> containing hazard from treatment equation
<u>lrmodel</u>	perform the likelihood-ratio model test instead of the default Wald test
<u>nocnsreport</u>	do not display constraints
<u>display_options</u>	control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling
Maximization	
<u>maximize_options</u>	control the maximization process; seldom used
<u>collinear</u>	keep collinear variables
<u>coeflegend</u>	display legend instead of statistics

**treat*(*depvar_t* = *indepvar_t* [, noconstant]) is required.

<i>etregress_ts_options</i>	Description
Model	
* treat()	equation for treatment effects
* twostep	produce two-step consistent estimate
<u>noconstant</u>	suppress constant term
SE	
vce(<i>vcetype</i>)	<i>vcetype</i> may be <u>conventional</u> , <u>bootstrap</u> , or <u>jackknife</u>
Reporting	
<u>level</u> (#)	set confidence level; default is <u>level</u> (95)
<u>first</u>	report first-step probit estimates
<u>hazard</u> (<i>newvar</i>)	create <i>newvar</i> containing hazard from treatment equation
<u>display_options</u>	control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling
<u>coeflegend</u>	display legend instead of statistics

treat*(*depvar_t* = *indepvar_t* [, noconstant]) and **twostep are required.

<i>etregress_cf_options</i>	Description
Model	
* <u>treat()</u>	equation for treatment effects
* <u>cfunction</u>	produce control-function estimate
<u>noconstant</u>	suppress constant term
<u>poutcomes</u>	use potential-outcome model with separate treatment and control group variance and correlation parameters
SE	
vce(<i>vcetype</i>)	<i>vcetype</i> may be <u>robust</u> , <u>bootstrap</u> , or <u>jackknife</u>
Reporting	
<u>level(#)</u>	set confidence level; default is <code>level(95)</code>
<u>first</u>	report first-step probit estimates
<u>hazard</u> (<i>newvar</i>)	create <i>newvar</i> containing hazard from treatment equation
<u>display_options</u>	control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling
Maximization	
<u>maximize_options</u>	control the maximization process; seldom used
<u>coeflegend</u>	display legend instead of statistics

* `treat(depvart = indepvarst [, noconstant])` and `cfunction` are required.

indepvars and *indepvar_{st}* may contain factor variables; see [\[U\] 11.4.3 Factor variables](#).

depvar, *indepvars*, *depvar_t*, and *indepvar_{st}* may contain time-series operators; see [\[U\] 11.4.4 Time-series varlists](#).

`bootstrap`, `by`, `fp`, `jackknife`, `rolling`, `statsby`, and `svy` are allowed; see [\[U\] 11.1.10 Prefix commands](#).

Weights are not allowed with the `bootstrap` prefix; see [\[R\] bootstrap](#).

`aweights` are not allowed with the `jackknife` prefix; see [\[R\] jackknife](#).

`twostep`, `cfunction`, `vce()`, `first`, `hazard()`, `lrm`, and weights are not allowed with the `svy` prefix; see [\[SVY\] svy](#).

`pweights`, `aweights`, `fweights`, and `iweights` are allowed with both maximum likelihood and control-function estimation; see [\[U\] 11.1.6 weight](#). No weights are allowed if `twostep` is specified.

`collinear` and `coeflegend` do not appear in the dialog box.

See [\[U\] 20 Estimation and postestimation commands](#) for more capabilities of estimation commands.

Options for maximum likelihood estimates

Model

`treat(depvart = indepvarst [, noconstant])` specifies the variables and options for the treatment equation. It is an integral part of specifying a treatment-effects model and is required.
`noconstant`; see [R] **Estimation options**.

`poutcomes` specifies that a potential-outcome model with separate variance and correlation parameters for each of the treatment and control groups be used.

`constraints(constraints)`; see [R] **Estimation options**.

SE/Robust

`vce(vcetype)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory (`oim`, `opg`), that are robust to some kinds of misspecification (`robust`), that allow for intragroup correlation (`cluster clustvar`), and that use bootstrap or jackknife methods (`bootstrap`, `jackknife`); see [R] **vce_option**.

Reporting

`level(#)`; see [R] **Estimation options**.

`first` specifies that the first-step probit estimates of the treatment equation be displayed before estimation.

`hazard(newvar)` will create a new variable containing the hazard from the treatment equation. The hazard is computed from the estimated parameters of the treatment equation.

`lrmodel, nocnsreport`; see [R] **Estimation options**.

`display_options`: `noci`, `nofvalues`, `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `nofvlabel`, `fwrap(#)`, `fwrapon(style)`, `cformat(%fmt)`, `pformat(%fmt)`, `sformat(%fmt)`, and `nolstretch`; see [R] **Estimation options**.

Maximization

`maximize_options`: `difficult`, `technique(algorithm_spec)`, `iterate(#)`, `[no]log`, `trace`, `gradient`, `showstep`, `hessian`, `showtolerance`, `tolerance(#)`, `ltolerance(#)`, `ntolerance(#)`, `nonrtolerance`, and `from(init_specs)`; see [R] **Maximize**. These options are seldom used.

Setting the optimization type to `technique(bhhh)` resets the default `vcetype` to `vce(opg)`.

The following options are available with `etregress` but are not shown in the dialog box:

`collinear, coeflegend`; see [R] **Estimation options**.

Options for two-step consistent estimates

Model

`treat(depvart = indepvarst [, noconstant])` specifies the variables and options for the treatment equation. It is an integral part of specifying a treatment-effects model and is required.

`twostep` specifies that two-step consistent estimates of the parameters, standard errors, and covariance matrix be produced, instead of the default maximum likelihood estimates.

`noconstant`; see [R] [Estimation options](#).

SE

`vce(vcetype)` specifies the type of standard error reported, which includes types that are derived from asymptotic theory (conventional) and that use bootstrap or jackknife methods (bootstrap, jackknife); see [R] [vce_option](#).

`vce(conventional)`, the default, uses the conventionally derived variance estimator for the two-step estimator of the treatment-effects model.

Reporting

`level(#)`; see [R] [Estimation options](#).

`first` specifies that the first-step probit estimates of the treatment equation be displayed before estimation.

`hazard(newvar)` will create a new variable containing the hazard from the treatment equation. The hazard is computed from the estimated parameters of the treatment equation.

`display_options`: `noci`, `nopvalues`, `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `nofvlabel`, `fvwrap(#)`, `fvrapon(style)`, `cformat(%fmt)`, `pformat(%fmt)`, `sformat(%fmt)`, and `nolstretch`; see [R] [Estimation options](#).

The following option is available with `etregress` but is not shown in the dialog box:

`coeflegend`; see [R] [Estimation options](#).

Options for control-function estimates

Model

`treat(depvart = indepvarst [, noconstant])` specifies the variables and options for the treatment equation. It is an integral part of specifying a treatment-effects model and is required.

`cfunction` specifies that control-function estimates of the parameters, standard errors, and covariance matrix be produced instead of the default maximum likelihood estimates. `cfunction` is required.

`noconstant`; see [R] [Estimation options](#).

`poutcomes` specifies that a potential-outcome model with separate variance and correlation parameters for each of the treatment and control groups be used.

SE

`vce(vcetype)` specifies the type of standard error reported, which includes types that are robust to some kinds of misspecification (`robust`) and that use bootstrap or jackknife methods (`bootstrap`, `jackknife`); see [R] [vce_option](#).

Reporting

`level(#)`; see [R] **Estimation options**.

`first` specifies that the first-step probit estimates of the treatment equation be displayed before estimation.

`hazard(newvar)` will create a new variable containing the hazard from the treatment equation. The hazard is computed from the estimated parameters of the treatment equation.

`display_options`: `noci`, `nopvalues`, `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `nofvlabel`, `fvwrap(#)`, `fvwrapon(style)`, `cformat(%fmt)`, `pformat(%fmt)`, `sformat(%fmt)`, and `nolstretch`; see [R] **Estimation options**.

Maximization

`maximize_options`: `iterate(#)`, `[no]log`, and `from(init_specs)`; see [R] **Maximize**. These options are seldom used.

`init_specs` is one of

```
matname [, skip copy]  
# [# ...] copy
```

The following option is available with **etregress** but is not shown in the dialog box:

`coeflegend`; see [R] **Estimation options**.

Remarks and examples

Remarks are presented under the following headings:

Overview
Basic examples
Average treatment effect (ATE)
Average treatment effect on the treated (ATET)

Overview

etregress estimates an ATE and the other parameters of a linear regression model that also includes an endogenous binary-treatment variable. In addition to the ATE, the parameters estimated by **etregress** can be used to estimate the ATET when the outcome is not conditionally independent of the treatment.

We call the model fit by **etregress** an endogenous treatment-regression model, although it is also known as an endogenous binary-variable model or as an endogenous dummy-variable model. The endogenous treatment-regression model is a specific endogenous treatment-effects model; it uses a linear model for the outcome and a normal distribution to model the deviation from the conditional independence assumption imposed by the estimators implemented in **teffects**; see [TE] **teffects intro**. In treatment-effects jargon, the endogenous binary-variable model is a linear potential-outcome model that allows for a specific correlation structure between the unobservables that affect the treatment and the unobservables that affect the potential outcomes. See [TE] **etpoisson** for an estimator that allows for a nonlinear outcome model and a similar model for the endogeneity of the treatment.

Heckman (1976, 1978) brought this model into the modern literature. Maddala (1983) derives the maximum likelihood and the control-function (CF) estimators of the model. Maddala (1983) also reviews some empirical applications and describes it as an endogenous-switching model. Barnow, Cain, and Goldberger (1981) provide another useful derivation of this model. They concentrate on deriving the conditions for which the self-selection bias of the simple OLS estimator of the treatment effect, δ , is nonzero and of a specific sign. Cameron and Trivedi (2005, sec. 16.7 and 25.3.4) and Wooldridge (2010, sec. 21.4.1) discuss the endogenous binary-variable model as an endogenous treatment-effects model and link it to recent work.

etregress performs CF estimation in one step by using the generalized method of moments (GMM) with stacked moments. See Newey (1984) and Wooldridge (2010, sec. 14.2) for a description of this technique. Many econometric and statistical models can be expressed as conditions on the population moments. The parameter estimates produced by GMM estimators make the sample-moment conditions as true as possible given the data. See [R] gmm for further information on GMM estimation and how Stata performs it. Two-step CF estimation is also supported by **etregress**.

Formally, the endogenous treatment-regression model is composed of an equation for the outcome y_j and an equation for the endogenous treatment t_j . The variables \mathbf{x}_j are used to model the outcome. When there are no interactions between t_j and \mathbf{x}_j , we have

$$\begin{aligned} y_j &= \mathbf{x}_j\beta + \delta t_j + \epsilon_j \\ t_j &= \begin{cases} 1, & \text{if } \mathbf{w}_j\gamma + u_j > 0 \\ 0, & \text{otherwise} \end{cases} \end{aligned}$$

where \mathbf{w}_j are the covariates used to model treatment assignment, and the error terms ϵ_j and u_j are bivariate normal with mean zero and covariance matrix

$$\begin{bmatrix} \sigma^2 & \rho\sigma \\ \rho\sigma & 1 \end{bmatrix}$$

The covariates \mathbf{x}_j and \mathbf{w}_j are unrelated to the error terms; in other words, they are exogenous. We call this the constrained model because the variance and correlation parameters are identical across the treatment and control groups.

This model can be generalized to a potential-outcome model with separate variance and correlation parameters for the treatment and control groups. The generalized model is

$$\begin{aligned} y_{0j} &= \mathbf{x}_j\beta_0 + \epsilon_{0j} \\ y_{1j} &= \mathbf{x}_j\beta_1 + \epsilon_{1j} \\ t_j &= \begin{cases} 1, & \text{if } \mathbf{w}_j\gamma + u_j > 0 \\ 0, & \text{otherwise} \end{cases} \end{aligned}$$

where y_{0j} is the outcome that person j obtains if person j selects treatment 0, and y_{1j} is the outcome that person j obtains if person j selects treatment 1. We never observe both y_{0j} and y_{1j} , only one or the other. We observe

$$y_j = t_j y_{1j} + (1 - t_j) y_{0j}$$

In this unconstrained model, the vector of error terms $(\epsilon_{0j}, \epsilon_{1j}, u_j)'$ comes from a mean zero trivariate normal distribution with covariance matrix

$$\begin{bmatrix} \sigma_0^2 & \sigma_{01} & \sigma_0\rho_0 \\ \sigma_{01} & \sigma_1^2 & \sigma_1\rho_1 \\ \sigma_0\rho_0 & \sigma_1\rho_1 & 1 \end{bmatrix}$$

The covariance σ_{01} cannot be identified because we never observe both y_{1j} and y_{0j} . However, identification of σ_{01} is not necessary to estimate the other parameters because all covariates and the outcome are observed in observations from each group. We normalize the treatment error variance to be 1 because we observe only whether an outcome occurs under treatment. More details are found in [Methods and formulas](#).

Rather than showing two separate regression equations, **etregress** reports one outcome equation with interaction terms between the treatment and outcome covariates. **etregress** can fit the constrained and generalized potential-outcome models using either the default maximum likelihood estimator or the one-step CF estimator obtained with option `cfunction`. The two-step CF estimator provides consistent estimates for the constrained model.

Basic examples

When there are no interactions between the treatment variable and the outcome covariates in the constrained model, **etregress** directly estimates the ATE and the ATET.

▷ Example 1: Basic example

We estimate the ATE of being a union member on wages of women in 1972 from a nonrepresentative extract of the National Longitudinal Survey on young women who were ages 14–26 in 1968. We will use the variables `wage` (wage), `grade` (years of schooling completed), `smsa` (an indicator for living in an SMSA—standard metropolitan statistical area), `black` (an indicator for being African-American), `tenure` (tenure at current job), and `south` (an indicator for living in the South).

We use `etregress` to estimate the parameters of the endogenous treatment-regression model.

```
. use https://www.stata-press.com/data/r16/union3
(National Longitudinal Survey. Young Women 14–26 years of age in 1968)
. etregress wage age grade smsa black tenure, treat(union = south black tenure)
Iteration 0: log likelihood = -3140.811
Iteration 1: log likelihood = -3053.6629
Iteration 2: log likelihood = -3051.5847
Iteration 3: log likelihood = -3051.575
Iteration 4: log likelihood = -3051.575
Linear regression with endogenous treatment          Number of obs      =     1,210
Estimator: maximum likelihood                      Wald chi2(6)       =     681.89
Log likelihood = -3051.575                         Prob > chi2        =     0.0000
```

	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
wage					
	age	.1487409	.0193291	7.70	0.000
	grade	.4205658	.0293577	14.33	0.000
	smsa	.9117044	.1249041	7.30	0.000
	black	-.7882471	.1367078	-5.77	0.000
	tenure	.1524015	.0369596	4.12	0.000
	1.union	2.945815	.2749621	10.71	0.000
union	_cons	-4.351572	.5283952	-8.24	0.000
	south	-.5807419	.0851111	-6.82	0.000
	black	.4557499	.0958042	4.76	0.000
	tenure	.0871536	.0232483	3.75	0.000
	_cons	-.8855758	.0724506	-12.22	0.000
/athrho	/lnsigma	-.6544347	.0910314	-7.19	0.000
		.7026769	.0293372	23.95	0.000
					.645177
rho					.7601767
	sigma	-.5746478	.060971		-.682005
	lambda	2.019151	.0592362		1.906325
		-1.1603	.1495097		-1.453334

LR test of indep. eqns. (rho = 0): chi2(1) = 19.84 Prob > chi2 = 0.0000

The likelihood-ratio test in the footer indicates that we can reject the null hypothesis of no correlation between the treatment-assignment errors and the outcome errors. The estimated correlation between the treatment-assignment errors and the outcome errors, ρ , is -0.575 . The negative relationship indicates that unobservables that raise observed wages tend to occur with unobservables that lower union membership. We discuss some details about this parameter in the technical note [below](#).

The estimated ATE of being a union member is 2.95. The ATET is the same as the ATE in this case because the treatment indicator variable has not been interacted with any of the outcome covariates, and the correlation and variance parameters are identical across the control and treatment groups.



□ Technical note

The results for the ancillary parameters ρ and σ require explanation. For numerical stability during optimization, **etregress** does not directly estimate ρ or σ . Instead, **etregress** estimates the inverse hyperbolic tangent of ρ ,

$$\operatorname{atanh} \rho = \frac{1}{2} \ln\left(\frac{1+\rho}{1-\rho}\right)$$

and $\ln\sigma$. Also **etregress** reports $\lambda = \rho\sigma$, along with an estimate of the standard error of the estimate and the confidence interval.

□

In contrast to the constrained model, **etregress** directly estimates the ATE only when there are no interactions between the treatment variable and the outcome covariates in the unconstrained model.

▷ Example 2: Allowing group-specific variance and correlation

We estimate the ATE of having health insurance on the natural logarithm of total out-of-pocket prescription drug expenditures from a simulated random sample of individuals between the ages of 25 and 64. We will use the variables `lndrug` (natural logarithm of spending on prescription drugs), `age` (age of the individual), `chron` (whether the individual has a chronic condition), `lninc` (natural logarithm of income), `married` (marriage status), and `work` (employment status). Our treatment is whether the person has health insurance, `ins`. We allow the outcome error variance and correlation parameters to vary between the treated (insured) and control (uninsured) groups in this example, rather than constraining them to be equal as in [example 1](#).

We use **etregress** to estimate the parameters of the endogenous treatment-effects model. To estimate separate variance and correlation parameters for each of the control and treatment groups, we specify the `poutcomes` option. We specify the `cfunction` option to use the CF estimator.

```
. use https://www.stata-press.com/data/r16/drugexp
(Prescription drug expenditures)

. etregress lndrug chron age lninc, treat(ins=age married lninc work) poutcomes
> cfunction

Iteration 0: GMM criterion Q(b) = 2.279e-15
Iteration 1: GMM criterion Q(b) = 6.358e-30

Linear regression with endogenous treatment      Number of obs      = 6,000
Estimator: control-function
```

	Robust					
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
lndrug						
chron	.4671725	.0319731	14.61	0.000	.4045064	.5298387
age	.1021359	.00292	34.98	0.000	.0964128	.1078589
lninc	.0550672	.0225036	2.45	0.014	.0109609	.0991735
1.ins	-.8598836	.3483648	-2.47	0.014	-1.542666	-.1771011
_cons	1.665539	.2527527	6.59	0.000	1.170153	2.160925
ins						
age	.021142	.0022961	9.21	0.000	.0166416	.0256424
married	.084631	.0359713	2.35	0.019	.0141286	.1551334
lninc	.1023032	.0225009	4.55	0.000	.0582022	.1464041
work	.288418	.0372281	7.75	0.000	.2154522	.3613837
_cons	-.622993	.108795	-5.73	0.000	-.8362273	-.4097587
/athrho0	.4035094	.1724539	2.34	0.019	.0655059	.7415129
/lnsigma0	.3159269	.0500476	6.31	0.000	.2178353	.4140184
/athrho1	.7929459	.2986601	2.66	0.008	.2075829	1.378309
/lnsigma1	.1865347	.0613124	3.04	0.002	.0663646	.3067048
rho0	.3829477	.1471637			.0654124	.6300583
sigma0	1.37153	.0686418			1.243382	1.512885
lambda0	.5252243	.226367			.0815532	.9688954
rho1	.6600746	.1685343			.2046518	.880572
sigma1	1.205066	.0738855			1.068616	1.35894
lambda1	.7954338	.2513036			.3028878	1.28798

Wald test of indep. (rho0 = rho1 = 0): chi2(2) = 8.88 Prob > chi2 = 0.0118

The Wald test reported in the footer indicates that we can reject the null hypothesis of no correlation between the treatment-assignment errors and the outcome errors for the control and treatment groups. The estimate of the correlation of the treatment-assignment errors for the control group (ρ_0) is positive, indicating that unobservables that increase spending on prescription drugs tend to occur with unobservables that increase health insurance coverage. Because ρ_1 is also positive, we make the same interpretation for individuals with insurance. The estimate ρ_1 is larger than the estimate ρ_0 , indicating a stronger relationship between the unobservables and treatment outcomes in the treated group.

The estimated ATE of having health insurance is -0.86 . Note that while the ATE and ATET were the same in [example 1](#), that is not the case here. We show how to calculate the ATET for a potential-outcome model in [example 6](#).

The estimate of the outcome error standard-deviation parameter for the control group (σ_0) is slightly larger than that of the treatment group parameter (σ_1), indicating a greater variability in the unobservables among the untreated group.



Average treatment effect (ATE)

When there is a treatment variable and outcome covariate interaction, the parameter estimates from **etregress** can be used by **margins** to estimate the ATE, the average difference of the treatment potential outcomes and the control potential outcomes.

▷ Example 3: Allowing interactions between treatment and outcome covariates, ATE

In [example 1](#), the coefficients on the outcome covariates do not vary by treatment level. The differences in wages between union members and nonmembers are modeled as a level shift captured by the coefficient on the indicator for union membership. In this example, we use factor-variable notation to allow some of the coefficients to vary over treatment level and then use **margins** (see [\[R\] margins](#)) to estimate the ATE. (See [\[U\] 11.4.3 Factor variables](#) for an introduction to factor-variable notation.)

We begin by estimating the parameters of the model in which the coefficients on `black` and `tenure` differ for union members and nonmembers. We specify the `vce(robust)` option because we need to specify `vce(unconditional)` when we use **margins** below.

```
. use https://www.stata-press.com/data/r16/union3
(National Longitudinal Survey. Young Women 14-26 years of age in 1968)
. etregress wage age grade smsa i.union#c.(black tenure),
> treat(union = south black tenure) vce(robust)

Iteration 0: log pseudolikelihood = -3614.6714
Iteration 1: log pseudolikelihood = -3218.8152
Iteration 2: log pseudolikelihood = -3057.0115
Iteration 3: log pseudolikelihood = -3049.3081
Iteration 4: log pseudolikelihood = -3049.2838
Iteration 5: log pseudolikelihood = -3049.2838

Linear regression with endogenous treatment      Number of obs      =      1,210
Estimator: maximum likelihood                  Wald chi2(8)      =     493.40
Log pseudolikelihood = -3049.2838             Prob > chi2      =     0.0000
```

	Robust					
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
wage						
age	.1489075	.0207283	7.18	0.000	.1082809	.1895342
grade	.4200493	.0377621	11.12	0.000	.3460371	.4940616
smsa	.9232615	.1201486	7.68	0.000	.6877746	1.158748
union#c.black						
0	-.6685582	.1444213	-4.63	0.000	-.9516187	-.3854977
1	-1.1831	.2574817	-4.59	0.000	-1.687755	-.6784455
union#c.tenure						
0	.168746	.0503107	3.35	0.001	.0701388	.2673532
1	.0836367	.0903669	0.93	0.355	-.0934792	.2607526
1.union	3.342859	.5586863	5.98	0.000	2.247854	4.437864
_cons	-4.42566	.6493003	-6.82	0.000	-5.698265	-3.153055
union						
south	-.5844678	.0833069	-7.02	0.000	-.7477464	-.4211893
black	.4740688	.093241	5.08	0.000	.2913197	.6568178
tenure	.0874297	.0253892	3.44	0.001	.0376678	.1371916
_cons	-.8910484	.0746329	-11.94	0.000	-1.037326	-.7447706
/athrho	-.6733149	.2215328	-3.04	0.002	-1.107511	-.2391185
/lnsigma	.7055907	.0749711	9.41	0.000	.55865	.8525313
rho	-.5871562	.1451589			-.8031809	-.234663
sigma	2.025042	.1518197			1.748311	2.345577
lambda	-1.189016	.3631079			-1.900695	-.4773378

Wald test of indep. eqns. (rho = 0): chi2(1) = 9.24 Prob > chi2 = 0.0024

The results indicate that the coefficients on `black` differ by union membership and that the coefficient on `tenure` for nonmembers is positive, while the coefficient on `tenure` for members is 0. The model fits well overall, so we proceed with interpretation. Because we interacted the treatment variable with two of the covariates, the estimated coefficient on the treatment level is not an estimate of the ATE. Below we use `margins` to estimate the ATE from these results. We specify the `vce(unconditional)` option to obtain the standard errors for the population ATE instead of the sample ATE. We specify the `contrast(nowald)` option to suppress the Wald tests, which `margins` displays by default for contrasts.

. margins r.union, vce(unconditional) contrast(nowald)			
Contrasts of predictive margins	Number of obs	=	1,210
Expression : Linear prediction, predict()			
<hr/>			
Unconditional Contrast Std. Err. [95% Conf. Interval]			
union (1 vs 0)	3.042688	.5305151	2.002898 4.082478

The ATE estimate is essentially the same as the one produced by the constrained model in [example 1](#).



We can use the same methods above to obtain the ATE in an unconstrained model.

▷ Example 4: Treatment interactions and group-specific variance and correlation, ATE

In [example 2](#), the coefficients on the outcome covariates do not vary by treatment level. Suppose we believe that the effect of having a chronic condition on out-of-pocket spending differs between the insured and uninsured. Again, we use an interaction term. Because we are using a CF estimator, the variance–covariance of the estimator (VCE) is already robust so we do not specify `vce(robust)`.

```
. use https://www.stata-press.com/data/r16/drugexp
(Prescription drug expenditures)
. etregress lndrug i.ins#i.chron age lninc, treat(ins=age married lninc work)
> poutcomes cfunction
Iteration 0: GMM criterion Q(b) = 2.279e-15
Iteration 1: GMM criterion Q(b) = 1.561e-28
Linear regression with endogenous treatment      Number of obs      = 6,000
Estimator: control-function
```

	Robust					
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
lndrug						
ins#chron						
0 1	.3798705	.0720713	5.27	0.000	.2386132	.5211277
1 1	.4957773	.0352571	14.06	0.000	.4266746	.5648801
age	.1022045	.0029228	34.97	0.000	.0964758	.1079331
lninc	.0548917	.0225219	2.44	0.015	.0107497	.0990337
1.ins	-.89703	.3493058	-2.57	0.010	-1.581657	-.2124031
_cons	1.691336	.2531222	6.68	0.000	1.195225	2.187446
ins						
age	.021142	.0022961	9.21	0.000	.0166416	.0256424
married	.084631	.0359713	2.35	0.019	.0141286	.1551334
lninc	.1023032	.0225009	4.55	0.000	.0582022	.1464041
work	.288418	.0372281	7.75	0.000	.2154522	.3613837
_cons	-.622993	.108795	-5.73	0.000	-.8362273	-.4097587
/athrho0	.4046007	.1725597	2.34	0.019	.0663899	.7428115
/lnsigma0	.3157561	.0501956	6.29	0.000	.2173746	.4141376
/athrho1	.7950592	.2992825	2.66	0.008	.2084763	1.381642
/lnsigma1	.1868903	.0614281	3.04	0.002	.0664934	.3072871
rho0	.3838786	.1471308			.0662925	.6308408
sigma0	1.371296	.0688329			1.24281	1.513065
lambda0	.5264111	.2264197			.0826366	.9701856
rho1	.6612655	.1684146			.2055076	.8813184
sigma1	1.205495	.0740512			1.068754	1.359731
lambda1	.7971523	.2514293			.3043599	1.289945

Wald test of indep. (rho0 = rho1 = 0): chi2(2) = 8.90 Prob > chi2 = 0.0117

The results indicate that the coefficient on chron differs by whether an individual has insurance. The model fits well overall, so we proceed with interpretation.

Because we interacted the treatment variable with one of the covariates, the estimated coefficient on the treatment level is not an estimate of the ATE. Below we use margins to estimate the ATE from these results. We specify the vce(unconditional) option to obtain the standard errors for the population ATE instead of the sample ATE. We specify the contrast(nowald) option to suppress the Wald tests.

Contrasts of predictive margins				Number of obs	=	6,000	
Expression : Linear prediction, predict()							
	Unconditional			[95% Conf. Interval]			
	Contrast	Std. Err.					
ins (1 vs 0)	-.8632045	.3484924		-1.546237	-.1801718		

The ATE estimate is similar to the one produced by the constrained model in [example 2](#).



Average treatment effect on the treated (ATET)

When there is a treatment variable and outcome covariate interaction, the parameter estimates from **etregress** can be used by **margins** to estimate the ATET, the average difference of the treatment potential outcomes and the control potential outcomes on the treated population.

▷ Example 5: Allowing interactions between treatment and outcome covariates, ATET

The ATET may differ from the ATE in [example 3](#) because the interaction between the treatment variable and some outcome covariates makes the ATE and the ATET vary over outcome covariate values. Below we use **margins** to estimate the ATET by specifying the **subpop(union)** option, which restricts the sample used by **margins** to union members.

. use https://www.stata-press.com/data/r16/union3								
(National Longitudinal Survey. Young Women 14–26 years of age in 1968)								
. etregress wage age grade smsa i.union#c.(black tenure),								
> treat(union = south black tenure) vce(robust)								
(output omitted)								
. margins r.union, vce(unconditional) contrast(nowald) subpop(union)								
Contrasts of predictive margins	Number of obs			=	1,210			
	Subpop. no. obs			=	253			
Expression : Linear prediction, predict()								
	Unconditional			[95% Conf. Interval]				
	Contrast	Std. Err.						
union (1 vs 0)	2.968977	.5358457		1.918739	4.019215			

The estimated ATET and ATE are close, indicating that the average predicted outcome for the treatment group is similar to the average predicted outcome for the whole population.



► Example 6: Treatment interactions and group-specific variance and correlation, ATET

The ATET may differ from the ATE in [example 4](#) because the interaction between the treatment variable and some outcome covariates makes the ATE and the ATET vary over values of the covariate in the outcome equation. Even if there is no interaction between treatment assignment and a covariate in the outcome equation, the estimated ATE and ATET will differ if the variances of the outcome errors and their correlations with the treatment-assignment errors differ across the control and treatment groups.

We can estimate the ATET of having health insurance by using the conditional treatment effect (conditional on exogenous covariates and treatment level) obtained using the `predict`, `cte` and the `margins` commands; see [Methods and formulas](#) below and [TE] **etregress postestimation** for more details about the use of `predict` after `etregress`.

We restrict estimation to the treated subpopulation by specifying the `subpop(ins)` option with `margins`.

```
. use https://www.stata-press.com/data/r16/drugexp
(Prescription drug expenditures)

. etregress lndrug i.ins#i.chron age lninc,
> treat(ins = age married lninc work) poutcomes cfunction
  (output omitted)

. margins, predict(cte) subpop(ins) vce(unconditional)
Predictive margins                               Number of obs      =      6,000
                                                Subpop. no. obs   =      4,556
Expression   : Conditional treatment effect, predict(cte)


```

	Unconditional					
	Margin	Std. Err.	z	P> z	[95% Conf. Interval]	
_cons	-.7558373	.3827579	-1.97	0.048	-1.506029	-.0056457

In absolute value, the treatment effect on the treated of -0.76 is smaller than the population average effect of -0.86 that we found in [example 4](#).



Stored results

etregress (maximum likelihood) stores the following in **e()**:

Scalars

e(N)	number of observations
e(k)	number of parameters
e(k_eq)	number of equations in e(b)
e(k_eq_model)	number of equations in overall model test
e(k_aux)	number of auxiliary parameters
e(k_dv)	number of dependent variables
e(df_m)	model degrees of freedom
e(l1)	log likelihood
e(l1_0)	log likelihood, constant-only model (lrmodel only)
e(N_clust)	number of clusters
e(lambda)	estimate of λ in constrained model
e(selambda)	standard error of λ in constrained model
e(sigma)	estimate of σ in constrained model
e(lambda0)	estimate of λ_0 in potential-outcome model
e(selambda0)	standard error of λ_0 in potential-outcome model
e(sigma0)	estimate of σ_0 in potential-outcome model
e(lambda1)	estimate of λ_1 in potential-outcome model
e(selambda1)	standard error of λ_1 in potential-outcome model
e(sigma1)	estimate of σ_1 in potential-outcome model
e(chi2)	χ^2
e(chi2_c)	χ^2 for comparison test
e(p)	<i>p</i> -value for model test
e(p_c)	<i>p</i> -value for comparison test
e(rho)	estimate of ρ in constrained model
e(rho0)	estimate of ρ_0 in potential-outcome model
e(rho1)	estimate of ρ_1 in potential-outcome model
e(rank)	rank of e(V)
e(rank0)	rank of e(V) for constant-only model
e(ic)	number of iterations
e(rc)	return code
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	etregress
e(cmdline)	command as typed
e(depvar)	name of dependent variable
e(hazard)	variable containing hazard
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(title2)	secondary title in estimation output
e(clustvar)	name of cluster variable
e(chi2type)	Wald or LR; type of model χ^2 test
e(chi2_ct)	Wald or LR; type of model χ^2 test corresponding to e(chi2_c)
e(vce)	<i>vcetype</i> specified in vce()
e(vcetype)	title used to label Std. Err.
e(opt)	type of optimization
e(which)	max or min; whether optimizer is to perform maximization or minimization
e(method)	ml
e(ml_method)	type of ml method
e(user)	name of likelihood-evaluator program
e(technique)	maximization technique
e(properties)	b V
e(predict)	program used to implement predict
e(footnote)	program used to implement the footnote display
e(marginsok)	predictions allowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved

Matrices

<code>e(b)</code>	coefficient vector
<code>e(Cns)</code>	constraints matrix
<code>e(ilog)</code>	iteration log (up to 20 iterations)
<code>e(gradient)</code>	gradient vector
<code>e(V)</code>	variance–covariance matrix of the estimators
<code>e(V_modelbased)</code>	model-based variance

Functions

<code>e(sample)</code>	marks estimation sample
------------------------	-------------------------

etregress (two-step) stores the following in `e()`:

Scalars

<code>e(N)</code>	number of observations
<code>e(df_m)</code>	model degrees of freedom
<code>e(lambda)</code>	λ
<code>e(selambda)</code>	standard error of λ
<code>e(sigma)</code>	estimate of sigma
<code>e(chi2)</code>	χ^2
<code>e(p)</code>	<i>p</i> -value for model test
<code>e(rho)</code>	ρ
<code>e(rank)</code>	rank of <code>e(V)</code>

Macros

<code>e(cmd)</code>	etregress
<code>e(cmdline)</code>	command as typed
<code>e(deparvar)</code>	name of dependent variable
<code>e(hazard)</code>	variable containing hazard
<code>e(title)</code>	title in estimation output
<code>e(title2)</code>	secondary title in estimation output
<code>e(chi2type)</code>	Wald or LR; type of model χ^2 test
<code>e(vce)</code>	<i>vcetype</i> specified in <code>vce()</code>
<code>e(method)</code>	<code>twostep</code>
<code>e(properties)</code>	<code>b V</code>
<code>e(predict)</code>	program used to implement <code>predict</code>
<code>e(footnote)</code>	program used to implement the footnote display
<code>e(marginsok)</code>	predictions allowed by <code>margins</code>
<code>e(marginsnotok)</code>	predictions disallowed by <code>margins</code>
<code>e(asbalanced)</code>	factor variables <code>fvset</code> as <code>asbalanced</code>
<code>e(asobserved)</code>	factor variables <code>fvset</code> as <code>asobserved</code>

Matrices

<code>e(b)</code>	coefficient vector
<code>e(V)</code>	variance–covariance matrix of the estimators

Functions

<code>e(sample)</code>	marks estimation sample
------------------------	-------------------------

etregress (control-function) stores the following in `e()`:

Scalars

<code>e(N)</code>	number of observations
<code>e(k)</code>	number of parameters
<code>e(k_eq)</code>	number of equations in <code>e(b)</code>
<code>e(k_aux)</code>	number of auxiliary parameters
<code>e(k_dv)</code>	number of dependent variables
<code>e(lambda)</code>	estimate of λ in constrained model
<code>e(selambda)</code>	standard error of λ in constrained model
<code>e(sigma)</code>	estimate of σ in constrained model
<code>e(lambdao)</code>	estimate of λ_0 in potential-outcome model
<code>e(selambdao)</code>	standard error of λ_0 in potential-outcome model
<code>e(sigma0)</code>	estimate of σ_0 in potential-outcome model
<code>e(lambda1)</code>	estimate of λ_1 in potential-outcome model
<code>e(selambda1)</code>	standard error of λ_1 in potential-outcome model
<code>e(sigma1)</code>	estimate of σ_1 in potential-outcome model
<code>e(chi2_c)</code>	χ^2 for comparison test
<code>e(p_c)</code>	p-value for comparison test
<code>e(rho)</code>	estimate of ρ in constrained model
<code>e(rho0)</code>	estimate of ρ_0 in potential-outcome model
<code>e(rho1)</code>	estimate of ρ_1 in potential-outcome model
<code>e(rank)</code>	rank of <code>e(V)</code>
<code>e(converged)</code>	1 if converged, 0 otherwise

Macros

<code>e(cmd)</code>	etregress
<code>e(cmdline)</code>	command as typed
<code>e(depvar)</code>	name of dependent variable
<code>e(hazard)</code>	variable containing hazard
<code>e(wtype)</code>	weight type
<code>e(wexp)</code>	weight expression
<code>e(title)</code>	title in estimation output
<code>e(title2)</code>	secondary title in estimation output
<code>e(chi2_ct)</code>	Wald; type of model χ^2 test corresponding to <code>e(chi2_c)</code>
<code>e(vce)</code>	<i>vcetype</i> specified in <code>vce()</code>
<code>e(vcetype)</code>	title used to label Std. Err.
<code>e(method)</code>	<code>cfunction</code>
<code>e(properties)</code>	<code>b V</code>
<code>e(predict)</code>	program used to implement <code>predict</code>
<code>e(footnote)</code>	program used to implement the footnote display
<code>e(marginsok)</code>	predictions allowed by <code>margins</code>
<code>e(asbalanced)</code>	factor variables <code>fvset</code> as <code>asbalanced</code>
<code>e(asobserved)</code>	factor variables <code>fvset</code> as <code>asobserved</code>

Matrices

<code>e(b)</code>	coefficient vector
<code>e(V)</code>	variance–covariance matrix of the estimators

Functions

<code>e(sample)</code>	marks estimation sample
------------------------	-------------------------

Methods and formulas

Maddala (1983, 117–122 and 223–228) derives both the maximum likelihood and the CF estimators implemented here. Greene (2012, 890–894) also provides an introduction to the treatment-effects model. Cameron and Trivedi (2005, sections 16.7 and 25.3.4) and Wooldridge (2010, section 21.4.1) discuss the endogenous binary-variable model as an endogenous treatment-effects model and link it to recent work.

Methods and formulas are presented under the following headings:

- Constrained model*
- General potential-outcome model*
- Average treatment effect*
- Average treatment effect on the treated*

Constrained model

The primary regression equation of interest is

$$y_j = \mathbf{x}_j \boldsymbol{\beta} + \delta t_j + \epsilon_j \quad (1)$$

where t_j is a binary-treatment variable that is assumed to stem from an unobservable latent variable:

$$t_j^* = \mathbf{w}_j \boldsymbol{\gamma} + u_j$$

The decision to obtain the treatment is made according to the rule

$$t_j = \begin{cases} 1, & \text{if } t_j^* > 0 \\ 0, & \text{otherwise} \end{cases}$$

where ϵ and u are bivariate normal with mean zero and covariance matrix

$$\begin{bmatrix} \sigma^2 & \rho\sigma \\ \rho\sigma & 1 \end{bmatrix}$$

Interactions between \mathbf{x}_j and the treatment t_j are also allowed in (1). The likelihood function for this model is given in [Maddala \(1983, 122\)](#). [Greene \(2000, 180\)](#) discusses the standard method of reducing a bivariate normal to a function of a univariate normal and the correlation ρ . The following is the log likelihood for observation j ,

$$\ln L_j = \begin{cases} \ln \Phi \left\{ \frac{\mathbf{w}_j \boldsymbol{\gamma} + (y_j - \mathbf{x}_j \boldsymbol{\beta} - \delta)\rho/\sigma}{\sqrt{1-\rho^2}} \right\} - \frac{1}{2} \left(\frac{y_j - \mathbf{x}_j \boldsymbol{\beta} - \delta}{\sigma} \right)^2 - \ln(\sqrt{2\pi}\sigma) & t_j = 1 \\ \ln \Phi \left\{ \frac{-\mathbf{w}_j \boldsymbol{\gamma} - (y_j - \mathbf{x}_j \boldsymbol{\beta})\rho/\sigma}{\sqrt{1-\rho^2}} \right\} - \frac{1}{2} \left(\frac{y_j - \mathbf{x}_j \boldsymbol{\beta}}{\sigma} \right)^2 - \ln(\sqrt{2\pi}\sigma) & t_j = 0 \end{cases}$$

where $\Phi(\cdot)$ is the cumulative distribution function of the standard normal distribution.

In the maximum likelihood estimation, σ and ρ are not directly estimated. Rather $\ln \sigma$ and $\operatorname{atanh} \rho$ are directly estimated, where

$$\operatorname{atanh} \rho = \frac{1}{2} \ln \left(\frac{1+\rho}{1-\rho} \right)$$

The standard error of $\lambda = \rho\sigma$ is approximated through the delta method, which is given by

$$\operatorname{Var}(\lambda) \approx \mathbf{D} \operatorname{Var}\{(\operatorname{atanh} \rho \ \ln \sigma)\} \mathbf{D}'$$

where \mathbf{D} is the Jacobian of λ with respect to $\operatorname{atanh} \rho$ and $\ln \sigma$.

Maddala (1983, 120–122) also derives the CF estimator as a two-step estimator. This estimator is implemented here. We will discuss it and then discuss the one-step CF estimator that is also implemented.

For the two-step estimator, probit estimates of the treatment equation

$$\Pr(t_j = 1 \mid \mathbf{w}_j) = \Phi(\mathbf{w}_j \boldsymbol{\gamma})$$

are obtained in the first stage. From these estimates, the hazard, h_j , for each observation j is computed as

$$h_j = \begin{cases} \phi(\mathbf{w}_j \hat{\boldsymbol{\gamma}})/\Phi(\mathbf{w}_j \hat{\boldsymbol{\gamma}}) & t_j = 1 \\ -\phi(\mathbf{w}_j \hat{\boldsymbol{\gamma}})/\{1 - \Phi(\mathbf{w}_j \hat{\boldsymbol{\gamma}})\} & t_j = 0 \end{cases}$$

where ϕ is the standard normal density function. If

$$d_j = h_j(h_j + \mathbf{w}_j \hat{\boldsymbol{\gamma}})$$

then

$$\begin{aligned} E(y_j \mid t_j, \mathbf{x}_j, \mathbf{w}_j) &= \mathbf{x}_j \boldsymbol{\beta} + \delta t_j + \rho \sigma h_j \\ \text{Var}(y_j \mid t_j, \mathbf{x}_j, \mathbf{w}_j) &= \sigma^2 (1 - \rho^2 d_j) \end{aligned}$$

The two-step parameter estimates of $\boldsymbol{\beta}$ and δ are obtained by augmenting the regression equation with the hazard h . Thus the regressors become $[\mathbf{x} \ \mathbf{t} \ h]$, and the additional parameter estimate β_h is obtained on the variable containing the hazard. A consistent estimate of the regression disturbance variance is obtained using the residuals from the augmented regression and the parameter estimate on the hazard

$$\hat{\sigma}^2 = \frac{\mathbf{e}' \mathbf{e} + \beta_h^2 \sum_{j=1}^N d_j}{N}$$

The two-step estimate of ρ is then

$$\hat{\rho} = \frac{\beta_h}{\hat{\sigma}}$$

To understand how the consistent estimates of the coefficient covariance matrix based on the augmented regression are derived, let $\mathbf{A} = [\mathbf{x} \ \mathbf{t} \ h]$ and \mathbf{D} be a square diagonal matrix of size N with $(1 - \hat{\rho}^2 d_j)$ on the diagonal elements. The conventional VCE is

$$\mathbf{V}_{\text{twostep}} = \hat{\sigma}^2 (\mathbf{A}' \mathbf{A})^{-1} (\mathbf{A}' \mathbf{D} \mathbf{A} + \mathbf{Q}) (\mathbf{A}' \mathbf{A})^{-1}$$

where

$$\mathbf{Q} = \hat{\rho}^2 (\mathbf{A}' \mathbf{D} \mathbf{A}) \mathbf{V}_{\mathbf{p}} (\mathbf{A}' \mathbf{D} \mathbf{A})$$

and $\mathbf{V}_{\mathbf{p}}$ is the variance–covariance estimate from the probit estimation of the treatment equation.

The one-step CF estimator is a GMM estimator with stacked moments. See Newey (1984) and Wooldridge (2010, sec. 14.2) for a description of this technique. Many econometric and statistical models can be expressed as conditions on the population moments. The parameter estimates produced by GMM estimators make the sample-moment conditions as true as possible given the data.

Under CF estimation, as in maximum likelihood estimation, we directly estimate $\operatorname{atanh} \rho$ and $\ln \sigma$ rather than ρ and σ , so the parameter vector is

$$\boldsymbol{\theta} = (\boldsymbol{\beta}', \delta, \boldsymbol{\gamma}', \operatorname{atanh} \rho, \ln \sigma)'$$

In this case, we have separate error functions for the treatment assignment

$$u_t(t_j, \mathbf{w}_j, \boldsymbol{\theta}) = \begin{cases} \phi(\mathbf{w}_j \boldsymbol{\gamma}) / \Phi(\mathbf{w}_j \boldsymbol{\gamma}) & t_j = 1 \\ -\phi(\mathbf{w}_j \boldsymbol{\gamma}) / \{1 - \Phi(\mathbf{w}_j \boldsymbol{\gamma})\} & t_j = 0 \end{cases}$$

for the outcome mean

$$u_m(y_j, t_j, \mathbf{x}_j, \mathbf{w}_j, \boldsymbol{\theta}) = y_j - \mathbf{x}_j \boldsymbol{\beta} - \delta t_j - \rho \sigma u_{t,j}$$

and for the outcome variance

$$u_v(y_j, t_j, \mathbf{x}_j, \mathbf{w}_j, \boldsymbol{\theta}) = u_{m,j}^2 - \sigma^2 [1 - \rho^2 \{u_{t,j}(u_{t,j} + \mathbf{w}_j \boldsymbol{\gamma})\}]$$

We calculate the hazard, h_j , prior to estimation from a probit regression of the treatment t_j on the treatment covariates \mathbf{w}_j . Let $\tilde{\mathbf{z}}_j = (\mathbf{x}_j, t_j, h_j)$. Now we define

$$\mathbf{Z}_j = \begin{bmatrix} \tilde{\mathbf{z}}_j & \mathbf{0} & 0 \\ 0 & \mathbf{w}_j & 0 \\ 0 & \mathbf{0} & 1 \end{bmatrix}$$

and

$$s_j(y_j, t_j, \mathbf{x}_j, \mathbf{w}_j, \boldsymbol{\theta}) = \mathbf{Z}'_j \begin{bmatrix} u_{m,j} \\ u_{t,j} \\ u_{v,j} \end{bmatrix}$$

The CF estimator $\hat{\boldsymbol{\theta}}$ is the value of $\boldsymbol{\theta}$ that satisfies the sample-moment conditions

$$\mathbf{0} = \frac{1}{N} \sum_i s_j(y_j, t_j, \mathbf{x}_j, \mathbf{w}_j, \boldsymbol{\theta})$$

The Huber/White/robust sandwich estimator is consistent for the VCE. See Wooldridge (2010, chap. 14), Cameron and Trivedi (2005, chap. 6), and Newey and McFadden (1994).

The formula is

$$\hat{\mathbf{V}} = (1/N) \bar{\mathbf{G}} \bar{\mathbf{S}} \bar{\mathbf{G}}'$$

where

$$\bar{\mathbf{G}} = \left\{ (1/N) \sum_i \frac{\partial s_j(y_j, t_j, \mathbf{x}_j, \mathbf{w}_j, \boldsymbol{\theta})}{\partial \hat{\boldsymbol{\theta}}} \right\}^{-1}$$

and

$$\bar{\mathbf{S}} = (1/N) \sum_i s_j(y_j, t_j, \mathbf{x}_j, \mathbf{w}_j, \boldsymbol{\theta}) s_j(y_j, t_j, \mathbf{x}_j, \mathbf{w}_j, \boldsymbol{\theta})'$$

The matrix $\bar{\mathbf{G}}$ is not symmetric because our estimator comes from stacking the moment conditions instead of optimizing one objective function. The implication is that the robust formula should always be used because, even under correct specification, the nonsymmetric $\bar{\mathbf{G}}$ and the symmetric $\bar{\mathbf{S}}$ converge to different matrices.

General potential-outcome model

Equation (1) can be generalized to a potential-outcome model with separate variance and correlation parameters for the control and treatment groups.

The generalized model is

$$\begin{aligned}y_{0j} &= \mathbf{x}_j \boldsymbol{\beta}_0 + \epsilon_{0j} \\y_{1j} &= \mathbf{x}_j \boldsymbol{\beta}_1 + \epsilon_{1j} \\t_j &= \begin{cases} 1, & \text{if } \mathbf{w}_j \boldsymbol{\gamma} + u_j > 0 \\ 0, & \text{otherwise} \end{cases}\end{aligned}$$

where y_{0j} is the outcome that person j obtains if person j selects treatment 0, and y_{1j} is the outcome that person j obtains if person j selects treatment 1. We never observe both y_{0j} and y_{1j} , only one or the other. We observe

$$y_j = t_j y_{1j} + (1 - t_j) y_{0j}$$

In this unconstrained model, the vector of error terms $(\epsilon_{0j}, \epsilon_{1j}, u_j)'$ comes from a mean zero trivariate normal distribution with covariance matrix

$$\begin{bmatrix} \sigma_0^2 & \sigma_{01} & \sigma_0 \rho_0 \\ \sigma_{01} & \sigma_1^2 & \sigma_1 \rho_1 \\ \sigma_0 \rho_0 & \sigma_1 \rho_1 & 1 \end{bmatrix}$$

The likelihood function for this model is given in Maddala (1983, 224).

$$\ln f_j = \begin{cases} \ln \Phi \left\{ \frac{\mathbf{w}_j \boldsymbol{\gamma} + (y_j - \mathbf{x}_j \boldsymbol{\beta}_1) \rho_1 / \sigma_1}{\sqrt{1 - \rho_1^2}} \right\} - \frac{1}{2} \left(\frac{y_j - \mathbf{x}_j \boldsymbol{\beta}_1}{\sigma_1} \right)^2 - \ln(\sqrt{2\pi} \sigma_1), & t_j = 1 \\ \ln \Phi \left\{ \frac{-\mathbf{w}_j \boldsymbol{\gamma} - (y_j - \mathbf{x}_j \boldsymbol{\beta}_0) \rho_0 / \sigma_0}{\sqrt{1 - \rho_0^2}} \right\} - \frac{1}{2} \left(\frac{y_j - \mathbf{x}_j \boldsymbol{\beta}_0}{\sigma_0} \right)^2 - \ln(\sqrt{2\pi} \sigma_0), & t_j = 0 \end{cases}$$

$$\ln L = \sum_{j=1}^n w_j \ln f_j$$

where $\Phi(\cdot)$ is the cumulative distribution function of the standard normal distribution, and w_j is an optional weight. The covariance between ϵ_{0j} and ϵ_{1j} , σ_{01} , cannot be estimated because the potential outcomes y_{0j} and y_{1j} are never observed simultaneously.

As in the constrained model, σ_0 and σ_1 are not directly estimated in the maximum likelihood estimation; rather, $\ln \sigma_0$ and $\ln \sigma_1$ are estimated.

The parameters ρ_0 and ρ_1 are also not directly estimated; rather, $\operatorname{atanh} \rho_0$ and $\operatorname{atanh} \rho_1$ are directly estimated.

The new parameter vector is

$$\boldsymbol{\theta} = (\boldsymbol{\beta}'_0, \boldsymbol{\beta}'_1, \boldsymbol{\gamma}', \operatorname{atanh} \rho_0, \ln \sigma_0, \operatorname{atanh} \rho_1, \ln \sigma_1)'$$

The CF estimator for this potential-outcome model uses new error functions for the outcome mean

$$\begin{aligned}u_m(y_j, t_j, \mathbf{x}_j, \mathbf{w}_j, \boldsymbol{\theta}) &= y_j - t_j (\mathbf{x}_j \boldsymbol{\beta}_1 + \rho_1 \sigma_1 u_{t,j}) \\&\quad - (1 - t_j) (\mathbf{x}_j \boldsymbol{\beta}_0 + \rho_0 \sigma_0 u_{t,j})\end{aligned}$$

and for the outcome variances

$$\begin{aligned} u_{v,0}(y_j, t_j, \mathbf{x}_j, \mathbf{w}_j, \boldsymbol{\theta}) &= (1 - t_j) (u_{m,j}^2 - \sigma_0^2 [1 - \rho_0^2 \{u_{t,j}(u_{t,j} + \mathbf{w}_j\gamma)\}]) \\ u_{v,1}(y_j, t_j, \mathbf{x}_j, \mathbf{w}_j, \boldsymbol{\theta}) &= t_j (u_{m,j}^2 - \sigma_1^2 [1 - \rho_1^2 \{u_{t,j}(u_{t,j} + \mathbf{w}_j\gamma)\}]) \end{aligned}$$

These error functions are derived based on the identities

$$\begin{aligned} E(y_j | t_j, \mathbf{x}_j, \mathbf{w}_j) &= t_j(\mathbf{x}_j\beta_1 + \rho_1\sigma_1 u_{t,j}) + (1 - t_j)(\mathbf{x}_j\beta_0 + \rho_0\sigma_0 u_{t,j}) \\ \text{Var}(y_j | t_j = 0, \mathbf{x}_j, \mathbf{w}_j) &= \sigma_0^2 [1 - \rho_0^2 \{u_{t,j}(u_{t,j} + \mathbf{w}_j\gamma)\}] \\ \text{Var}(y_j | t_j = 1, \mathbf{x}_j, \mathbf{w}_j) &= \sigma_1^2 [1 - \rho_1^2 \{u_{t,j}(u_{t,j} + \mathbf{w}_j\gamma)\}] \end{aligned}$$

We calculate the hazard, h_j , prior to estimation from a probit regression of the treatment, t_j , on the treatment covariates, \mathbf{w}_j . Let $\tilde{\mathbf{z}}_j = \{\mathbf{x}_j, t_j h_j, (1 - t_j)h_j\}$. Now we define

$$\mathbf{Z}_j = \begin{bmatrix} \tilde{\mathbf{z}}_j & \mathbf{0} & 0 & 0 \\ 0 & \mathbf{w}_j & 0 & 0 \\ 0 & \mathbf{0} & 1 & 0 \\ 0 & \mathbf{0} & 0 & 1 \end{bmatrix}$$

and

$$s_j(y_j, t_j, \mathbf{x}_j, \mathbf{w}_j, \boldsymbol{\theta}) = \mathbf{Z}'_j \begin{bmatrix} u_{m,j} \\ u_{t,j} \\ u_{v,0,j} \\ u_{v,1,j} \end{bmatrix}$$

The CF estimator $\hat{\boldsymbol{\theta}}$ is the value of $\boldsymbol{\theta}$ that satisfies the sample-moment conditions

$$\mathbf{0} = \frac{1}{N} \sum_i s_j(y_j, t_j, \mathbf{x}_j, \mathbf{w}_j, \boldsymbol{\theta})$$

The Huber/White/robust sandwich estimator is consistent for the VCE. See Wooldridge (2010, chap. 14), Cameron and Trivedi (2005, chap. 6), and Newey and McFadden (1994).

The formula is

$$\hat{\mathbf{V}} = (1/N) \bar{\mathbf{G}} \bar{\mathbf{S}} \bar{\mathbf{G}}'$$

where

$$\bar{\mathbf{G}} = \left\{ (1/N) \sum_i \frac{\partial s_j(y_j, t_j, \mathbf{x}_j, \mathbf{w}_j, \boldsymbol{\theta})}{\partial \hat{\boldsymbol{\theta}}} \right\}^{-1}$$

and

$$\bar{\mathbf{S}} = (1/N) \sum_i s_j(y_j, t_j, \mathbf{x}_j, \mathbf{w}_j, \boldsymbol{\theta}) s_j(y_j, t_j, \mathbf{x}_j, \mathbf{w}_j, \boldsymbol{\theta})'$$

The matrix $\bar{\mathbf{G}}$ is not symmetric because our estimator comes from stacking the moment conditions instead of optimizing one objective function. The implication is that the robust formula should always be used because, even under correct specification, the nonsymmetric $\bar{\mathbf{G}}$ and the symmetric $\bar{\mathbf{S}}$ converge to different matrices.

Average treatment effect

The ATE is the average difference of the treated potential outcomes and the control potential outcomes.

By the law of iterated expectations, the ATE is

$$\begin{aligned} E(y_{1j} - y_{0j}) &= E\{E(y_{1j} - y_{0j} | \mathbf{x}_j, \epsilon_{0j}, \epsilon_{1j})\} \\ &= E(\mathbf{x}_j \beta_1 + \epsilon_1 - \mathbf{x}_j \beta_0 - \epsilon_0) \\ &= E\{\mathbf{x}_j (\beta_1 - \beta_0)\} \end{aligned}$$

This expectation can be estimated as a predictive margin when $\mathbf{x}_j (\beta_1 - \beta_0)$ varies in \mathbf{x}_j . Otherwise, the ATE is estimated as the coefficient of t_j in the model.

Average treatment effect on the treated

The ATE is the average difference of the treated potential outcomes and the control potential outcomes on the treated population.

The conditional means of the potential outcomes y_{tj} , $t \in (0, 1)$ for exogenous covariates \mathbf{x}_j and treatment covariates \mathbf{w}_j at treatment $t_j = 1$ are

$$E(y_{tj} | \mathbf{x}_j, \mathbf{w}_j, t_j = 1) = \mathbf{x}_j \beta_t + \rho_t \sigma_t \phi(\mathbf{w}_j \gamma) / \Phi(\mathbf{w}_j \gamma)$$

By the law of iterated expectations, the ATET is

$$\begin{aligned} E(y_{1j} - y_{0j} | t_j = 1) &= E\{E(y_{1j} - y_{0j} | \mathbf{x}_j, \mathbf{w}_j, t_j = 1)\} \\ &= E\{\mathbf{x}_j (\beta_1 - \beta_0) + (\rho_1 \sigma_1 - \rho_0 \sigma_0) \phi(\mathbf{w}_j \gamma) / \Phi(\mathbf{w}_j \gamma) | t_j = 1\} \end{aligned}$$

This expectation can be estimated as a predictive margin on the treated population when $\mathbf{x}_j (\beta_1 - \beta_0)$ varies in \mathbf{x}_j or when the variance and correlation parameters differ by treatment group. Otherwise, the ATET is estimated as the coefficient of t_j in the model.

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Also see

- [TE] **etregress postestimation** — Postestimation tools for etregress
- [TE] **etpoisson** — Poisson regression with endogenous treatment effects
- [ERM] **eregress** — Extended linear regression
- [R] **heckman** — Heckman selection model
- [R] **probit** — Probit regression
- [R] **regress** — Linear regression
- [SVY] **svy estimation** — Estimation commands for survey data
- [U] **20 Estimation and postestimation commands**

etregress postestimation — Postestimation tools for etregress

Postestimation commands predict margins Remarks and examples
 Also see

Postestimation commands

The following postestimation commands are available after `etregress`:

Command	Description
<code>contrast</code>	contrasts and ANOVA-style joint tests of estimates
* <code>estat ic</code>	Akaike's and Schwarz's Bayesian information criteria (AIC and BIC)
<code>estat summarize</code>	summary statistics for the estimation sample
<code>estat vce</code>	variance–covariance matrix of the estimators (VCE)
<code>estat (svy)</code>	postestimation statistics for survey data
<code>estimates</code>	cataloging estimation results
* <code>hausman</code>	Hausman's specification test
<code>lincom</code>	point estimates, standard errors, testing, and inference for linear combinations of coefficients
* <code>lrtest</code>	likelihood-ratio test
<code>margins</code>	marginal means, predictive margins, marginal effects, and average marginal effects
<code>marginsplot</code>	graph the results from margins (profile plots, interaction plots, etc.)
<code>nlcom</code>	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
<code>predict</code>	predictions, residuals, influence statistics, and other diagnostic measures
<code>predictnl</code>	point estimates, standard errors, testing, and inference for generalized predictions
<code>pwcompare</code>	pairwise comparisons of estimates
* <code>suest</code>	seemingly unrelated estimation
<code>test</code>	Wald tests of simple and composite linear hypotheses
<code>testnl</code>	Wald tests of nonlinear hypotheses

* `estat ic`, `lrtest`, and `suest` are not appropriate after `etregress`, `twostep` or `etregress`, `cfunction`.
`hausman` and `lrtest` are not appropriate with `svy` estimation results.

predict

Description for predict

`predict` creates a new variable containing predictions such as linear predictions, conditional treatment effects, standard errors, expected values, and probabilities.

Menu for predict

Statistics > Postestimation

Syntax for predict

After *ML*, *twostep*, or *cfunction*

```
predict [type] newvar [if] [in] [, statistic]
```

After *ML* or *cfunction* for constrained model

```
predict [type] { stub* | newvarreg newvartreat newvarathrho newvarlnsigma }
[if] [in], scores
```

After *ML* or *cfunction* for general potential-outcome model

```
predict [type] { stub* | newvarreg newvartreat newvarathrho0 newvarlnsigma0
newvarathrho1 newvarlnsigma1 } [if] [in], scores
```

statistic	Description
<hr/>	
Main	
<code>xb</code>	linear prediction; the default
<code>cte</code>	conditional treatment effect at treatment level
<code>stdp</code>	standard error of the prediction
<code>stdf</code>	standard error of the forecast
<code>yctr</code>	$E(y_j \mid \text{treatment} = 1)$
<code>ycntr</code>	$E(y_j \mid \text{treatment} = 0)$
<code>ptrt</code>	$\Pr(\text{treatment} = 1)$
<code>xbtr</code>	linear prediction for treatment equation
<code>stdptrt</code>	standard error of the linear prediction for treatment equation

These statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample.

`stdf` is not allowed with `svy` estimation results.

Options for predict

Main

xb, the default, calculates the linear prediction, $\mathbf{x}_j \mathbf{b}$.

cte calculates the treatment effect, the difference of potential-outcome means, conditioned on treatment level.

stdp calculates the standard error of the prediction, which can be thought of as the standard error of the predicted expected value or mean for the observation's covariate pattern. The standard error of the prediction is also referred to as the standard error of the fitted value.

stdf calculates the standard error of the forecast, which is the standard error of the point prediction for one observation. It is commonly referred to as the standard error of the future or forecast value. By construction, the standard errors produced by **stdf** are always larger than those produced by **stdp**; see [Methods and formulas in \[R\] regress postestimation](#).

yctr calculates the expected value of the dependent variable conditional on the presence of the treatment: $E(y_j | \text{treatment} = 1)$.

ycntr calculates the expected value of the dependent variable conditional on the absence of the treatment: $E(y_j | \text{treatment} = 0)$.

ptrt calculates the probability of the presence of the treatment:

$$\Pr(\text{treatment} = 1) = \Pr(\mathbf{w}_j \boldsymbol{\gamma} + u_j > 0).$$

xbtrt calculates the linear prediction for the treatment equation.

stdptrt calculates the standard error of the linear prediction for the treatment equation.

scores, not available with **twostep**, calculates equation-level score variables.

The first new variable will contain $\partial \ln L / \partial (\mathbf{x}_j \boldsymbol{\beta})$.

The second new variable will contain $\partial \ln L / \partial (\mathbf{w}_j \boldsymbol{\gamma})$.

Under the constrained model, the third new variable will contain $\partial \ln L / \partial \text{atanh } \rho$.

Under the constrained model, the fourth new variable will contain $\partial \ln L / \partial \ln \sigma$.

Under the general potential-outcome model, the third new variable will contain $\partial \ln L / \partial \text{atanh } \rho_0$.

Under the general potential-outcome model, the fourth new variable will contain $\partial \ln L / \partial \ln \sigma_0$.

Under the general potential-outcome model, the fifth new variable will contain $\partial \ln L / \partial \text{atanh } \rho_1$.

Under the general potential-outcome model, the sixth new variable will contain $\partial \ln L / \partial \ln \sigma_1$.

margins

Description for margins

`margins` estimates margins of response for linear predictions, conditional treatment effects, expected values, and probabilities.

Menu for margins

Statistics > Postestimation

Syntax for margins

```
margins [marginlist] [, options]
margins [marginlist], predict(statistic ...) [predict(statistic ...) ...] [options]
```

Maximum likelihood and control-function estimation results

statistic	Description
<code>xb</code>	linear prediction; the default
<code>cte</code>	conditional treatment effect at treatment level
<code>yctr</code>	$E(y_j \text{treatment} = 1)$
<code>ycntr</code>	$E(y_j \text{treatment} = 0)$
<code>ptrt</code>	$\Pr(\text{treatment} = 1)$
<code>xbtrt</code>	linear prediction for treatment equation
<code>stdp</code>	not allowed with <code>margins</code>
<code>stdf</code>	not allowed with <code>margins</code>
<code>stdptrt</code>	not allowed with <code>margins</code>

Two-step estimation results

statistic	Description
<code>xb</code>	linear prediction; the default
<code>ptrt</code>	$\Pr(\text{treatment} = 1)$
<code>xbtrt</code>	linear prediction for treatment equation
<code>cte</code>	not allowed with <code>margins</code>
<code>yctr</code>	not allowed with <code>margins</code>
<code>ycntr</code>	not allowed with <code>margins</code>
<code>stdp</code>	not allowed with <code>margins</code>
<code>stdf</code>	not allowed with <code>margins</code>
<code>stdptrt</code>	not allowed with <code>margins</code>

Statistics not allowed with `margins` are functions of stochastic quantities other than `e(b)`.

For the full syntax, see [\[R\] margins](#).

Remarks and examples

The average treatment effect (ATE) and the average treatment effect on the treated (ATET) are the parameters most frequently estimated by postestimation techniques after **etregress**.

When there are no interactions between the treatment variable and the outcome covariates in the constrained model, **etregress** directly estimates the ATE and the ATET; see [example 1](#) of [\[TE\] etregress](#).

When there are no interactions between the treatment variable and the outcome covariates in the general potential-outcome model, **etregress** directly estimates the ATE; see [example 2](#) of [\[TE\] etregress](#).

When there are interactions between the treatment variable and the outcome covariates, you can use **margins** after **etregress** to estimate the ATE. See [example 3](#) and [example 4](#) of [\[TE\] etregress](#) for examples of ATE estimation.

When there are interactions between the treatment variable and the outcome covariates in the constrained model, you can use **margins** after **etregress** to estimate the ATET. See [example 5](#) of [\[TE\] etregress](#) for an example of ATET estimation in the constrained model.

In the general potential-outcome model, you can use **margins** after **etregress** to estimate the ATET. See [example 6](#) of [\[TE\] etregress](#) for an example of ATET estimation in the general potential-outcome model.

Also see

[\[TE\] etregress](#) — Linear regression with endogenous treatment effects

[\[U\] 20 Estimation and postestimation commands](#)

stteffects — Treatment-effects estimation for observational survival-time data

Description Syntax Also see

Description

stteffects estimates average treatment effects, average treatment effects on the treated, and potential-outcome means using observational survival-time data. The available estimators are regression adjustment, inverse-probability weighting, and more efficient methods that combine regression adjustment and inverse-probability weighting.

For a brief description and example of each estimator, see *Remarks and examples* in [TE] **stteffects intro**.

Syntax

stteffects *subcommand* ... [, *options*]

<i>subcommand</i>	Description
ra	regression adjustment
ipw	inverse-probability weighting
ipwra	inverse-probability-weighted regression adjustment
wra	weighted regression adjustment

Also see

[TE] **stteffects intro** — Introduction to treatment effects for observational survival-time data

Description

This entry provides an overview of the treatment-effects estimators that use observational survival-time data and are implemented in **stteffects**. It also provides an overview of the potential-outcomes framework and its application to survival-time data and to the interpretation of the treatment-effects parameters estimated.

The **stteffects** command estimates average treatment effects (ATEs), average treatment effects on the treated (ATETs), and potential-outcome means (POMs). Each of these effect parameters is discussed in this entry. **stteffects** implements a variety of estimators for the ATE, ATET, and POM. The treatment effects can be estimated using regression adjustment (RA), inverse-probability weights (IPW), inverse-probability-weighted regression adjustment (IPWRA), and weighted regression adjustment (WRA). This entry also provides some intuition for the estimators and discusses the trade-offs between them.

Remarks and examples

Remarks are presented under the following headings:

Introduction
A quick tour of the estimators
 Regression adjustment
 Inverse-probability weighting
 Combinations of RA and IPW
 Weighted regression adjustment
Average treatment effect on the treated
Comparison of treatment-effects estimators
Assumptions and trade-offs
 The conditional independence assumption
 The sufficient overlap assumption
 The correct adjustment for censoring assumption
 Assumptions for the ATET
Specification diagnostics and tests
Multivalued treatments

Introduction

The **stteffects** command estimates treatment effects using observational survival-time data.

For some intuition about the methods implemented in the **stteffects** command, consider the following question: Does smoking decrease the time to a second heart attack in the population of women aged 45–55 who have had one heart attack? Three aspects of this question stand out.

1. For ethical reasons, these data will be observational.
2. This question is about the time to an event, and such data are commonly known as survival-time data or time-to-event data. These data are nonnegative and, frequently, right-censored.
3. Many researchers and practitioners want an effect estimate in easy-to-understand units of time.

[Aspect 1](#) is one of the most common reasons for using observational data, and [aspect 2](#) focuses interest on survival-time data.

We are most concerned with [aspect 3](#) because it helps us define and understand the effect of interest. In particular, we would like to know the average change in time to a second heart attack that would occur in the population if all women smoked instead of if no women smoked. This effect is an ATE.

We must solve a missing-data problem to estimate the ATE. The ATE is the population average of the contrast in outcomes when everyone gets the treatment and when no one gets the treatment. Formally, we write this as

$$\text{ATE} = E(t_1 - t_0)$$

where t_1 is the survival time when a subject gets the treatment and t_0 is the survival time when a subject does not get the treatment. For each treatment level, there is a potential outcome that would be observed if a subject received that treatment level: t_1 is the potential outcome that would occur if someone gets the treatment and t_0 is the potential outcome that would occur if someone does not get the treatment. The missing-data problem arises because each subject receives only one treatment level, and so we observe only one of the two potential outcomes.

Much of the survival-time literature uses a hazard ratio as the effect of interest. The ATE has three advantages over the hazard ratio as an effect measure.

1. The ATE measures the effect in the same time units as the outcome instead of in relative conditional probabilities.
2. The ATE is much easier to explain to nontechnical audiences.
3. The models used to estimate the ATE can be much more flexible. Hazard ratios are useful for population effects when they are constant, which occurs when the treatment enters linearly and the distribution of the outcome has a proportional-hazards form. Neither linearity in treatment nor proportional-hazards form is required for the ATE, and neither is imposed on the models fit by the estimators implemented in `stteffects`.

The estimators implemented in `stteffects` use the common missing-data techniques of regression modeling, weighting, and combinations thereof to account for data lost to censoring and to unobserved potential outcomes.

Here we note only a few contributions and entry points to the vast literature on estimating ATEs. The use of potential outcomes to define treatment effects has proved extraordinarily useful; see [Holland \(1986\)](#), [Rubin \(1974\)](#), and [Heckman \(1997\)](#). [Cameron and Trivedi \(2005, chap. 25\)](#), [Wooldridge \(2010, chap. 21\)](#), and [Vittinghoff et al. \(2012, chap. 9\)](#) provide excellent general introductions to estimating ATEs.

□ Technical note

Left-truncation would be another type of missing data. The estimators implemented in `stteffects` do not adjust for left-truncation, so `stteffects` cannot be used with delayed-entry data.

`stteffects` cannot be used with time-varying covariates or multiple-record data because these add a repeated-measure structure that significantly complicates the estimation problem.



A quick tour of the estimators

The **stteffects** command implements five estimators of treatment effects. We introduce each one by showing the basic syntax used to apply it to a common example dataset. See each command's entry for detailed information.

We have some fictional data on the time to a second heart attack among women aged 45–55 years. The treatment, smoking, is stored in the 0/1 indicator `smoke`. These data also contain each woman's age at the time of her first heart attack (`age`), and indices of her exercise level (`exercise`), diet quality (`diet`), and education attainment (`education`) prior to her first heart attack.

Like `streg` and other survival-time commands, **stteffects** uses the outcome variable and the failure indicator computed by `stset`. In this dataset, `atime` is the observed time in years to the second heart attack, and `fail` is the 0/1 indicator that a second heart attack was observed and recorded in `atime`. (When `fail` is 1, `atime` records the time to the second attack; when `fail` is 0, `atime` records a censored observation of the time to the second attack.)

We begin our examples by first reading in the data and then specifying the raw outcome and failure variables to `stset`.

```
. use https://www.stata-press.com/data/r16/sheart
(Time to second heart attack (fictional))

. stset atime, failure(fail)
    failure event: fail != 0 & fail < .
obs. time interval: (0, atime]
exit on or before: failure

2,000  total observations
      0  exclusions

2,000  observations remaining, representing
1,208  failures in single-record/single-failure data
3,795.226  total analysis time at risk and under observation
                           at risk from t =          0
                           earliest observed entry t =      0
                           last observed exit t = 34.17743
```

The output indicates that 1,208 of the 2,000 observations record actual time to a second heart attack. The remaining observations were censored. Now that we have `stset` the data, we can use `stteffects`.

Regression adjustment

Regression modeling of the outcome variable is a venerable approach to solving the missing-data problem in treatment-effects estimation. Known as the regression-adjustment (RA) estimator, this method uses averages of predicted outcomes to estimate the ATE. If the outcome model is well specified, this approach is surprisingly robust.

► Example 1: RA estimation

We now use `stteffects ra` to estimate the ATE by RA. We model the outcome as a function of age, exercise, diet, and education, and we specify that `smoke` is the treatment variable.

```
. stteffects ra (age exercise diet education) (smoke)
    failure _d: fail
    analysis time _t: atime
Iteration 0:  EE criterion = 1.006e-14
Iteration 1:  EE criterion = 2.305e-25
Survival treatment-effects estimation          Number of obs      =      2,000
Estimator       : regression adjustment
Outcome model   : Weibull
Treatment model: none
Censoring model: none
```

<code>_t</code>	Robust Coef.	Std. Err.	<code>z</code>	<code>P> z </code>	[95% Conf. Interval]
ATE smoke (Smoker vs Nonsmoker)	-1.956657	.3331787	-5.87	0.000	-2.609676 -1.303639
P0mean smoke Nonsmoker	4.243974	.2620538	16.20	0.000	3.730358 4.75759

When all women in the population smoke, the average time to a second heart attack is estimated to be 1.96 years less than when no women smoke. The estimated average time to a second heart attack when no women smoke is 4.24 years.

The output reports that a Weibull model was used for the outcome. The other outcome models available are exponential, gamma, and log normal. See [example 2](#) in [TE] `stteffects ra` for an application of the gamma parameterization to this model.

The ratio of the ATE to control-level POM measures the importance of the effect. In this example, when all women smoke, the time to a second heart attack falls by an estimated 46% relative to the case in which none of them smoke. See [example 3](#) in [TE] `stteffects ra` for an example that uses `nlcom` to compute a point estimate and a confidence interval for this ratio.

Unlike the IPW estimator discussed in the next section, RA does not model treatment assignment or the censoring process. Treatment assignment is handled by fitting separate models for each treatment level and averaging the predicted outcomes. As is standard in the survival-time literature, the censoring term in the log-likelihood function accounts for censoring; see [Kalbfleisch and Prentice \(2002, chap. 3\)](#), [Cameron and Trivedi \(2005, chap. 17\)](#), [Cleves, Gould, and Marchenko \(2016, chap. 13\)](#), and [Wooldridge \(2010, chap. 22\)](#).

See [\[TE\] stteffects ra](#) for further discussion of this command and the RA estimator.

Inverse-probability weighting

Sometimes researchers are more comfortable modeling treatment assignment than the outcome. Inverse-probability-weighted (IPW) estimators use weighted averages of the observed outcome to estimate the POMs and the ATE. The weights correct for the missing data. When there is no censoring, the missing potential outcome is the only missing data, and the weights are constructed from a model of treatment assignment. When the data may be censored, the weights must control for censoring and the missing potential outcome. In this case, IPW estimators construct the weights from two models, one for the censoring time and one for treatment assignment.

▷ Example 2: IPW estimation

Here we use `stteffects ipw` to estimate the effect of smoking on the time to a second heart attack. The model of assignment to the treatment `smoke` depends on `age`, `exercise`, `diet`, and `education`. The time-to-censoring model also depends on `age`, `exercise`, `diet`, and `education`.

<code>_t</code>	<code>Robust</code>	<code>Coef.</code>	<code>Std. Err.</code>	<code>z</code>	<code>P> z </code>	<code>[95% Conf. Interval]</code>
ATE smoke (Smoker vs Nonsmoker)		-2.187297	.6319837	-3.46	0.001	-3.425962 -.9486314
P0mean smoke Nonsmoker		4.225331	.517501	8.16	0.000	3.211047 5.239614

When all women in the population smoke, the average time to a second heart attack is estimated to be 2.19 years less than when no women smoke. The estimated average time to a second heart attack when no women smoke is 4.23 years. When all women smoke, the average time to a second heart attack falls by an estimated 52% relative to the case when no women smoke.

The estimates have changed; however, the interpretation is the same as for the RA estimator because the IPW and RA estimators are estimating the same population effects. Under correct model specification, the estimates will differ in finite samples, but the size of these differences will decrease as the sample size gets larger. For the case at hand, the estimated ATE and control-level POM are roughly similar to those produced by the RA estimator using the Weibull model for the outcome.

Recall that IPW estimators are weighted averages of observed outcomes and that the weights control for the missing outcomes. Weights in survival-time data have two components: one for the missing potential outcome and one for data lost to censoring. We used a logit model for treatment assignment, so the component of the weights that controls for the missing potential outcome comes from the

estimated logit parameters. We used a Weibull model for the time to censoring, so the component of the weights that controls for data lost to censoring comes from the estimated Weibull parameters.



Using weighting from an estimated treatment-assignment model to control for the missing potential outcome is standard in the treatment-effects literature; for example, see [TE] **teffects intro advanced**, Wooldridge (2010, chap. 21), Vittinghoff et al. (2012, chap. 9), Hirano, Imbens, and Ridder (2003), Cattaneo (2010), and Cattaneo, Drukker, and Holland (2013). Modeling the time to censoring is specific to the survival-time treatment-effects literature; see Bai, Tsiatis, and O'Brien (2013) and Robins and Rotnitzky (2006). See *Methods and formulas* in [TE] **stteffects ipwra** for more details.

See [TE] **stteffects ipw** for further discussion of this command and the IPW estimator.

Combinations of RA and IPW

More efficient estimators are obtained by combining IPW and RA, due to Wooldridge (2007) and Wooldridge (2010, chap. 21) and denoted by IPWRA. Unlike the estimators discussed in Wooldridge (2010, chap. 21), both the treatment and the outcome models must be correctly specified to estimate the ATE.

The IPWRA estimator uses estimated weights that control for missing data to obtain missingness-adjusted regression coefficients that are used to compute averages of predicted outcomes to estimate the POMs. The estimated ATE is a contrast of the estimated POMs. These weights always involve a model for treatment assignment. You choose whether to account for censoring by including a term in the log-likelihood function or whether to use weights that also account for the data lost to censoring.

▷ Example 3: Likelihood-adjusted-censoring IPWRA estimation

We model the outcome (time to a second heart attack) as a function of `age`, `exercise`, `diet`, and `education`. We model assignment to the treatment `smoke` as a function of the same covariates.

```
. stteffects ipwra (age exercise diet education)
> (smoke age exercise diet education)
    failure _d: fail
    analysis time _t: atime
Iteration 0:  EE criterion =  6.476e-15
Iteration 1:  EE criterion =  1.116e-26
Survival treatment-effects estimation          Number of obs      =      2,000
Estimator       : IPW regression adjustment
Outcome model   : Weibull
Treatment model: logit
Censoring model: none
```

<code>_t</code>	Robust						
	Coef.	Std. Err.	<code>z</code>	<code>P> z </code>	[95% Conf. Interval]		
ATE							
smoke (Smoker vs Nonsmoker)	-1.592494	.4872777	-3.27	0.001	-2.54754	- .637447	
P0mean							
smoke Nonsmoker	4.214523	.2600165	16.21	0.000	3.7049	4.724146	

The estimated ATE of -1.59 and control-level POM of 4.21 are similar to the reported values of -1.96 and 4.24 in example 1.

We did not specify a model for the time to censoring, so censoring is handled by including a term in the log-likelihood function in the Weibull outcome model. We denote this likelihood-adjusted-censoring (LAC) version of the IPWRA estimator by LAC-IPWRA.



▷ Example 4: Weighted-adjusted-censoring IPWRA estimation

Instead of including a term in the log-likelihood function, the weighted-adjusted-censoring IPWRA (WAC-IPWRA) estimator uses estimated weights to adjust for censoring. We model the time to a second heart attack as a function of `age`, `exercise`, `diet`, and `education`; we model assignment to the treatment `smoke` as a function of the same covariates; and we model the time to censoring as a function of `age`, `exercise`, and `diet`.

```
. stteffects ipwra (age exercise diet education)
> (smoke age exercise diet education) (age exercise diet)
    failure _d: fail
    analysis time _t: atime
Iteration 0:  EE criterion =  2.797e-13
Iteration 1:  EE criterion =  2.032e-25
Survival treatment-effects estimation          Number of obs      =      2,000
Estimator       : IPW regression adjustment
Outcome model   : Weibull
Treatment model: logit
Censoring model: Weibull

```

<code>_t</code>	Robust					[95% Conf. Interval]
	Coef.	Std. Err.	<code>z</code>	<code>P> z </code>		
ATE smoke (Smoker vs Non-smoker)	-2.037944	.6032549	-3.38	0.001	-3.220302	-.855586
P0mean smoke Non-smoker	4.14284	.4811052	8.61	0.000	3.199891	5.085789

The estimated ATE of -2.04 and control-level POM of 4.14 are similar to the reported values of -1.96 and 4.24 in [example 1](#).

The weights for censoring are constructed from the estimated parameters because we specified a time-to-censoring model.



Under correct specification, both versions of the IPWRA estimator estimate the same ATE and control-level POM as estimated by RA and IPW.

The addition of the time-to-censoring model makes the WAC-IPWRA somewhat less robust than the LAC-IPWRA estimator. Weighting methods to control for censoring also place more restrictive assumptions on the censoring process. For example, the censoring time must be random, otherwise it would be impossible to construct the weights. In [Assumptions and trade-offs](#) below, we discuss the trade-offs among the estimators and the assumptions that each requires. For the moment, we note that we believe the LAC-IPWRA estimator is more robust than the WAC-IPWRA estimator.

See [TE] `stteffects ipwra` for further discussion of this command and the IPWRA estimator.

Weighted regression adjustment

When estimating the parameters of an outcome model, the weighted regression-adjustment (WRA) estimator uses weights instead of a term in the log-likelihood function to adjust for censoring. These weights are constructed from a model for the censoring process. The estimated parameters are subsequently used to compute averages of predicted outcomes that estimate the POMs. A contrast of the estimated POMs estimates the ATE.

▷ Example 5: WRA estimation

We model the time to a second heart attack as a function of `age`, `exercise`, `diet`, and `education`; we specify that `smoke` is the treatment; and we model the time to censoring as a function of `age`, `exercise`, and `diet`.

```
. stteffects wra (age exercise diet education) (smoke) (age exercise diet)
    failure _d: fail
    analysis time _t: atime
Iteration 0: EE criterion = 7.116e-15
Iteration 1: EE criterion = 5.859e-27
Survival treatment-effects estimation           Number of obs      =      2,000
Estimator       : weighted regression adjustment
Outcome model   : Weibull
Treatment model: none
Censoring model: Weibull
```

<code>_t</code>	Robust					
	Coef.	Std. Err.	<code>z</code>	<code>P> z </code>	[95% Conf. Interval]	
ATE smoke (Smoker vs Nonsmoker)	-2.152014	.4986005	-4.32	0.000	-3.129253	-1.174775
P0mean smoke Nonsmoker	4.079273	.4379517	9.31	0.000	3.220903	4.937642

The estimated ATE of -2.15 and control-level POM of 4.08 are similar to the reported values of -1.96 and 4.24 in [example 1](#). Like the other estimators discussed, the WRA estimators estimate the same effect parameters as the RA estimator, so the interpretation is the same.



In many survival-time applications, using weights to adjust for censoring is probably less robust than just including a term in the log-likelihood function for the outcome model. The model used to construct the weights is just as complicated as the outcome model, and including the term in the log-likelihood function places fewer restrictions on the censoring process, as discussed in [The correct adjustment for censoring assumption](#) below.

See [TE] `stteffects wra` for further discussion of this command and the WRA estimator.

Average treatment effect on the treated

Intuitively, the average treatment effect on the treated (ATET) is the effect in a well-defined, at-risk subpopulation. Sometimes the subpopulation that gets the treatment defines such an at-risk subpopulation. For example, we may want to know the average change in time to a second heart attack among female smokers aged 45–55 who have had a heart attack if they all became nonsmokers. This effect is the ATET.

Below, we use `stteffects ra` to estimate the ATET by RA.

```
. stteffects ra (age exercise diet education) (smoke), atet
    failure _d: fail
    analysis time _t: atime
Iteration 0: EE criterion = 1.006e-14
Iteration 1: EE criterion = 2.970e-26
Survival treatment-effects estimation           Number of obs      =      2,000
Estimator       : regression adjustment
Outcome model   : Weibull
Treatment model: none
Censoring model: none
```

<u>_t</u>	Robust					
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
ATET						
smoke (Smoker vs Nonsmoker)	-1.527476	.2489203	-6.14	0.000	-2.015351	-1.039602
P0mean						
smoke Nonsmoker	3.436937	.2217808	15.50	0.000	3.002255	3.87162

Now, all effects are calculated only for the subpopulation of women aged 45–55 years who smoke after their first heart attack. If no women in the subpopulation were to smoke, the average time to a second heart attack would be 3.44 years. When all women in the subpopulation smoke (the observed behavior), the average time to a second heart attack is estimated to be 1.53 years less than if no women in the subpopulation had smoked. In other words, if we could somehow turn all smokers in the subpopulation into nonsmokers, the average time to a second heart attack would be 3.44 years instead of 1.91 years ($3.44 - 1.53 = 1.91$).

These point estimates are a little different than those for the ATE and the control-level POM in the full population of women aged 45–55 years who have had one heart attack. The difference indicates that this particular health cost of smoking may be smaller among women who choose to smoke than in the full population.

Comparison of treatment-effects estimators

We can classify the estimators implemented in `stteffects` into five categories: 1) estimators based on a model for the outcome variable; 2) estimators based on models for the treatment assignment and the censoring time; 3) estimators based on models for the outcome variable and the treatment assignment; 4) estimators based on models for the outcome variable, the treatment assignment, and the censoring time; and 5) estimators based on models for the outcome variable and the censoring time.

Because there are several categories of estimators, the user must decide whether to model the outcome, the probability of treatment, the time to censoring, or some combination thereof.

Each category of estimator contains a variety of choices about the functional forms for the models.

We now provide some intuition behind each category of estimator and discuss the relationships.

1. When modeling only the outcome, separate outcome models for each treatment level account for treatment assignment, and censoring is adjusted for in the log-likelihood function. This approach is used in the RA estimators.
2. Some researchers would rather avoid modeling the outcome. Some estimators use weighted averages of the observed outcome to estimate the effect. When estimating treatment effects from observational survival-time data, the weights used must account for treatment assignment and censoring. Models for treatment assignment and time to censoring are used to construct the weights. This approach is used in the IPW estimators.
3. When seeking a more efficient estimator, it is natural to model both the outcome and the treatment and to adjust for censoring in the outcome model. This approach is used in the LAC-IPWRA estimators.
4. When seeking a more efficient estimator, another natural approach is to model both the outcome and the treatment and to adjust for censoring by weights that come from a time-to-censoring model. This approach is used in the WAC-IPWRA estimators.
5. We could modify approach 1 to model the outcome and the time to censoring so that censoring is handled by weighting and its own model instead of by likelihood adjustment. This approach is used in the WRA estimators.

While researcher preferences over what to model largely dictate the approach selected, we quickly note two points that could affect which approach works best. First, we can adjust for censoring by weighting only when censoring time is random. Second, weighting estimators become unstable if the weights get too large.

In the next section, we elaborate on the assumptions needed and the trade-offs among the approaches to estimation.

Assumptions and trade-offs

The estimators implemented in `stteffects` require three assumptions: conditional independence, sufficient overlap, and correct adjustment for censoring.

The conditional independence assumption

All estimators implemented in `stteffects` require the potential outcomes to be independent of the treatment assignment after conditioning on the covariates. Randomized experiments and the Heckman selection model are two motivating frameworks for the conditional independence assumption.

When the treatment is assigned randomly, the randomization ensures that the potential outcomes are independent of the treatment assignment. In observational data, the treatment is not randomly assigned. However, many important questions can only be answered using observational data because it would be unethical to randomly allocate hazardous treatments, for example, smoking. The conditional independence assumption in observational data says that treatment assignment is as good as random after conditioning on the covariates.

We can also understand conditional independence from a modeling framework. The Heckman selection model specifies that each of the potential outcomes and the treatment assignment process are functions of observable covariates and unobservable errors. The potential outcomes are conditionally independent of the treatment assignment when the unobservable errors in the treatment-assignment process are independent of the unobservable errors in each of the potential-outcome processes. See [The CI assumption](#) in [\[TE\] teffects intro advanced](#) for a detailed example.

Both frameworks lead to the same conclusion: we need to observe and to condition on a sufficient number of covariates.

Essentially, all the estimators in `stteffects` are equally susceptible to violations of the conditional independence assumption. No one estimator is any more robust to the conditional independence assumption than any other one.

Estimating the ATE among the subpopulation of those who get the treatment requires a significantly weaker version of the CI assumption; see [Assumptions for the ATET](#) below.

For more details about the conditional independence assumption, see [The CI assumption](#) in [\[TE\] teffects intro advanced](#), and see Rosenbaum and Rubin (1983), Heckman (1997), Imbens and Wooldridge (2009), Cameron and Trivedi (2005, sec. 25.2), Wooldridge (2010, chap. 21), and Vittinghoff et al. (2012, chap. 9).

The sufficient overlap assumption

The sufficient overlap assumption requires that each individual have a sufficiently positive probability of being assigned to each treatment level. We believe that the RA estimator is more robust than the other estimators to near violations of the sufficient overlap condition, under correct model specification.

The overlap condition has no specification test, but using `teffects overlap` and then summarizing the predicted treatment probabilities presents good diagnostics of overlap problems.

The correct adjustment for censoring assumption

The correct adjustment for censoring assumption has two parts. First, either the censoring time must be fixed or the process must be conditionally-on-covariates independent of the potential outcomes and the treatment-assignment process. This assumption is standard in survival analysis; see, for example, Kalbfleisch and Prentice (2002, chap. 3).

Second, the method used to adjust to censoring must be correct. For the RA and LAC-IPWRA estimators, which use likelihood-adjusted censoring, the second assumption is no more restrictive than assuming correct specification of the outcome model. For the IPW, WAC-IPWRA, and WRA estimators, which adjust by weighting, the second assumption requires that the censoring be random and that the censoring process be correctly modeled.

Under correct specification, all the estimators in `stteffects` perform well. However, we believe that estimators that use likelihood adjustment instead of weighting are more robust for three reasons.

1. The estimators that use weighting to adjust for censoring cannot handle fixed censoring processes. If the censoring process is not random, the weights are not well defined.
2. The estimators that use weighting to adjust for censoring do not allow the random censoring process to vary by treatment level.
3. The estimators that use weighting to adjust for censoring require an additional sufficient overlap condition: the probability of not being censored must be sufficiently greater than 0 or else the weights that adjust for censoring get too large.

While the estimators that use WAC instead of LAC require a few more assumptions, some researchers are more comfortable modeling the treatment and censoring than the outcome. In this case, the IPW or WAC-IPWRA estimator would be the estimator of choice.

See [Specification diagnostics and tests](#) below for information about testing these assumptions.

Assumptions for the ATET

We noted in [Average treatment effect on the treated](#) that the ATET is sometimes more interesting than the ATE. We can also estimate the ATET under less restrictive versions of the conditional independence assumption and the sufficient overlap assumption than those required for the ATE.

While ATE estimation requires that the potential outcomes for both the treated and the not treated be conditionally independent of treatment assignment, ATET estimation requires that only the not treated potential outcome be conditionally independent of treatment assignment.

This weaker version of conditional independence allows the gains from the treatment to be related to treatment assignment, after conditioning on the covariates. We can estimate the ATET, but not the ATE, if some unobserved factor increases (or decreases) the likelihood of assignment to the treatment, increases (or decreases) the time to event in the treatment group, and has no effect on the time to event when not in the treatment group.

For example, suppose that smoking is an acquired taste and that individuals who acquire the taste for smoking more easily are less adversely affected by smoking and otherwise similar to everyone else when not smoking. Taste for smoking is unobservable, and our data have no measure of this variable. In this case, we could estimate the ATET but not the ATE.

The weaker version of the sufficient overlap assumption only requires that each individual in the treated subpopulation have a positive probability of not getting treated. In contrast, ATE estimation requires that each individual in the population have a positive probability of getting each treatment level. In particular, we can estimate the ATET, but not the ATE, when some individuals in the population have zero chance of getting the treatment. For example, we could estimate the ATET, but not the ATE, if some women will never smoke for religious reasons.

Even when the conditions for ATE estimation hold, the ATE and ATET may differ. Finding that the ATET is significantly different from the ATE does not mean that the ATE is incorrectly estimated.

See [Heckman \(1997\)](#) and [Wooldridge \(2010, 911–912\)](#) for more information about the assumptions necessary to estimate the ATET.

Specification diagnostics and tests

After `stteffects ipw` and `stteffects ipwra`, some specification checks for the treatment-assignment model and the overlap condition are available.

The checks for the treatment-assignment model are known as balance checks. When the covariate distributions are invariant to the treatment level, the covariates are said to be balanced. The concept of balanced covariates comes from the experimental literature, in which random treatment assignment ensures that the covariates are balanced.

In observational data, the covariates are almost never balanced in the raw data. Weighting methods can be viewed as using a treatment-assignment model to balance the covariates. If the treatment-assignment model is well specified, the weights constructed from this model will balance the covariates. One of the nice features of balance checks is that they do not depend on the outcome or its distribution. This fact is especially useful for survival-time outcomes because censoring of the outcome has no effect on the balance checks, so the balance checks implemented in `tebalance` work without modification.

Conditional on the treatment-assignment model being well specified, we can use the estimated probabilities of treatment, known as the propensity scores, to look for signs that the overlap condition is violated. These checks depend only on the estimated treatment probabilities and are not affected by any censoring of the outcome, so the methods implemented in `teffects overlap` work without modification.

We begin examining our model by using `tebalance summarize` after refitting the models used by the LAC-IPWRA estimator.

```
. quietly stteffects ipwra (age exercise diet education)
> (smoke age exercise diet education)
. tebalance summarize
```

Covariate balance summary

			Raw	Weighted
Number of obs =			2,000	2,000.0
Treated obs =			738	994.1
Control obs =			1,262	1,005.9

	Standardized differences		Variance ratio	
	Raw	Weighted	Raw	Weighted
age	-.3122094	-.0184574	.8547308	.9370065
exercise	-.4975269	-.0458412	.4966778	.8342339
diet	-.2479756	.0021802	.7937645	1.095347
education	-.4801442	-.0216366	.6015139	.978078

The weighted standardized differences are much closer to 0 than the raw standardized differences, and the weighted variance ratios are much closer to 1 than the raw variance ratios. These results indicate that the model-based treatment weights balanced the covariates; see [TE] `tebalance` and [TE] `tebalance summarize` for details.

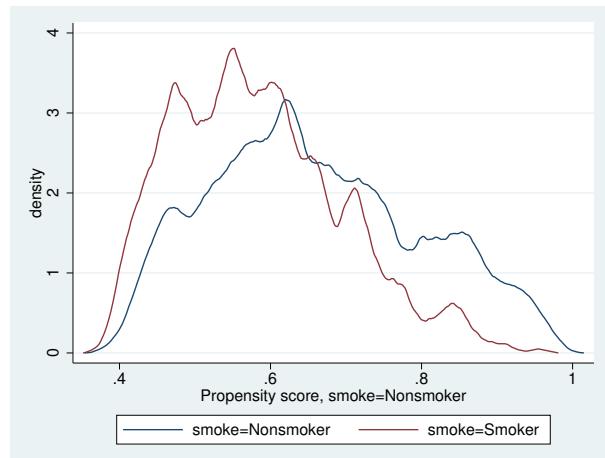
The diagnostics presented by `tebalance summarize` are not a formal test. However, we can use `tebalance overid` to conduct a formal test of the hypothesis that the weights constructed from the treatment-assignment model balanced the covariates.

```
. tebalance overid
Iteration 0: criterion = .22681884
Iteration 1: criterion = .22692316 (backed up)
Iteration 2: criterion = .23090158
Iteration 3: criterion = .2311461
Iteration 4: criterion = .23256285
Iteration 5: criterion = .23286304
Iteration 6: criterion = .23335858
Iteration 7: criterion = .2335567
Iteration 8: criterion = .2335671
Iteration 9: criterion = .23356711
Overidentification test for covariate balance
H0: Covariates are balanced:
chi2(5)      =  3.28142
Prob > chi2  =  0.6567
```

There is no significant evidence against the null hypothesis. The interpretation is that we do not reject the null hypothesis that the treatment-assignment model is well specified; see [TE] `tebalance` and [TE] `tebalance overid` for details.

Given that we do not reject the treatment-assignment model, we can use this model to look for evidence that the overlap condition is violated. We begin by using `teffects overlap`.

```
. teffects overlap, plevel(Smoker)
```



The densities of the propensity scores for the smokers and nonsmokers appear to have the same support, indicating that there is no violation of the overlap condition. The only indicator of a possible problem is that the support of the density for nonsmokers gets very close to 0. This problem would affect ATE estimation but not ATET estimation, as discussed in [Assumptions and trade-offs](#). To further investigate, we compute and summarize the predicted propensity score by treatment level.

```
. predict ps1, ps tlevel(Smoker)
```

```
. summarize ps1 if smoke == 0
```

Variable	Obs	Mean	Std. Dev.	Min	Max
ps1	1,262	.3410001	.1381673	.014819	.6161401

Variable	Obs	Mean	Std. Dev.	Min	Max
ps1	738	.4168805	.1107557	.0454891	.6216282

To interpret these results, recall that ATE estimation requires that the minimum propensity score for each treatment level be sufficiently greater than 0 and that the maximum propensity score for each treatment level be sufficiently less than 1. Also recall that ATET estimation only requires that the maximum propensity score for each treatment level be sufficiently less than 1.

For ATE estimation, only the minimum predicted propensity score for nonsmokers presents a challenge, and 0.015 is probably not too small. For ATET estimation, neither maximum causes concern.

For information about choosing among the `stteffects` estimators and their functional forms for the different models, see [Model choice](#) under Remarks and examples in [TE] [teffects intro advanced](#).

Multivalued treatments

`stteffects` can estimate treatment effects for multivalued treatments; here we provide some examples. See [TE] [teffects multivalued](#) for an introduction to interpreting effects from multivalued treatments.

▷ Example 6: Multivalued ATE estimation

We have another fictional dataset that records the time to a second heart attack among women aged 45–55 years. In this dataset, `atime` is the observed time in years to the second heart attack, and `fail` is the 0/1 indicator that a second heart attack was observed and recorded in `atime`. (When `fail` is 1, `atime` records the time to the second attack; when `fail` is 0, `atime` records a censored observation of the time to the second attack.)

These data also contain the age at the time of the first heart attack (`age`), and indices of each woman's exercise level (`exercise`), diet quality (`diet`), and education attainment (`education`) prior to her first heart attack.

The treatment, smoking, is stored in the categorical variable `smoke`, which has the following value labels. The women who never smoked are labeled as N; the women who previously smoked but quit before their first heart attack are labeled as B; the women who previously smoked but quit after their first heart attack are labeled as A; and the women who continued to smoke after their first heart attack are labeled as S.

We begin by first reading in the data and then reviewing information previously stored using `stset`.

```
. use https://www.stata-press.com/data/r16/sheartm, clear
(Time to second heart attack (fictional))

. stset
-> stset atime, failure(fail)

    failure event: fail != 0 & fail < .
obs. time interval: (0, atime]
exit on or before: failure

10,000  total observations
      0  exclusions

10,000  observations remaining, representing
      9,741  failures in single-record/single-failure data
27,999.155  total analysis time at risk and under observation
                           at risk from t =          0
                           earliest observed entry t =      0
                           last observed exit t = 17.40826
```

We continue by tabulating the treatment variable `smoke`.

Smoking level	Freq.	Percent	Cum.
N	3,167	31.67	31.67
B	2,263	22.63	54.30
A	1,924	19.24	73.54
S	2,646	26.46	100.00
Total	10,000	100.00	

We see that 31.67% of the women never smoked, 22.63% of the women previously smoked but quit before their first heart attack, 19.24% of the women previously smoked but quit after their first heart attack, and 26.46% of the women continued to smoke after their first heart attack.

We now use `stteffects ra` to estimate the ATE by RA. We model the outcome as a function of age, exercise, diet, and education, and we specify that `smoke` is the treatment variable.

Robust						
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
Survival treatment-effects estimation						
Number of obs	=				10,000	
Estimator	:	regression adjustment				
Outcome model	:	Weibull				
Treatment model:	none					
Censoring model:	none					
_t						
ATE						
smoke						
(B vs N)	-.4129793	.0317	-13.03	0.000	-.47511	-.3508485
(A vs N)	-1.281031	.032866	-38.98	0.000	-1.345447	-1.216614
(S vs N)	-2.167359	.0338994	-63.93	0.000	-2.233801	-2.100917
P0mean						
smoke						
N	3.745919	.0289014	129.61	0.000	3.689273	3.802565

The average time to a second heart attack is 0.41 years sooner when all the women smoked at some point but quit before their first heart attack than when all the women never smoked. The average time to a second heart attack is 1.28 years sooner when all the women smoked at some point but quit after their first heart attack than when all the women never smoked. The average time to a second heart attack is 2.17 years sooner when all the women continued to smoke after their first heart attack than when all the women never smoked.



▷ Example 7: Multivalued ATET estimation

In the at-risk subpopulation of women who continued to smoke, we want to estimate the effect of continuing to smoke (S) versus quitting after the first heart attack (A). Below we estimate the ATETs by RA, specifying A to be the control level and S to be the treatment level.

```
. stteffects ra (age exercise diet education) (smoke), atet control(A) tlevel(S)
    failure _d: fail
    analysis time _t: atime
Iteration 0:  EE criterion = 1.390e-20
Iteration 1:  EE criterion = 1.167e-29
Survival treatment-effects estimation          Number of obs      =     10,000
Estimator       : regression adjustment
Outcome model   : Weibull
Treatment model: none
Censoring model: none
```

<u>_t</u>	Robust					
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
ATET						
smoke						
(N vs A)	1.290123	.0377552	34.17	0.000	1.216125	1.364122
(B vs A)	.8748349	.0239595	36.51	0.000	.8278751	.9217946
(S vs A)	-.8869257	.0272301	-32.57	0.000	-.9402958	-.8335557
POmean						
smoke						
A	2.500108	.0217833	114.77	0.000	2.457413	2.542802

The parameter (S vs A) is the one of interest. The estimate implies that the average time to a second heart attack among women who continue to smoke is 0.89 years sooner when they all continue to smoke than when they all quit smoking after their first heart attack.



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Also see

- [TE] **stteffects postestimation** — Postestimation tools for stteffects
- [TE] **teffects intro advanced** — Advanced introduction to treatment effects for observational data
- [ST] **streg** — Parametric survival models
- [ST] **stset** — Declare data to be survival-time data
- [U] **20 Estimation and postestimation commands**

stteffects ipw — Survival-time inverse-probability weighting

Description	Quick start	Menu	Syntax
Options	Remarks and examples	Stored results	Methods and formulas
References	Also see		

Description

stteffects ipw estimates the average treatment effect (ATE), the average treatment effect on the treated (ATET), and the potential-outcome means (POMs) from observational survival-time data with random time to censoring. Estimation is by inverse-probability weighting (IPW). IPW estimators use weighted averages of the observed outcome. The estimated weights correct for missing data on the potential outcomes and for censored survival times. **stteffects ipw** offers several choices for the functional forms of the treatment model and the time-to-censoring model. Binary and multivalued treatments are accommodated.

See [TE] **stteffects intro** for an overview of estimating treatment effects from observational survival-time data.

Quick start

Specify `time` as observed failure time and `fail` as failure indicator

```
stset time, failure(fail)
```

ATE of binary `treat2` on `time` by IPW using a logistic model of `treat2` on `x` and `w` and using `x` and `w` in a Weibull model for the censoring time

```
stteffects ipw (treat2 x w) (x w)
```

As above, but estimate the ATET

```
stteffects ipw (treat2 x w) (x w), atet
```

ATE of `treat2` on `time` by IPW using a probit model of `treat2` on `x` and `w` and using `x` and `w` in a gamma model for the censoring time

```
stteffects ipw (treat2 x w, probit) (x w, gamma)
```

ATE for treatment levels 2 and 3 of three-valued treatment `treat3`

```
stteffects ipw (treat3 x w) (x w)
```

As above, and specify that `treat3 = 3` is the control level using the value label "MyControl" for 3

```
stteffects ipw (treat3 x w) (x w), control("MyControl")
```

Menu

Statistics > Treatment effects > Survival outcomes > Inverse-probability weighting (IPW)

Syntax

```
stteffects ipw (tvar tmvarlist [ , tmoptions ]) (cmvarlist [ , cmoptions ])
[ if ] [ in ] [ , stat options ]
```

tvar must contain integer values representing the treatment levels.

tmvarlist specifies the variables that predict treatment assignment in the treatment model.

cmvarlist specifies the variables that predict censoring in the censoring model.

<i>tmoptions</i>	Description
Model	
<u>logit</u>	logistic treatment model; the default
<u>probit</u>	probit treatment model
<u>hetprobit</u> (<i>varlist</i>)	heteroskedastic probit treatment model
<u>noconstant</u>	suppress constant from treatment model
<i>cmoptions</i>	Description
Model	
<u>weibull</u>	Weibull; the default
<u>exponential</u>	exponential
<u>gamma</u>	two-parameter gamma
<u>lnormal</u>	lognormal
<u>ancillary</u> (<i>avarlist</i> [, <u>noconstant</u>])	specify variables used to model ancillary parameter
<u>noconstant</u>	suppress constant from censoring model
<i>stat</i>	Description
Stat	
<u>ate</u>	estimate average treatment effect in population; the default
<u>atet</u>	estimate average treatment effect on the treated
<u>pomeans</u>	estimate potential-outcome means

options	Description
SE/Robust	
vce(vcetype)	<i>vcetype</i> may be <code>robust</code> , <code>cluster</code> <i>clustvar</i> , <code>bootstrap</code> , or <code>jackknife</code>
Reporting	
level(#)	set confidence level; default is <code>level(95)</code>
aequations	display auxiliary-equation results
noshow	do not show st setting information
display_options	control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling
Maximization	
maximize_options	control the maximization process; seldom used
iterinit(#)	specify starting-value iterations; seldom used
Advanced	
pstolerance(#)	set the tolerance for the overlap assumption
osample(newvar)	identify observations that violate the overlap assumption
control(# label)	specify the level of <i>tvar</i> that is the control
tlevel(# label)	specify the level of <i>tvar</i> that is the treatment
coeflegend	display legend instead of statistics

You must `stset` your data before using `stteffects`; see [ST] `stset`.

tmvarlist, *cmvarlist*, and *avarlist* may contain factor variables; see [U] 11.4.3 Factor variables.

`bootstrap`, `by`, `jackknife`, and `statsby` are allowed; see [U] 11.1.10 Prefix commands.

Weights are not allowed with the `bootstrap` prefix; see [R] `bootstrap`.

`fweights`, `iweights`, and `pweights` may be specified using `stset`; see *Weights* under Remarks and examples in [ST] `stset`. However, weights may not be specified if you are using the `bootstrap` prefix.

`coeflegend` does not appear in the dialog box.

See [U] 20 Estimation and postestimation commands for more capabilities of estimation commands.

Options

Model

ancillary(avarlist [, noconstant]) specifies the variables used to model the ancillary parameter. By default, the ancillary parameter does not depend on covariates. Specifying `ancillary(avarlist, noconstant)` causes the constant to be suppressed in the model for the ancillary parameter. `noconstant`; see [R] Estimation options.

Stat

stat is one of three statistics: `ate`, `atet`, or `pomeans`. `ate` is the default.

`ate` specifies that the average treatment effect be estimated.

`atet` specifies that the average treatment effect on the treated be estimated.

`pomeans` specifies that the potential-outcome means for each treatment level be estimated.

SE/Robust

`vce(vcetype)` specifies the type of standard error reported, which includes types that are robust to some kinds of misspecification (`robust`), that allow for intragroup correlation (`cluster clustvar`), and that use bootstrap or jackknife methods (`bootstrap`, `jackknife`); see [R] [vce_option](#).

Reporting

`level(#)`; see [R] [Estimation options](#).

`aequations` specifies that the results for the outcome-model or the treatment-model parameters be displayed. By default, the results for these auxiliary parameters are not displayed.

`noshow` prevents `stteffects ipw` from showing the key st variables. This option is rarely used because most people type `stset`, `show` or `stset`, `noshow` to permanently set whether they want to see these variables mentioned at the top of the output of every st command; see [ST] [stset](#).

`display_options`: `noci`, `nocvalues`, `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `nofvlabel`, `fvwrap(#)`, `fvrapon(style)`, `cformat(%fmt)`, `pformat(%fmt)`, `sformat(%fmt)`, and `nolstretch`; see [R] [Estimation options](#).

Maximization

`maximize_options`: `iterate(#)`, `[no]log`, and `from(init_specs)`; see [R] [Maximize](#). These options are seldom used.

`init_specs` is one of

```
matname [, skip copy]
# [, # ...], copy
```

`iterinit(#)` specifies the maximum number of iterations used to calculate the starting values. This option is seldom used.

Advanced

`pstolerance(#)` specifies the tolerance used to check the overlap assumption. The default value is `pstolerance(1e-5)`. `stteffects` will exit with an error if an observation has an estimated propensity score smaller than that specified by `pstolerance()`.

`osample(newvar)` specifies that indicator variable `newvar` be created to identify observations that violate the overlap assumption.

`control(#|label)` specifies the level of `tvar` that is the control. The default is the first treatment level. You may specify the numeric level `#` (a nonnegative integer) or the label associated with the numeric level. `control()` may not be specified with the statistic `pomeans`. `control()` and `tlevel()` may not specify the same treatment level.

`tlevel(#|label)` specifies the level of `tvar` that is the treatment for the statistic `atet`. The default is the second treatment level. You may specify the numeric level `#` (a nonnegative integer) or the label associated with the numeric level. `tlevel()` may only be specified with statistic `atet`. `tlevel()` and `control()` may not specify the same treatment level.

The following option is available with `stteffects` but is not shown in the dialog box:
`coeflegend`; see [R] [Estimation options](#).

Remarks and examples

If you are not familiar with the framework for treatment-effects estimation from observational survival-time data, please see [TE] **stteffects intro**.

IPW estimators use contrasts of weighted averages of observed outcomes to estimate treatment effects. The estimated weights correct for data that are missing because each subject is only observed after receiving one of the possible treatment levels and because some survival-time outcomes are censored.

The IPW estimators implemented in **stteffects ipw** use a three-step approach to estimating the ATE:

1. Estimate the parameters of a treatment-assignment model, and compute the component of the estimated weights that accounts for data missing because each subject is only observed after receiving one of the possible treatment levels.
2. Estimate the parameters of a time-to-censoring model, and compute the component of the estimated weights that accounts for data lost to censoring.
3. Use the estimated weights to compute weighted averages of the outcomes for each treatment level.

To estimate the ATET, we use different weights in step 2.

The time to censoring must be random to use **stteffects ipw** because the model in step 2 is not well defined if the time to censoring is fixed. See [TE] **stteffects intro** for more details. For information about estimators that accommodate a fixed time to censoring, see [TE] **stteffects ra** and [TE] **stteffects ipwra**.

Here we note only a few entry points to the vast literature on IPW estimators. Hirano, Imbens, and Ridder (2003), Imbens (2000, 2004), Imbens and Wooldridge (2009), Rosenbaum and Rubin (1983), Robins and Rotnitzky (2006), Wooldridge (2002, 2007), Cameron and Trivedi (2005, chap. 25), Wooldridge (2010, chap. 21), and Vittinghoff et al. (2012, chap. 9) provide excellent general introductions to estimating ATEs and to the IPW estimators in particular.

Like **streg** and other survival-time commands, **stteffects ipw** uses the outcome variable and the failure indicator computed by, and optionally weights specified with, **stset**. **stteffects ipw** is not appropriate for data with time-varying covariates, also known as multiple-record survival-time data, or for delayed-entry data.

▷ Example 1: Estimating the ATE

Suppose we wish to study the effect of smoking on the time to a second heart attack among women aged 45–55 years. In our fictional **sheart** dataset, **atime** is the observed time in years to a second heart attack or censoring, and **fail** is the 0/1 indicator that a second heart attack was observed. (When **fail** is 1, **atime** records the time to the second heart attack; when **fail** is 0, **atime** records a censored observation of the time to a second heart attack.) We previously **stset** these data; see [A quick tour of the estimators](#) in [TE] **stteffects intro**.

The treatment, smoking, is stored in the 0/1 indicator **smoke**. These data also contain age at the time of the first heart attack (**age**), and indices of the level of exercise (**exercise**), diet quality (**diet**), and education (**education**) prior to the first heart attack.

We can use **stteffects ipw** to estimate the ATE. We model treatment assignment using the default logit model with covariates on **age**, **exercise**, and **education**. We model the time to censoring using the default Weibull model with covariates on **age**, **exercise**, **diet**, and **education**.

```
. use https://www.stata-press.com/data/r16/sheart
(Time to second heart attack (fictional))
. stteffects ipw (smoke age exercise education) (age exercise diet education)
    failure _d: fail
    analysis time _t: atime
Iteration 0: EE criterion = 2.042e-18
Iteration 1: EE criterion = 5.191e-31
Survival treatment-effects estimation           Number of obs      = 2,000
Estimator       : inverse-probability weights
Outcome model   : weighted mean
Treatment model: logit
Censoring model: Weibull
```

$_t$	Robust					
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
ATE smoke (Smoker vs Nonsmoker)	-2.22226	.6307573	-3.52	0.000	-3.458522	-.9859983
P0mean smoke Nonsmoker	4.235569	.5210937	8.13	0.000	3.214244	5.256894

When every woman smoked in the population of women aged 45–55 years who have had a heart attack, the average time to a second heart attack is estimated to be 2.22 years less than when no women in the population of interest smoked. The estimated average time to a second heart attack when no women in the population of interest smoked is 4.24 years.

The ratio of the ATE to the control-level POM measures the importance of the effect. In this example, when every woman smoked, the average time to a second heart attack falls by an estimated 52% relative to the case when none of them smoked. See [example 3](#) in [TE] **stteffects ra** for an example that uses **nlcom** to compute a point estimate and a confidence interval for this ratio.



▷ Example 2: Different treatment and censoring models

Instead of a logit model for the treatment assignment, we could have used a probit or a heteroskedastic probit model. Instead of a Weibull model for the censoring time, we could have used an exponential, a gamma, or a lognormal model. For a quick comparison, we now estimate the ATE using a probit model for the treatment assignment and using a gamma model for the censoring time.

```
. stteffects ipw (smoke age exercise education, probit)
> (age exercise diet education, gamma)
    failure _d: fail
    analysis time _t: atime
Iteration 0: EE criterion = 3.534e-15
Iteration 1: EE criterion = 5.263e-27
Survival treatment-effects estimation           Number of obs      =     2,000
Estimator       : inverse-probability weights
Outcome model   : weighted mean
Treatment model: probit
Censoring model: gamma
```

<u>t</u>	Coef.	Robust Std. Err.	z	P> z	[95% Conf. Interval]
ATE smoke (Smoker vs Nonsmoker)	-2.646808	.8368254	-3.16	0.002	-4.286956 -1.006661
P0mean smoke Nonsmoker	4.702301	.7404567	6.35	0.000	3.251033 6.15357

The estimated ATE of -2.65 and control-level POM of 4.70 are similar to the values of -2.22 and 4.24 reported in [example 1](#).



▷ Example 3: Estimating the ATET

Intuitively, the ATET measures the effect of the treatment on an at-risk subpopulation. Sometimes the subpopulation that gets the treatment defines such an at-risk subpopulation. The ATET has the added benefit that it can be estimated under weaker conditions than the ATE; see [Assumptions and trade-offs](#) under Remarks and examples in [\[TE\] stteffects intro](#).

```
. stteffects ipw (smoke age exercise education) (age exercise diet education),
> atet
    failure _d: fail
    analysis time _t: atime
Iteration 0: EE criterion = 2.042e-18
Iteration 1: EE criterion = 1.248e-32
Survival treatment-effects estimation           Number of obs      = 2,000
Estimator       : inverse-probability weights
Outcome model   : weighted mean
Treatment model: logit
Censoring model: Weibull
```

<u>_t</u>	Robust					
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
ATET smoke (Smoker vs Non-smoker)	-1.846136	.5076872	-3.64	0.000	-2.841185	-.8510877
P0mean smoke Non-smoker	3.543788	.474395	7.47	0.000	2.613991	4.473585

When every woman in the subpopulation smoked, the average time to a second heart attack is estimated to be 1.85 years less than when no women in the subpopulation smoked. The estimated average time to a second heart attack when no women in the subpopulation smoked is 3.54 years.



Stored results

stteffects ipw stores the following in e():

Scalars

e(N)	number of observations
e(nj)	number of observations for treatment level <i>j</i>
e(N_clust)	number of clusters
e(k_eq)	number of equations in e(b)
e(k_levels)	number of levels in treatment variable
e(treated)	level of treatment variable defined as treated
e(control)	level of treatment variable defined as control
e(converged)	1 if converged, 0 otherwise

Macros

e(cmd)	stteffects
e(cmdline)	command as typed
e(dead)	_d
e(depyar)	_t
e(tvar)	name of treatment variable
e(subcmd)	ipw
e(tmodel)	treatment model: logit, probit, or hetprobit
e(cmodel)	censoring model: weibull, exponential, gamma, or lognormal
e(stat)	statistic estimated: ate, atet, or pomeans
e(wtype)	weight type
e(wexp)	weight expression
e(title)	title in estimation output
e(clustvar)	name of cluster variable
e(tlevels)	levels of treatment variable

e(vce)	vcetype specified in vce()
e(vcetype)	title used to label Std. Err.
e(properties)	b V
e(estat_cmd)	program used to implement estat
e(predict)	program used to implement predict
e(marginsnotok)	predictions disallowed by margins
e(asbalanced)	factor variables fvset as asbalanced
e(asobserved)	factor variables fvset as asobserved
Matrices	
e(b)	coefficient vector
e(V)	variance-covariance matrix of the estimators
Functions	
e(sample)	marks estimation sample

Methods and formulas

The methods and formulas for the IPW estimators implemented in **stteffects ipw** are given in *Methods and formulas* of [TE] **stteffects ipwra**.

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Also see

- [TE] **stteffects postestimation** — Postestimation tools for stteffects
- [TE] **stteffects intro** — Introduction to treatment effects for observational survival-time data
- [ST] **streg** — Parametric survival models
- [ST] **stset** — Declare data to be survival-time data
- [U] **20 Estimation and postestimation commands**

stteffects ipwra — Survival-time inverse-probability-weighted regression adjustment

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Methods and formulas

Description

stteffects ipwra estimates the average treatment effect (ATE), the average treatment effect on the treated (ATET), and the potential-outcome means (POMs) from observational survival-time data by inverse-probability-weighted regression adjustment (IPWRA). IPWRA estimators use missingness-adjusted regression coefficients to compute averages of treatment-level predicted outcomes. Contrasts of these averages estimate the treatment effects. **stteffects ipwra** offers several choices for the functional forms of the outcome model, of the treatment model, and of the optional time-to-censoring model. Binary and multivalued treatments are accommodated.

See [TE] **stteffects intro** for an overview of estimating treatment effects from observational survival-time data.

Quick start

Specify `time` as observed failure time and `fail` as failure indicator

```
stset time, failure(fail)
```

ATE of binary treatment `treat2` estimated by IPWRA using a Weibull model for `time` on `x1` and `x2` and a logistic model for `treat2` on `x1` and `w`

```
stteffects ipwra (x1 x2) (treat2 x1 w)
```

As above, but estimate the ATET

```
stteffects ipwra (x1 x2) (treat2 x1 w), atet
```

Gamma model for `time` and probit model for `treat2`

```
stteffects ipwra (x1 x2, gamma) (treat2 x1 w, probit)
```

ATE for each level of three-valued treatment `treat3`

```
stteffects ipwra (x1 x2) (treat3 x1 w)
```

As above, and specify that `treat3 = 3` is the control level using the value label "MyControl" for 3

```
stteffects ipwra (x1 x2) (treat3 x1 w), control("MyControl")
```

ATE of `treat2` estimated by IPWRA using a Weibull model for `time` on `x1` and `x2`, a logistic model for `treat2` on `x1` and `w`, and a Weibull model for the time to censoring with covariates `x1` and `x2`

```
stteffects ipwra (x1 x2) (treat2 x1 w) (x1 x2)
```

Gamma model for `time`, probit model for `treat2`, and gamma model for censoring

```
stteffects ipwra (x1 x2, gamma) (treat2 x1 w, probit) (x1 x2, gamma)
```

Menu

Statistics > Treatment effects > Survival outcomes > Regression adjustment with IPW

Syntax

```
stteffects ipwra (omvarlist [ , omoptions ]) (tvar tmvarlist [ , tmoptions ]) 
    [ (cmvarlist [ , cmoptions ]) ] [if] [in] [ , stat options ]
```

omvarlist specifies the variables that predict the survival-time variable in the outcome model.
tvar must contain integer values representing the treatment levels.

tmvarlist specifies the variables that predict treatment assignment in the treatment model.

cmvarlist specifies the variables that predict censoring in the censoring model.

<i>omoptions</i>	Description
Model	
<u>weibull</u>	Weibull; the default
<u>exponential</u>	exponential
<u>gamma</u>	two-parameter gamma
<u>lnormal</u>	lognormal
<u>ancillary</u> (<i>avarlist</i> [, <u>noconstant</u>])	specify variables used to model ancillary parameter
<u>noconstant</u>	suppress constant from outcome model
<i>tmoptions</i>	Description
Model	
<u>logit</u>	logistic treatment model; the default
<u>probit</u>	probit treatment model
<u>hetprobit</u> (<i>varlist</i>)	heteroskedastic probit treatment model
<u>noconstant</u>	suppress constant from treatment model
<i>cmoptions</i>	Description
Model	
<u>weibull</u>	Weibull; the default
<u>exponential</u>	exponential
<u>gamma</u>	two-parameter gamma
<u>lnormal</u>	lognormal
<u>ancillary</u> (<i>avarlist</i> [, <u>noconstant</u>])	specify variables used to model ancillary parameter
<u>noconstant</u>	suppress constant from censoring model

stat	Description
Stat	
ate	estimate average treatment effect in population; the default
atet	estimate average treatment effect on the treated
pomeans	estimate potential-outcome means
options	Description
SE/Robust	
vce(vcetype)	vcetype may be robust, cluster clustvar, bootstrap, or jackknife
Reporting	
level(#)	set confidence level; default is level(95)
aequations	display auxiliary-equation results
noshow	do not show st setting information
display_options	control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling
Maximization	
maximize_options	control the maximization process; seldom used
iterinit(#)	specify starting-value iterations; seldom used
Advanced	
pstolerance(#)	set the tolerance for the overlap assumption
osample(newvar)	identify observations that violate the overlap assumption
control(# label)	specify the level of tvar that is the control
tlevel(# label)	specify the level of tvar that is the treatment
coeflegend	display legend instead of statistics

You must `stset` your data before using `stteffects`; see [ST] `stset`.

`omvarlist`, `tmvarlist`, `cmvarlist`, and `avarlist` may contain factor variables; see [U] 11.4.3 Factor variables.

`bootstrap`, `by`, `jackknife`, and `statsby` are allowed; see [U] 11.1.10 Prefix commands.

Weights are not allowed with the `bootstrap` prefix; see [R] `bootstrap`.

`fweights`, `iweights`, and `pweights` may be specified using `stset`; see `Weights` under Remarks and examples in [ST] `stset`. However, weights may not be specified if you are using the `bootstrap` prefix.

`coeflegend` does not appear in the dialog box.

See [U] 20 Estimation and postestimation commands for more capabilities of estimation commands.

Options

Model

`ancillary(avarlist [, noconstant])` specifies the variables used to model the ancillary parameter. By default, the ancillary parameter does not depend on covariates. Specifying `ancillary(avarlist, noconstant)` causes the constant to be suppressed in the model for the ancillary parameter.

`ancillary()` may be specified for the model for survival-time outcome, for the model for the censoring variable, or for both. If `ancillary()` is specified for both, the varlist used for each model may be different.

`noconstant`; see [R] **Estimation options**.

Stat

`stat` is one of three statistics: `ate`, `atet`, or `pomeans`. `ate` is the default.

`ate` specifies that the average treatment effect be estimated.

`atet` specifies that the average treatment effect on the treated be estimated.

`pomeans` specifies that the potential-outcome means for each treatment level be estimated.

SE/Robust

`vce(vcetype)` specifies the type of standard error reported, which includes types that are robust to some kinds of misspecification (`robust`), that allow for intragroup correlation (`cluster clustvar`), and that use bootstrap or jackknife methods (`bootstrap`, `jackknife`); see [R] **vce_option**.

Reporting

`level(#)`; see [R] **Estimation options**.

`aequations` specifies that the results for the outcome-model or treatment-model parameters be displayed. By default, the results for these auxiliary parameters are not displayed.

`noshow` prevents `stteffects ipwra` from showing the key `st` variables. This option is rarely used because most people type `stset`, `show` or `stset`, `noshow` to permanently set whether they want to see these variables mentioned at the top of the output of every `st` command; see [ST] **stset**.

`display_options`: `noci`, `nopvalues`, `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `nofvlabel`, `fvwrap(#)`, `fvwrapon(style)`, `cformat(%fmt)`, `pformat(%fmt)`, `sformat(%fmt)`, and `nolstretch`; see [R] **Estimation options**.

Maximization

`maximize_options`: `iterate(#)`, `[no]log`, and `from(init_specs)`; see [R] **Maximize**. These options are seldom used.

`init_specs` is one of

`matname [, skip copy]`

`# [, # ...], copy`

`iterinit(#)` specifies the maximum number of iterations used to calculate the starting values. This option is seldom used.

Advanced

`pstolerance(#)` specifies the tolerance used to check the overlap assumption. The default value is `pstolerance(1e-5)`. `stteffects` will exit with an error if an observation has an estimated propensity score smaller than that specified by `pstolerance()`.

`osample(newvar)` specifies that indicator variable `newvar` be created to identify observations that violate the overlap assumption.

`control(#|label)` specifies the level of `tvar` that is the control. The default is the first treatment level. You may specify the numeric level # (a nonnegative integer) or the label associated with the numeric level. `control()` may not be specified with the statistic `pomeans`. `control()` and `tlevel()` may not specify the same treatment level.

`tlevel(#|label)` specifies the level of `tvar` that is the treatment for the statistic `atet`. The default is the second treatment level. You may specify the numeric level # (a nonnegative integer) or the label associated with the numeric level. `tlevel()` may only be specified with statistic `atet`. `tlevel()` and `control()` may not specify the same treatment level.

The following option is available with `stteffects` but is not shown in the dialog box:
`coeflegend`; see [R] **Estimation options**.

Remarks and examples

If you are not familiar with the framework for treatment-effects estimation from observational survival-time data, please see [TE] **stteffects intro**.

IPWRA estimators use estimated weights to obtain missingness-adjusted outcome-regression parameters. The missingness-adjusted outcome-regression parameters are used to compute averages of treatment-level predicted outcomes. Contrasts of these averages estimate the treatment effects.

The estimated weights account for the missing potential outcome and, optionally, for data lost to censoring. The weights are estimated using a treatment-assignment model and, optionally, a model for the censoring time. A term in the estimator for the outcome-regression parameters accounts for data lost to censoring when estimated weights are not used.

There are two versions of the IPWRA estimator because there are two methods of accounting for the data lost to censoring.

1. IPWRA estimators that adjust for censoring by including a term in the likelihood function for the outcome-model parameters are known as likelihood-adjusted-censoring IPWRA (LAC-IPWRA) estimators.
2. IPWRA estimators that adjust for censoring by weighting the likelihood function for the outcome-model parameters by estimated inverse-probability-of-censoring weights are known as weighted-adjusted-censoring IPWRA (WAC-IPWRA) estimators.

The LAC-IPWRA estimators require fewer assumptions than the WAC-IPWRA estimators. Outlining the steps performed by LAC-IPWRA and WAC-IPWRA estimators allows us to be more specific about the trade-offs between the estimators.

LAC-IPWRA estimators use a three-step approach to estimating treatment effects:

1. Estimate the parameters of a treatment-assignment model and compute inverse-probability-of-treatment weights.
2. Obtain the treatment-specific predicted mean outcomes for each subject by using the weighted maximum likelihood estimators. Estimated inverse-probability-of-treatment weights are used to weight the maximum likelihood estimator. A term in the likelihood function adjusts for right-censored survival times.
3. Compute the means of the treatment-specific predicted mean outcomes. Contrasts of these averages provide the estimates of the ATEs. By restricting the computations of the means to the subset of treated subjects, we can obtain the ATETs.

WAC-IPWRA estimators use a four-step approach to estimating treatment effects:

1. Estimate the parameters of a treatment-assignment model and compute inverse-probability-of-treatment weights.
2. Estimate the parameters of a time-to-censoring model and compute inverse-probability-of-censoring weights.
3. Obtain the treatment-specific predicted mean outcomes for each subject by using the weighted maximum likelihood estimators. Estimated inverse-probability-of-treatment weights and inverse-probability-of-censoring weights are used to weight the maximum likelihood estimator. The inverse-probability-of-censoring weights account for right-censored survival times.
4. Compute the means of the treatment-specific predicted mean outcomes. Contrasts of these averages provide the estimates of the ATEs. By restricting the computations of the means to the subset of treated subjects, we can obtain the ATETs.

The WAC-IPWRA estimators require that the censoring time be random and that the time-to-censoring model be well specified. The implemented WAC-IPWRA estimators also require that the time-to-censoring process not vary by treatment level. The LAC-IPWRA estimators do not require these extra assumptions because they use a likelihood term instead of weights to adjust for the data lost to censoring.

Here we note only a few entry points to the vast literature on estimators that combine IPW and RA methods. Hirano, Imbens, and Ridder (2003), Imbens (2000, 2004), Imbens and Wooldridge (2009), Rosenbaum and Rubin (1983), Robins and Rotnitzky (1995, 2006), Robins, Rotnitzky, and Zhao (1995), Wooldridge (2002, 2007), Cameron and Trivedi (2005, chap. 25), Wooldridge (2010, chap. 21), and Vittinghoff et al. (2012, chap. 9) provide excellent general introductions to estimating ATEs and to the IPWRA estimators in particular.

Like `streg` and other survival-time commands, `stteffects ipwra` uses the outcome variable and the failure indicator computed by, and optionally weights specified with, `stset`. `stteffects ipwra` is not appropriate for data with time-varying covariates, also known as multiple-record survival-time data, or for delayed-entry data.

▷ Example 1: Estimating the ATE by LAC-IPWRA

Suppose we wish to study the effect of smoking on the time to a second heart attack among women aged 45–55 years. In our fictional `sheart` dataset, `atime` is the observed time in years to a second heart attack or censoring, and `fail` is the 0/1 indicator that a second heart attack was observed. (When `fail` is 1, `atime` records the time to the second heart attack; when `fail` is 0, `atime` records a censored observation of the time to a second heart attack.) We previously `stset` these data; see [A quick tour of the estimators in \[TE\] stteffects intro](#).

The treatment, smoking, is stored in the 0/1 indicator `smoke`. These data also contain age at the time of the first heart attack (`age`), and indices of the level of exercise (`exercise`), diet quality (`diet`), and education (`education`) prior to the first heart attack.

We can use `stteffects ipwra` to estimate the ATE. We model the mean survival time using the default Weibull model, controlling for `age`, `exercise`, `diet`, and `education`. We model treatment assignment using the default logit model with covariates `age`, `exercise`, and `education`. We do not specify a time-to-censoring model so that we obtain the LAC estimator.

```
. use https://www.stata-press.com/data/r16/sheart
(Time to second heart attack (fictional))

. stteffects ipwra (age exercise diet education) (smoke age exercise education)
  failure _d: fail
  analysis time _t: atime

Iteration 0:  EE criterion = 7.439e-15
Iteration 1:  EE criterion = 1.756e-26

Survival treatment-effects estimation           Number of obs      =      2,000
Estimator          : IPW regression adjustment
Outcome model     : Weibull
Treatment model: logit
Censoring model: none
```

$_t$	Robust					[95% Conf. Interval]
	Coef.	Std. Err.	z	P> z		
ATE smoke (Smoker vs Nonsmoker)	-1.591874	.4837332	-3.29	0.001	-2.539973	-.643774
P0mean smoke Nonsmoker	4.214263	.2598689	16.22	0.000	3.704929	4.723597

When every woman smoked in the population of women aged 45–55 years who have had a heart attack, the average time to a second heart attack is estimated to be 1.59 years less than when no women in the population of interest smoked. The estimated average time to a second heart attack when no women in the population of interest smoked is 4.21 years.

The ratio of the ATE to the control-level potential-outcome mean (POM) measures the importance of the effect. In this example, when all women smoked, the time to the second heart attack falls by an estimated 38% relative to the case in which no women smoked. See [example 3](#) in [TE] stteffects ra for an example that uses nlcom to compute a point estimate and a confidence interval for this ratio.



► Example 2: Different outcome and treatment models

Instead of a Weibull model for the outcome model, we could have used an exponential, a gamma, or a lognormal model. Instead of a logit model for the treatment assignment, we could have used a probit or a heteroskedastic probit model. This example uses a gamma model for the outcome and a probit model for the treatment assignment.

		Robust					
		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
ATE							
smoke	(Smoker						
	vs						
Nonsmoker)		-1.387303	.4786032	-2.90	0.004	-2.325348	-.4492583
P0mean							
smoke							
	Nonsmoker	3.97986	.2258474	17.62	0.000	3.537207	4.422512

The estimated ATE of -1.39 and control-level POM of 3.98 are similar to the values of -1.59 and 4.21 that we obtained in [example 1](#).



► Example 3: Estimating the ATE by WAC-IPWRA

Rather than using LAC, we may want to specify a time-to-censoring model. We now use `stteffects ipwra` to estimate the ATE by WAC-IPWRA. We use the same specification of the outcome and treatment models that we used in [example 1](#). However, now we specify a time-to-censoring model, using the default Weibull model with covariates `age`, `exercise`, `diet`, and `education`.

```
. stteffects ipwra (age exercise diet education) (smoke age exercise education)
> (age exercise diet education)

    failure _d: fail
    analysis time _t: atime

Iteration 0:   EE criterion =  3.673e-18
Iteration 1:   EE criterion =  3.383e-31

Survival treatment-effects estimation           Number of obs      =      2,000
Estimator       : IPW regression adjustment
Outcome model   : Weibull
Treatment model: logit
Censoring model: Weibull


```

<code>_t</code>	Robust					
	Coef.	Std. Err.	<code>z</code>	<code>P> z </code>	[95% Conf. Interval]	
ATE smoke (Smoker vs Non-smoker)	-2.285057	.7318456	-3.12	0.002	-3.719448	-.8506656
P0mean smoke Non-smoker	4.385841	.6427521	6.82	0.000	3.12607	5.645612

The estimated ATE of -2.29 differs from the ATE of -1.59 estimated by LAC-IPWRA, but the estimates of the control-level POM are similar between the two models: 4.39 for the WAC compared with 4.21 for the LAC.



► Example 4: Estimating the ATET by LAC-IPWRA

Intuitively, the ATET measures the effect of the treatment on an at-risk subpopulation. Sometimes the subpopulation that gets the treatment defines such an at-risk subpopulation. The ATET has the added benefit that it can be estimated under weaker conditions than the ATE; see [Assumptions and trade-offs](#) under Remarks and examples in [TE] stteffects intro.

<code>_t</code>	Robust Coef.	Std. Err.	<code>z</code>	<code>P> z </code>	[95% Conf. Interval]	
ATET smoke (Smoker vs Nonsmoker)	-1.775107	.3437506	-5.16	0.000	-2.448846	-1.101368
P0mean smoke Nonsmoker	4.062424	.2779877	14.61	0.000	3.517578	4.60727

When all women in the subpopulation smoked, the average time to a second heart attack is estimated to be 1.78 years less than when no women in the subpopulation of interest smoked. If no women in the subpopulation of interest smoked, the average time to a second heart attack is 4.06 years.



Stored results

`stteffects ipwra` stores the following in `e()`:

Scalars

<code>e(N)</code>	number of observations
<code>e(nj)</code>	number of observations for treatment level j
<code>e(N_clust)</code>	number of clusters
<code>e(k_eq)</code>	number of equations in <code>e(b)</code>
<code>e(k_levels)</code>	number of levels in treatment variable
<code>e(treated)</code>	level of treatment variable defined as treated
<code>e(control)</code>	level of treatment variable defined as control
<code>e(converged)</code>	1 if converged, 0 otherwise

Macros

<code>e(cmd)</code>	<code>stteffects</code>
<code>e(cmdline)</code>	command as typed
<code>e(dead)</code>	<code>_d</code>
<code>e(depvar)</code>	<code>_t</code>
<code>e(tvar)</code>	name of treatment variable

<code>e(subcmd)</code>	<code>ipwra</code>
<code>e(omodel)</code>	outcome model: <code>weibull</code> , <code>exponential</code> , <code>gamma</code> , or <code>lognormal</code>
<code>e(tmodel)</code>	treatment model: <code>logit</code> , <code>probit</code> , or <code>hetprobit</code>
<code>e(cmodel)</code>	censoring model: <code>weibull</code> , <code>exponential</code> , <code>gamma</code> , or <code>lognormal</code> (if specified)
<code>e(stat)</code>	statistic estimated: <code>ate</code> , <code>atet</code> , or <code>pomeans</code>
<code>e(wtype)</code>	weight type
<code>e(wexp)</code>	weight expression
<code>e(title)</code>	title in estimation output
<code>e(clustvar)</code>	name of cluster variable
<code>e(tlevels)</code>	levels of treatment variable
<code>e(vce)</code>	<code>vcetype</code> specified in <code>vce()</code>
<code>e(vcetype)</code>	title used to label Std. Err.
<code>e(properties)</code>	<code>b</code> <code>V</code>
<code>e(estat_cmd)</code>	program used to implement <code>estat</code>
<code>e(predict)</code>	program used to implement <code>predict</code>
<code>e(marginsnotok)</code>	predictions disallowed by <code>margins</code>
<code>e(asbalanced)</code>	factor variables <code>fvset</code> as <code>asbalanced</code>
<code>e(asobserved)</code>	factor variables <code>fvset</code> as <code>asobserved</code>
Matrices	
<code>e(b)</code>	coefficient vector
<code>e(V)</code>	variance–covariance matrix of the estimators
Functions	
<code>e(sample)</code>	marks estimation sample

Methods and formulas

Methods and formulas are presented under the following headings:

- Introduction*
- Regression-adjusted estimators*
- Weighted-adjusted-censoring assumptions*
- Weighted regression-adjusted estimators*
- Inverse-probability-weighted estimators*
 - Uncensored data*
 - Inverse-probability-weighted regression-adjustment estimators*
 - Weighted-adjusted-censoring IPWRA*
 - Likelihood-adjusted-censoring IPWRA*
 - Functional-form details*

Introduction

This section presents the methods and formulas used by the estimators implemented in `stteffects ra`, `stteffects wra`, `stteffects ipw`, and `stteffects ipwra`. This section assumes that you are familiar with the concepts and intuition from the estimators discussed in [TE] **teffects intro advanced**.

Each of the estimators implemented in `stteffects` has a multistep logic but is implemented as one step by simultaneously solving the estimating equations that define each step. This one-step estimating-equation approach provides consistent point estimates and a consistent variance–covariance of the estimator (VCE); see [Newey \(1984\)](#), [Wooldridge \(2010\)](#), and [Drukker \(2014\)](#).

Survival-time treatment-effects estimators handle two types of missing data. First, only one of the potential outcomes is observed, as is standard in causal inference. Second, the potential outcome for the received treatment may be censored. The data missing because of censoring may be handled by an outcome model, a censoring model, or both, just like the data missing due to observing only one potential outcome.

□ Technical note

Delayed entry would be a third type of missing data. The left-truncation process caused by delayed entry would also need to be modeled to estimate ATE parameters. The estimators implement in `stteffects` do not allow for delayed entry because they do not have a method for modeling how the left-truncation process selects the sample, conditional on the covariates.



All the implemented estimators are combinations of regression-adjustment (RA) and inverse-probability-weighted (IPW) techniques. RA estimators use an outcome model to account for the missing potential outcome and for censoring. IPW estimators use models for treatment assignment and censoring to construct weights that account for the missing potential outcome and for censoring.

The remainder of this section provides technical details about how the estimators in `stteffects` were implemented. We provide details only for the two-treatment-level case to simplify the formulas. We provide outlines for how the extensions to the multiple-treatment-level case were implemented.

Regression-adjusted estimators

We begin with the RA estimators implemented in `stteffects ra`. The RA estimators have the following logic:

- RA1. For each treatment level $\tau \in \{0, 1\}$, estimate by maximum likelihood (ML) the parameters β_τ of a parametric model for the survival-time outcome t in which $F(t|\mathbf{x}, \tau, \beta_\tau)$ is the distribution of t conditional on covariates \mathbf{x} and treatment level τ . Denote the estimates β_τ by $\hat{\beta}_{ra,\tau}$.
- RA2. Use the estimated $\hat{\beta}_{ra,\tau}$ and the functional form implied by $F(t|\mathbf{x}, \tau, \beta_\tau)$ to estimate the mean survival time, conditional on \mathbf{x} and treatment level τ , for each sample observation, denoted by $\hat{E}(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{ra,\tau})$. Conditional independence of the treatment and the survival-time potential outcomes ensures that $E(t|\mathbf{x}, \tau, \beta_\tau) = E(t_\tau|\mathbf{x}, \beta_\tau)$, where t_τ is the potential survival-time outcome corresponding to treatment level τ . Under correct model specification, sample averages of $\hat{E}(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{ra,\tau})$ consistently estimate the POM for treatment level τ , denoted by POM_τ .
- RA3. A contrast of the estimated POMs estimates the ATE.

If estimating an ATET, step RA2 is modified to use only the treated observations when estimating the POMs. A contrast of these POMs then estimates the ATET.

The contribution of the i th observation to the log likelihood that is maximized in step RA1 is

$$L_{ra}(t_i, \mathbf{x}_i, \tau, \hat{\beta}_{ra,\tau}) = \varpi_i(\tau_i == \tau) \left[(1 - c_i) \ln\{f(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{ra,\tau})\} + c_i \ln\{1 - F(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{ra,\tau})\} \right] \quad (1)$$

where ϖ_i is the observation-level weight, c_i is the 0/1 indicator for whether the survival-time observation on person i was censored, and $f(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{ra,\tau})$ is the density corresponding to distribution $F(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{ra,\tau})$. The first term inside the curly braces in (1) accounts for the noncensored observations, and the second term inside the curly braces accounts for the censored observations.

The RA estimators for the POMs simultaneously solve estimating equations (2a) through (2d) for $\widehat{\beta}_{\text{ra},0}$, $\widehat{\beta}_{\text{ra},1}$, $\widehat{\text{POM}}_{\text{ra},0}$, and $\widehat{\text{POM}}_{\text{ra},1}$.

$$1/N \sum_{i=1}^N \mathbf{s}_{\text{ra}}(t_i, \mathbf{x}_i, 0, \widehat{\beta}_{\text{ra},0}, F) = \mathbf{0} \quad (2a)$$

$$1/N \sum_{i=1}^N \mathbf{s}_{\text{ra}}(t_i, \mathbf{x}_i, 1, \widehat{\beta}_{\text{ra},1}, F) = \mathbf{0} \quad (2b)$$

$$1/N \sum_{i=1}^N \varpi_i \left\{ \widehat{E}(t_i | \mathbf{x}_i, \tau = 0, \widehat{\beta}_{\text{ra},0}) - \widehat{\text{POM}}_{\text{ra},0} \right\} = 0 \quad (2c)$$

$$1/N \sum_{i=1}^N \varpi_i \left\{ \widehat{E}(t_i | \mathbf{x}_i, \tau = 1, \widehat{\beta}_{\text{ra},1}) - \widehat{\text{POM}}_{\text{ra},1} \right\} = 0 \quad (2d)$$

where

$\mathbf{s}_{\text{ra}}(t_i, \mathbf{x}_i, 0, \widehat{\beta}_{\text{ra},0}, F) = \frac{\partial L_{\text{ra}}(t_i, \mathbf{x}_i, 0, \widehat{\beta}_{\text{ra},0})}{\partial \widehat{\beta}_{\text{ra},0}}$ is the vector of score equations from the ML estimator

for $\widehat{\beta}_{\text{ra},0}$ based on survival-time model F ,

$\mathbf{s}_{\text{ra}}(t_i, \mathbf{x}_i, 1, \widehat{\beta}_{\text{ra},1}, F) = \frac{\partial L_{\text{ra}}(t_i, \mathbf{x}_i, 1, \widehat{\beta}_{\text{ra},1})}{\partial \widehat{\beta}_{\text{ra},1}}$ is the vector of score equations from the ML estimator

for $\widehat{\beta}_{\text{ra},1}$ based on survival-time model F ,

$\widehat{E}(t_i | \mathbf{x}_i, \tau = 0, \widehat{\beta}_{\text{ra},0})$ is the predicted mean survival time assuming treatment level 0 for observation i conditional on \mathbf{x}_i , and

$\widehat{E}(t_i | \mathbf{x}_i, \tau = 1, \widehat{\beta}_{\text{ra},1})$ is the predicted mean survival time assuming treatment level 1 for observation i conditional on \mathbf{x}_i .

The ATE is estimated by replacing (2d) with

$$1/N \sum_{i=1}^N \varpi_i \left\{ \widehat{E}(t_i | \mathbf{x}_i, \tau = 1, \widehat{\beta}_{\text{ra},1}) - \widehat{\text{POM}}_{\text{ra},0} - \widehat{\text{ATE}}_{\text{ra}} \right\} = 0 \quad (3)$$

and the ATET is estimated by replacing (2c) and (3) with

$$1/N_1 \sum_{i=1}^N \varpi_i (\tau_i == 1) \left\{ \widehat{E}(t_i | \mathbf{x}_i, \tau = 0, \widehat{\beta}_{\text{ra},0}) - \widehat{\text{POM}}_{\text{ra,cot},0} \right\} = 0$$

$$1/N_1 \sum_{i=1}^N \varpi_i (\tau_i == 1) \left\{ \widehat{E}(t_i | \mathbf{x}_i, \tau = 1, \widehat{\beta}_{\text{ra},1}) - \widehat{\text{POM}}_{\text{ra,cot},0} - \widehat{\text{ATET}}_{\text{ra}} \right\} = 0$$

where $N_1 = \sum_{i=1}^N (\tau_i == 1)$ and $\widehat{\text{POM}}_{\text{ra,cot},0}$ is the estimated conditional-on-treatment POM for treatment level 0.

Asymptotic standard errors for estimating equation estimators, also known as exactly identified generalized method of moments estimators, are standard in the literature; see Newey (1984), Newey and McFadden (1994), Tsiatis (2006), and Wooldridge (2010). These standard errors always have a robust structure and have been generalized to cluster-robust standard errors (see Wooldridge [2010]).

The score equations and the functional form for the predicted mean survival time depend on the model for survival-time outcome F . We provide these details below, under *Functional-form details*.

Weighted-adjusted-censoring assumptions

All estimators that permit you to model the time to censoring are subject to three assumptions:

1. The censoring time must be random.
2. The censoring time must be from a known distribution.
3. The distribution of the censoring time cannot vary by treatment level.

We call these three requirements the WAC assumptions. If the WAC assumptions are violated, you can use either an RA estimator or the LAC version of the IPWRA estimator.

□ Technical note

We now describe how the observed survival-time outcome t is generated from the random censoring time t_c , the received treatment τ , and the potential-outcome survival times t_0 and t_1 under the WAC assumptions. First, each potential outcome is either censored or not censored.

$$\begin{aligned}\tilde{t}_0 &= t_c(t_0 \geq t_c) + t_0\{1 - (t_0 \geq t_c)\} \\ \tilde{t}_1 &= t_c(t_1 \geq t_c) + t_1\{1 - (t_1 \geq t_c)\}\end{aligned}$$

Under the WAC assumptions, t_c is a random variable from a known distribution, and t_c does not vary by treatment level.

Next, the received treatment $\tau \in \{0, 1\}$ determines which, possibly censored, potential outcome is observed.

$$t = (1 - \tau)\tilde{t}_0 + \tau\tilde{t}_1$$

The 0/1 indicator for whether the observed t was censored, denoted by c , is given by

$$c = (1 - \tau)(t_0 \geq t_c) + \tau(t_1 \geq t_c)$$

□

Weighted regression-adjusted estimators

As is standard in the survival literature, the RA estimators account for censored survival times by adding a term to the log-likelihood function for censored observations [see (1)]. In contrast, weighted regression-adjustment (WRA) estimators use weights to account for censored observations and are subject to the [WAC assumptions](#).

Wooldridge (2007) and Lin (2000) derived estimators for the regression parameters that maximize a weighted objective function of the uncensored observations. Each observation-level weight is the inverse of the probability of not being censored. Like the RA estimators, the WRA estimators use averages of the predicted mean survival times to estimate treatment-effect parameters.

The WRA estimators have the following logic.

- WRA1. Estimate by ML the parameters γ of a parametric survival-time model for the time to censoring t_c , in which $F_c(t_c|\mathbf{w}, \gamma)$ is the distribution of t_c conditional on covariates \mathbf{w} . Note that the censoring process does not vary by treatment level and that we only observe t_c when the observed potential outcome was censored. Denote the estimates of γ by $\hat{\gamma}$.
- WRA2. For each treatment level $\tau \in \{0, 1\}$, estimate by weighted maximum likelihood (WML) the β_τ parameters of a parametric survival-time model, denoted by $F(t|\mathbf{x}, \tau, \beta_\tau)$, where t is the survival-time outcome and \mathbf{x} are the covariates. The weights are the inverse of the estimated probabilities of not being censored, $1/\{1 - F_c(t_c|\mathbf{w}, \hat{\gamma})\}$, and only the uncensored observations are used. Denote the estimates of β_τ by $\hat{\beta}_{wra,\tau}$.
- WRA3. Use the estimated $\hat{\beta}_{wra,\tau}$ and the functional form implied by $F(t|\mathbf{x}, \tau, \beta_\tau)$ to estimate the mean survival time, conditional on \mathbf{x} and treatment level τ , for each sample observation, denoted by $\hat{E}(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{wra,\tau})$. Conditional independence of the treatment and the survival-time potential outcomes ensures that $E(t|\mathbf{x}, \tau, \beta_\tau) = E(t_\tau|\mathbf{x}, \beta_\tau)$, where t_τ is the potential survival-time outcome corresponding to treatment level τ . Under correct model specification, sample averages of $\hat{E}(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{wra,\tau})$ consistently estimate the POM for treatment level τ , denoted by POM_τ .
- WRA4. A contrast of the estimated POMs estimates the ATE.

If estimating an ATET, step WRA3 is modified to use only the treated observations when estimating the POMs. A contrast of these POMs then estimates the ATET.

The contribution of the i th observation to the log likelihood that is maximized in step WRA1 is

$$L_{c,wra}(t_i, \mathbf{w}_i, \hat{\gamma}) = \varpi_i [c_i \ln\{f_c(t_i|\mathbf{w}_i, \hat{\gamma})\} + (1 - c_i) \ln\{1 - F_c(t_i|\mathbf{w}_i, \hat{\gamma})\}] \quad (4)$$

where ϖ_i is the observation-level weight, c_i is the 0/1 indicator for whether the survival-time observation on person i was censored, t_i is the observed failure time, and $f_c(t_i|\mathbf{w}_i, \hat{\gamma})$ is the density corresponding to conditional time-to-censoring distribution $F_c(t_i|\mathbf{w}_i, \hat{\gamma})$. When $c_i = 1$, t_i is the time to censoring. When $c_i = 0$, the censoring time is not observed; we only know that it is greater than the observed t_i . The first term accounts for the observations in which t_i is observed to be the censoring time, and the second term accounts for the observations in which the censoring time is greater than the observed t_i .

The contribution of the i th observation to the log likelihood that is maximized in step WRA2 is

$$L_{wra}(t_i, \mathbf{x}_i, \tau, \hat{\beta}_{wra,\tau}) = \varpi_i(\tau_i == \tau) \left[\frac{(1 - c_i)}{\{1 - F_c(t_i|\mathbf{w}_i, \hat{\gamma})\}} \right] \ln\{f(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{wra,\tau})\} \quad (5)$$

where $f(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{wra,\tau})$ is the density corresponding to distribution $F(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{wra,\tau})$. Equation (5) does not contain a term that adjusts for censoring; see (1) for a comparison. Rather, it uses inverse-probability weights to account for both the censored and the uncensored observations.

The WRA estimators for the POMs simultaneously solve estimating equations (6a) through (6e) for $\hat{\gamma}$, $\hat{\beta}_{wra,0}$, $\hat{\beta}_{wra,1}$, $\widehat{POM}_{wra,0}$, and $\widehat{POM}_{wra,1}$.

$$1/N \sum_{i=1}^N \mathbf{s}_{wra}(t_i, \mathbf{w}_i, \hat{\gamma}, F_c) = \mathbf{0} \quad (6a)$$

$$1/N \sum_{i=1}^N \mathbf{s}_{wra}(t_i, \mathbf{x}_i, 0, \hat{\beta}_{wra,0}, F) = \mathbf{0} \quad (6b)$$

$$1/N \sum_{i=1}^N \mathbf{s}_{\text{wra}}(t_i, \mathbf{x}_i, 1, \hat{\beta}_{\text{wra},1}, F) = \mathbf{0} \quad (6c)$$

$$1/N \sum_{i=1}^N \varpi_i \left\{ \hat{E}(t_i | \mathbf{x}_i, \tau = 0, \hat{\beta}_{\text{wra},0}) - \widehat{\text{POM}}_{\text{wra},0} \right\} = 0 \quad (6d)$$

$$1/N \sum_{i=1}^N \varpi_i \left\{ \hat{E}(t_i | \mathbf{x}_i, \tau = 1, \hat{\beta}_{\text{wra},1}) - \widehat{\text{POM}}_{\text{wra},1} \right\} = 0 \quad (6e)$$

where

$\mathbf{s}_{\text{wra}}(t_i, \mathbf{w}_i, \hat{\gamma}, F_c) = \frac{\partial L_{c,\text{wra}}(t_i, \mathbf{w}_i, \hat{\gamma})}{\partial \hat{\gamma}}$ is the vector of score equations from the ML estimator for $\hat{\gamma}$ based on survival-time model F_c ,

$\mathbf{s}_{\text{wra}}(t_i, \mathbf{x}_i, 0, \hat{\beta}_{\text{wra},0}, F) = \frac{\partial L(t_i, \mathbf{x}_i, 0, \hat{\beta}_{\text{wra},0})}{\partial \hat{\beta}_{\text{wra},0}}$ is the vector of score equations from the WML estimator for $\hat{\beta}_{\text{wra},0}$ based on survival-time model F ,

$\mathbf{s}_{\text{wra}}(t_i, \mathbf{x}_i, 1, \hat{\beta}_{\text{wra},1}, F) = \frac{\partial L(t_i, \mathbf{x}_i, 1, \hat{\beta}_{\text{wra},1})}{\partial \hat{\beta}_{\text{wra},1}}$ is the vector of score equations from the WML estimator for $\hat{\beta}_{\text{wra},1}$ based on survival-time model F ,

$\hat{E}(t_i | \mathbf{x}_i, \tau = 0, \hat{\beta}_{\text{wra},0})$ is the predicted mean survival time assuming treatment level 0 for observation i conditional on \mathbf{x}_i , and

$\hat{E}(t_i | \mathbf{x}_i, \tau = 1, \hat{\beta}_{\text{wra},1})$ is the predicted mean survival time assuming treatment level 1 for observation i conditional on \mathbf{x}_i .

The observation-level scores $\mathbf{s}_{\text{wra}}(t_i, \mathbf{x}_i, 0, \hat{\beta}_{\text{wra},0}, F)$ and $\mathbf{s}_{\text{wra}}(t_i, \mathbf{x}_i, 1, \hat{\beta}_{\text{wra},1}, F)$ also depend on c_i , \mathbf{w}_i , $\hat{\gamma}$, and F_c , but we ignored this dependence to simplify the notation.

The ATE is estimated by replacing (6e) with

$$1/N \sum_{i=1}^N \varpi_i \left\{ \hat{E}(t_i | \mathbf{x}_i, \tau = 1, \hat{\beta}_{\text{wra},1}) - \widehat{\text{POM}}_{\text{wra},0} - \widehat{\text{ATE}}_{\text{wra}} \right\} = 0 \quad (7)$$

and the ATET is estimated by replacing (6e) and (7) with

$$1/N_1 \sum_{i=1}^N \varpi_i (\tau_i == 1) \left\{ \hat{E}(t_i | \mathbf{x}_i, \tau = 0, \hat{\beta}_{\text{wra},0}) - \widehat{\text{POM}}_{\text{wra,cot},0} \right\} = 0$$

$$1/N_1 \sum_{i=1}^N \varpi_i (\tau_i == 1) \left\{ \hat{E}(t_i | \mathbf{x}_i, \tau = 1, \hat{\beta}_{\text{wra},1}) - \widehat{\text{POM}}_{\text{wra,cot},0} - \widehat{\text{ATET}}_{\text{wra}} \right\} = 0$$

where $\widehat{\text{POM}}_{\text{wra,cot},0}$ is the estimated conditional-on-treatment POM.

Inverse-probability-weighted estimators

IPW estimators are weighted averages of the observed outcome. The weights correct for missing data due to unobserved potential outcomes and censoring. Each weight is the inverse of the probability that a given value is observed. Observed values that were not likely to be observed have higher weights.

When the outcome variable is never censored, the missing data are the unobserved potential outcome and an observation's weight is the inverse of a treatment probability. When the outcome may be censored, the censoring is an additional source of missing data. In this case, an observation's weight is the inverse of the joint probability that an observation is uncensored and has a particular treatment level.

To define this joint probability, the censoring time must be random. In practice, we make the [WAC assumptions](#).

As is standard in the survival-time literature, we assume that the censoring-time process is independent of treatment assignment after conditioning on the covariates. This conditional independence assumption implies that the probability that observation i receives treatment level 1 and is not censored is the product of the probability that i gets treatment level 1 and the probability that i is not censored at time t_i , which we denote by

$$p(\mathbf{z}_i, \boldsymbol{\alpha})\{1 - F_c(t_i|\mathbf{w}_i, \boldsymbol{\gamma})\}$$

where

$p(\mathbf{z}_i, \boldsymbol{\alpha})$ is the modeled probability that i gets treatment level 1, conditional on covariates \mathbf{z}_i with parameters $\boldsymbol{\alpha}$, and

$F_c(t_i|\mathbf{w}_i, \boldsymbol{\gamma})$ is the survival-time model for the censoring time, conditional on covariates \mathbf{w}_i with parameters $\boldsymbol{\gamma}$, and evaluated at time t_i .

Bai, Tsiatis, and O'Brien (2013) formally derive these weights to control jointly for the missing potential outcome and censoring.

The IPW estimators have the following logic.

IPW1. Estimate by ML the parameters $\boldsymbol{\gamma}$ of a parametric survival-time model for the time to censoring, in which $F_c(t_c|\mathbf{w}, \boldsymbol{\gamma})$ is the distribution of censoring time, conditional on covariates \mathbf{w} . Denote the estimates of $\boldsymbol{\gamma}$ by $\hat{\boldsymbol{\gamma}}$.

IPW2. Estimate by ML the parameters $\boldsymbol{\alpha}$ of a parametric model for the probability of treatment model $p(\mathbf{z}_i, \boldsymbol{\alpha})$. Denote the estimates of $\boldsymbol{\alpha}$ by $\hat{\boldsymbol{\alpha}}$.

IPW3. Use the $\hat{\boldsymbol{\gamma}}$ estimated in IPW1 and the $\hat{\boldsymbol{\alpha}}$ estimated in IPW2 to construct inverse-probability weights by (8a) for treatment level 1 and by (8b) for treatment level 0.

$$\omega_{i,1} = \frac{(\tau_i == 1)(c_i == 0)}{[p(\mathbf{z}_i, \hat{\boldsymbol{\alpha}})\{1 - F_c(t_i|\mathbf{w}_i, \hat{\boldsymbol{\gamma}})\}]} \quad (8a)$$

$$\omega_{i,0} = \frac{(\tau_i == 0)(c_i == 0)}{[\{1 - p(\mathbf{z}_i, \hat{\boldsymbol{\alpha}})\}\{1 - F_c(t_i|\mathbf{w}_i, \hat{\boldsymbol{\gamma}})\}]} \quad (8b)$$

IPW4. Use the estimated weights to estimate each POM_τ by a weighted average of the uncensored observations on the observed potential outcome.

The contribution of the i th observation to the log likelihood that is maximized in step IPW1 is

$$L_{c,\text{ipw}}(t_i, \mathbf{w}_i, \hat{\gamma}) = \varpi_i [c_i \ln\{f_c(t_i|\mathbf{w}_i, \hat{\gamma})\} + (1 - c_i) \ln\{1 - F_c(t_i|\mathbf{w}_i, \hat{\gamma})\}]$$

where the definitions and intuition are as described after (4).

The contribution of the i th observation to the log likelihood that is maximized in step IPW2 is

$$L_{p,\text{ipw}}(\tau_i, \mathbf{z}_i, \hat{\alpha}) = \varpi_i [(\tau_i == 1) \ln\{p(\mathbf{z}_i, \hat{\alpha})\} + \{1 - (\tau_i == 1)\} \ln\{1 - p(\mathbf{z}_i, \hat{\alpha})\}]$$

where $p(\mathbf{z}_i, \hat{\alpha})$ is the model for the probability that i gets treatment level 1.

The IPW estimators for the POMs simultaneously solve estimating equations (9a) through (9d) for $\hat{\gamma}$, $\hat{\alpha}$, $\widehat{\text{POM}}_{\text{ipw},0}$, and $\widehat{\text{POM}}_{\text{ipw},1}$.

$$1/N \sum_{i=1}^N \mathbf{s}_{\text{ipw}}(t_i, \mathbf{w}_i, \hat{\gamma}, F_c) = \mathbf{0} \quad (9a)$$

$$1/N \sum_{i=1}^N \mathbf{s}_{\text{ipw}}(\tau_i, \mathbf{z}_i, \hat{\alpha}, p) = \mathbf{0} \quad (9b)$$

$$1/N \sum_{i=1}^N \varpi_i \omega_{i,0} (t_i - \widehat{\text{POM}}_{\text{ipw},0}) = 0 \quad (9c)$$

$$1/N \sum_{i=1}^N \varpi_i \omega_{i,1} (t_i - \widehat{\text{POM}}_{\text{ipw},1}) = 0 \quad (9d)$$

where

$\mathbf{s}_{\text{ipw}}(t_i, \mathbf{w}_i, \hat{\gamma}, F_c) = \frac{\partial L_{c,\text{ipw}}(t_i, \mathbf{w}_i, \hat{\gamma})}{\partial \hat{\gamma}}$ is the vector of score equations from the ML estimator for $\hat{\gamma}$ based on survival-time model F_c , and

$\mathbf{s}_{\text{ipw}}(\tau_i, \mathbf{z}_i, \hat{\alpha}, p) = \frac{\partial L_{p,\text{ipw}}(\tau_i, \mathbf{z}_i, \hat{\alpha})}{\partial \hat{\alpha}}$ is the vector of score equations from the ML estimator for $\hat{\alpha}$ based on probability model p .

The literature on IPW estimators discusses using normalized versus unnormalized weights, with normalized weights doing better in simulation studies; see Busso, DiNardo, and McCrary (2014) for example. The way that weights enter moment equations (9c) and (9d) implies that they are normalized, because the scale of the weights does not affect the estimates.

The estimated ATE is computed as

$$\widehat{\text{POM}}_{\text{ipw},1} - \widehat{\text{POM}}_{\text{ipw},0} = \widehat{\text{ATE}}_{\text{ipw}}$$

The estimated ATET uses weights

$$\omega_{i,\text{cot},1} = \frac{(\tau_i == 1)(c_i == 0)}{[\{1 - F_c(t_i|\mathbf{w}_i, \hat{\gamma})\}]} \quad (10a)$$

for treatment level 1 and

$$\omega_{i,\text{cot},0} = \frac{p(\mathbf{z}_i, \hat{\alpha})(\tau_i == 0)(c_i == 0)}{[\{1 - p(\mathbf{z}_i, \hat{\alpha})\}\{1 - F_c(t_i|\mathbf{w}_i, \hat{\gamma})\}]} \quad (10b)$$

for treatment level 0, and replaces (9c) and (9d) with

$$\frac{1}{N_1} \sum_{i=1}^N \varpi_i \omega_{i,\text{cot},0} (t_i - \widehat{\text{POM}}_{\text{ipw},\text{cot},0}) = 0 \quad (11\text{a})$$

$$\frac{1}{N_1} \sum_{i=1}^N \varpi_i \omega_{i,\text{cot},1} (t_i - \widehat{\text{POM}}_{\text{ipw},\text{cot},1}) = 0 \quad (11\text{b})$$

and then computes

$$\widehat{\text{POM}}_{\text{ipw},\text{cot},1} - \widehat{\text{POM}}_{\text{ipw},\text{cot},0} = \widehat{\text{ATE}}_{\text{ipw}}$$

These IPW estimators can be viewed as weighted IPW estimators and are thus related to those in Hirano, Imbens, and Ridder (2003).

Uncensored data

As mentioned, when the outcome variable is never censored, the missing data are the unobserved potential outcome and an observation's weight is the inverse of a treatment probability. In the never-censored case, the IPW estimators are identical to those implemented in **teffects ipw**; see **IPW estimators** under *Methods and formulas* in [TE] **teffects aipw**.

stteffects ipw computes the estimator for never-censored data when a censoring model is not specified and there are no censored observations in the sample. In the never-censored case, the following changes are made to the IPW estimator for the POMs and the ATE.

1. Step **IPW1** is not performed.
2. The weights in (8a) and (8b) for the POMs and the ATE are replaced with (12a) for treatment level 1 and (12b) for treatment level 0.

$$\omega_{i,1} = \frac{(\tau_i == 1)}{p(\mathbf{z}_i, \widehat{\boldsymbol{\alpha}})} \quad (12\text{a})$$

$$\omega_{i,0} = \frac{(\tau_i == 0)}{\{1 - p(\mathbf{z}_i, \widehat{\boldsymbol{\alpha}})\}} \quad (12\text{b})$$

3. Only moment conditions (9b), (9c), and (9d) are used.

The following changes also are made to the IPW estimator for the ATET.

1. Step **IPW1** is not performed.
2. The weights in (10a) and (10b) are replaced with (13a) for treatment level 1 and (13b) for treatment level 0.

$$\omega_{i,\text{cot},1} = (\tau_i == 1) \quad (13\text{a})$$

$$\omega_{i,\text{cot},0} = \frac{p(\mathbf{z}_i, \widehat{\boldsymbol{\alpha}})(\tau_i == 0)}{\{1 - p(\mathbf{z}_i, \widehat{\boldsymbol{\alpha}})\}} \quad (13\text{b})$$

3. Only moment conditions (9b), (11a), and (11b) are used.

Inverse-probability-weighted regression-adjustment estimators

IPWRA estimators are averages of treatment-specific predicted conditional means that were made using missingness-adjusted regression parameters. These estimators are Wooldridge's IPWRA for survival-time outcomes; see [Wooldridge \(2010, chap. 21\)](#) and [Wooldridge \(2007\)](#).

The censored observations can be handled either by weighting under the WAC assumptions to obtain the WAC-IPWRA estimator or by adding a term to the log-likelihood function (which we call likelihood-adjusted censoring) to obtain the LAC-IPWRA estimator. Correspondingly, there are two versions of formulas for the IPWRA estimator.

1. When a censoring model is specified, `stteffects ipwra` uses the formulas for the WAC-IPWRA estimator given in [Weighted-adjusted-censoring IPWRA](#).
2. When a censoring model is not specified, `stteffects ipwra` uses the formulas for the LAC-IPWRA given in [Likelihood-adjusted-censoring IPWRA](#), below.

The WAC-IPWRA estimator requires that some observations be censored and that the WAC assumptions hold; see [Weighted-adjusted-censoring assumptions](#), above. The LAC-IPWRA estimator handles the case in which no observations are censored and requires the weaker independent censoring assumptions, which allows for fixed censoring times.

Weighted-adjusted-censoring IPWRA

When a censoring model is specified, `stteffects ipwra` uses the formulas for the WAC-IPWRA estimator to obtain the model-based weights that account for censoring. For notational conciseness and to reinforce its dependence on random censoring, we denote the WAC-IPWRA estimator by IPWRAR in lists and formulas. The WAC-IPWRA estimators have the following logic.

- IPWRAR1. Estimate by ML the parameters γ of a parametric survival-time model for the time to censoring, in which $F_c(t_c|\mathbf{w}, \gamma)$ is the censoring-time distribution, conditional on covariates \mathbf{w} . We denote the estimates of γ by $\hat{\gamma}$.
- IPWRAR2. Estimate by ML the parameters α of a parametric model for the probability of treatment model $p(\mathbf{z}_i, \alpha)$. We denote the estimates of α by $\hat{\alpha}$.
- IPWRAR3. For each treatment level $\tau \in \{0, 1\}$, estimate by WML the parameters β_τ of a parametric model for the survival-time outcome t , in which $F(t|\mathbf{x}, \tau, \beta_\tau)$ is the distribution of t conditional on covariates \mathbf{x} and treatment level τ . For the ATE, the weights are those in equations (8a) and (8b). For the ATET, the weights are those in equations (10a) and (10b). We denote the estimates of $\beta_{ipwrar, \tau}$ by $\hat{\beta}_\tau$.
- IPWRAR4. Use the estimated $\hat{\beta}_{ipwrar, \tau}$ and the functional form implied by $F(t|\mathbf{x}, \tau, \beta_\tau)$ to estimate the mean survival time, conditional on \mathbf{x} and treatment level τ , for each sample observation, denoted by $\hat{E}(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{ipwrar, \tau})$. Conditional independence of the treatment and the survival-time potential outcomes ensures that $E(t|\mathbf{x}, \tau, \beta_\tau) = E(t_\tau|\mathbf{x}, \beta_\tau)$, where t_τ is the potential survival-time outcome corresponding to treatment level τ . Under correct model specification, sample averages of $\hat{E}(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{ipwrar, \tau})$ consistently estimate the POM for treatment level τ , denoted by POM_τ .

The contribution of the i th observation to the log likelihood that is maximized in step IPWRAR1 is

$$L_{c, ipwrar}(t_i, \mathbf{w}_i, \hat{\gamma}) = \varpi_i [c_i \ln\{f_c(t_i|\mathbf{w}_i, \hat{\gamma})\} + (1 - c_i) \ln\{1 - F_c(t_i|\mathbf{w}_i, \hat{\gamma})\}]$$

where the definitions and intuition are as described after (4).

The contribution of the i th observation to the log likelihood that is maximized in step IPWRAR2 is

$$L_{p,\text{ipwrar}}(\tau_i, \mathbf{z}_i, \hat{\boldsymbol{\alpha}}) = \varpi_i [(\tau_i == 1) \ln\{p(\mathbf{z}_i, \hat{\boldsymbol{\alpha}})\} + \{1 - (\tau_i == 1)\} \ln\{1 - p(\mathbf{z}_i, \hat{\boldsymbol{\alpha}})\}]$$

where $p(\mathbf{z}_i, \hat{\boldsymbol{\alpha}})$ is the model for the probability that i gets treatment level 1.

The weights and the parameters in step IPWRAR3 used to estimate the ATE differ from those used to estimate the ATET. For the ATE, the contribution of the i th observation to the log likelihood that is maximized in step IPWRAR3 is

$$L_{\text{ipwrar}}(t_i, \mathbf{x}_i, \tau, \hat{\boldsymbol{\beta}}_{\text{ipwrar,ate},\tau}) = \varpi_i \omega_{i,\tau} \ln\{f(t_i | \mathbf{x}_i, \tau, \hat{\boldsymbol{\beta}}_{\text{ipwrar,ate},\tau})\}$$

where $\omega_{i,1}$ is given in (8a), $\omega_{i,0}$ is given in (8b), and $f(t_i | \mathbf{x}_i, \tau, \hat{\boldsymbol{\beta}}_{\text{ipwrar,ate},\tau})$ is the density corresponding to distribution $F(t_i | \mathbf{x}_i, \tau, \hat{\boldsymbol{\beta}}_{\text{ipwrar,ate},\tau})$. Like WRA, only the uncensored observations are used because the weights account for censoring.

The IPWRAR estimators for the POMs simultaneously solve estimating equations (14a) through (14f) for $\hat{\gamma}$, $\hat{\boldsymbol{\alpha}}$, $\hat{\boldsymbol{\beta}}_{\text{ipwrar,ate},0}$, $\hat{\boldsymbol{\beta}}_{\text{ipwrar,ate},0}$, $\widehat{\text{POM}}_{\text{ipwrar},0}$, and $\widehat{\text{POM}}_{\text{ipwrar},1}$.

$$1/N \sum_{i=1}^N \mathbf{s}_{\text{ipwrar}}(t_i, \mathbf{w}_i, \hat{\boldsymbol{\gamma}}, F_c) = \mathbf{0} \quad (14a)$$

$$1/N \sum_{i=1}^N \mathbf{s}_{\text{ipwrar}}(\tau_i, \mathbf{z}_i, \hat{\boldsymbol{\alpha}}, p) = \mathbf{0} \quad (14b)$$

$$1/N \sum_{i=1}^N \mathbf{s}_{\text{ipwrar}}(t_i, \mathbf{x}_i, 0, \hat{\boldsymbol{\beta}}_{\text{ipwrar,ate},0}, F) = \mathbf{0} \quad (14c)$$

$$1/N \sum_{i=1}^N \mathbf{s}_{\text{ipwrar}}(t_i, \mathbf{x}_i, 1, \hat{\boldsymbol{\beta}}_{\text{ipwrar,ate},1}, F) = \mathbf{0} \quad (14d)$$

$$1/N \sum_{i=1}^N \varpi_i \left\{ \hat{E}(t_i | \mathbf{x}_i, \tau = 0, \hat{\boldsymbol{\beta}}_{\text{ipwrar,ate},0}) - \widehat{\text{POM}}_{\text{ipwrar},0} \right\} = 0 \quad (14e)$$

$$1/N \sum_{i=1}^N \varpi_i \left\{ \hat{E}(t_i | \mathbf{x}_i, \tau = 1, \hat{\boldsymbol{\beta}}_{\text{ipwrar,ate},1}) - \widehat{\text{POM}}_{\text{ipwrar},1} \right\} = 0 \quad (14f)$$

where

$\mathbf{s}_{\text{ipwrar}}(t_i, \mathbf{w}_i, \hat{\boldsymbol{\gamma}}, F_c) = \frac{\partial L_{c,\text{ipwrar}}(t_i, \mathbf{w}_i, \hat{\boldsymbol{\gamma}})}{\partial \hat{\boldsymbol{\gamma}}}$ is the vector of score equations from the ML estimator for $\hat{\boldsymbol{\gamma}}$ based on survival-time model F_c ,

$\mathbf{s}_{\text{ipwrar}}(\tau_i, \mathbf{z}_i, \hat{\boldsymbol{\alpha}}, p) = \frac{\partial L_{p,\text{ipwrar}}(\tau_i, \mathbf{z}_i, \hat{\boldsymbol{\alpha}})}{\partial \hat{\boldsymbol{\alpha}}}$ is the vector of score equations from the ML estimator for $\hat{\boldsymbol{\alpha}}$ based on probability model p ,

$\mathbf{s}_{\text{ipwrar}}(t_i, \mathbf{x}_i, 0, \hat{\boldsymbol{\beta}}_{\text{ipwrar,ate},0}, F) = \frac{\partial L_{\text{ipwrar}}(t_i, \mathbf{x}_i, 0, \hat{\boldsymbol{\beta}}_{\text{ipwrar,ate},0})}{\partial \hat{\boldsymbol{\beta}}_{\text{ipwrar,ate},0}}$ is the vector of score equations from the ML estimator for $\hat{\boldsymbol{\beta}}_{\text{ipwrar,ate},0}$ based on survival-time model F ,

$s_{ipwrar}(t_i, \mathbf{x}_i, 1, \hat{\beta}_{ipwrar,ate,1}, F) = \frac{\partial L_{ipwrar}(t_i, \mathbf{x}_i, 1, \hat{\beta}_{ipwrar,ate,1})}{\partial \hat{\beta}_{ipwrar,ate,1}}$ is the vector of score equations from the ML estimator for $\hat{\beta}_{ipwrar,ate,1}$ based on survival-time model F ,

$\hat{E}(t_i | \mathbf{x}_i, \tau = 0, \hat{\beta}_{ipwrar,ate,0})$ is the predicted mean survival time assuming treatment level 0 for observation i conditional on \mathbf{x}_i , and

$\hat{E}(t_i | \mathbf{x}_i, \tau = 1, \hat{\beta}_{ipwrar,ate,1})$ is the predicted mean survival time assuming treatment level 1 for observation i conditional on \mathbf{x}_i .

The ATE is estimated by replacing (14f) with

$$1/N \sum_{i=1}^N \varpi_i \left\{ \hat{E}(t_i | \mathbf{x}_i, \tau = 1, \hat{\beta}_{ipwrar,ate,1}) - \widehat{POM}_{ipwrar,0} - \widehat{ATE}_{ipwrar} \right\} = 0$$

For the ATET, the contribution of the i th observation to the weighted log likelihood that is maximized in step IPWRAR3 is

$$L_{ipwrar}(t_i, \mathbf{x}_i, \tau, \hat{\beta}_{ipwrar,ate,\tau}) = \varpi_i \omega_{i,cot,\tau}(\tau_i == \tau) \ln\{f(t_i | \mathbf{x}_i, \tau, \hat{\beta}_{ipwrar,atet,\tau})\}$$

where $\omega_{i,cot,1}$ is given in (10a), $\omega_{i,cot,0}$ is given in (10b), and $f(t_i | \mathbf{x}_i, \tau, \hat{\beta}_{ipwrar,atet,\tau})$ is the density corresponding to distribution $F(t_i | \mathbf{x}_i, \tau, \hat{\beta}_{ipwrar,atet,\tau})$.

The WAC-IPWRA estimators for the conditional-on-treatment POMs simultaneously solve estimating equations (15a) through (15f) for $\hat{\beta}_{ipwrar,atet,0}$, $\hat{\beta}_{ipwrar,atet,0}$, $\hat{\gamma}$, $\hat{\alpha}$, $\widehat{POM}_{ipwrar,cot,0}$, and $\widehat{POM}_{ipwrar,cot,1}$.

$$1/N \sum_{i=1}^N \mathbf{s}_{ipwrar}(t_i, \mathbf{w}_i, \hat{\gamma}, F_c) = \mathbf{0} \quad (15a)$$

$$1/N \sum_{i=1}^N \mathbf{s}_{ipwrar}(\tau_i, \mathbf{z}_i, \hat{\alpha}, p) = \mathbf{0} \quad (15b)$$

$$1/N \sum_{i=1}^N \mathbf{s}_{ipwrar}(t_i, \mathbf{x}_i, 0, \hat{\beta}_{ipwrar,atet,0}, F) = \mathbf{0} \quad (15c)$$

$$1/N \sum_{i=1}^N \mathbf{s}_{ipwrar}(t_i, \mathbf{x}_i, 1, \hat{\beta}_{ipwrar,atet,1}, F) = \mathbf{0} \quad (15d)$$

$$1/N \sum_{i=1}^N \varpi_i \left\{ \hat{E}(t_i | \mathbf{x}_i, \tau = 0, \hat{\beta}_{ipwrar,atet,0}) - \widehat{POM}_{ipwrar,cot,0} \right\} = 0 \quad (15e)$$

$$1/N \sum_{i=1}^N \varpi_i \left\{ \hat{E}(t_i | \mathbf{x}_i, \tau = 1, \hat{\beta}_{ipwrar,atet,1}) - \widehat{POM}_{ipwrar,cot,1} \right\} = 0 \quad (15f)$$

where

$\mathbf{s}_{ipwrar}(t_i, \mathbf{w}_i, \hat{\gamma}, F_c) = \frac{\partial L_{c,ipwrar}(t_i, \mathbf{w}_i, \hat{\gamma})}{\partial \hat{\gamma}}$ is the vector of score equations from the ML estimator for $\hat{\gamma}$ based on survival-time model F_c ,

$\mathbf{s}_{\text{ipwrar}}(\tau_i, \mathbf{z}_i, \hat{\boldsymbol{\alpha}}, p) = \frac{\partial L_{p,\text{ipwrar}}(\tau_i, \mathbf{z}_i, \hat{\boldsymbol{\alpha}})}{\partial \hat{\boldsymbol{\alpha}}}$ is the vector of score equations from the ML estimator for $\hat{\boldsymbol{\alpha}}$ based on probability model p ,

$\mathbf{s}_{\text{ipwrar}}(t_i, \mathbf{x}_i, 0, \hat{\boldsymbol{\beta}}_{\text{ipwrar},\text{atet},0}, F) = \frac{\partial L_{\text{ipwrar}}(t_i, \mathbf{x}_i, 0, \hat{\boldsymbol{\beta}}_{\text{ipwrar},\text{atet},0})}{\partial \hat{\boldsymbol{\beta}}_{\text{ipwrar},\text{atet},0}}$ is the vector of score equations from the WML estimator for $\hat{\boldsymbol{\beta}}_{\text{ipwrar},\text{atet},0}$ based on survival-time model F ,

$\mathbf{s}_{\text{ipwrar}}(t_i, \mathbf{x}_i, 1, \hat{\boldsymbol{\beta}}_{\text{ipwrar},\text{atet},1}, F) = \frac{\partial L_{\text{ipwrar}}(t_i, \mathbf{x}_i, 1, \hat{\boldsymbol{\beta}}_{\text{ipwrar},\text{atet},1})}{\partial \hat{\boldsymbol{\beta}}_{\text{ipwrar},\text{atet},1}}$ is the vector of score equations from the WML estimator for $\hat{\boldsymbol{\beta}}_{\text{ipwrar},\text{atet},1}$ based on survival-time model F ,

$\hat{E}(t_i | \mathbf{x}_i, \tau = 0, \hat{\boldsymbol{\beta}}_{\text{ipwrar},\text{atet},0})$ is the predicted mean survival time assuming treatment level 0 for observation i conditional on \mathbf{x}_i , and

$\hat{E}(t_i | \mathbf{x}_i, \tau = 1, \hat{\boldsymbol{\beta}}_{\text{ipwrar},\text{atet},1})$ is the predicted mean survival time assuming treatment level 1 for observation i conditional on \mathbf{x}_i .

The ATET is estimated by replacing (15f) with

$$1/N \sum_{i=1}^N \varpi_i \left\{ \hat{E}(t_i | \mathbf{x}_i, \tau = 1, \hat{\boldsymbol{\beta}}_{\text{ipwrar},\text{atet},1}) - \widehat{\text{POM}}_{\text{ipwrar},\text{cot},0} - \widehat{\text{ATET}}_{\text{ipwrar}} \right\} = 0$$

Likelihood-adjusted-censoring IPWRA

When a censoring model is not specified, **stteffects ipwra** uses the formulas for the LAC-IPWRA estimator that add a term to the log-likelihood function. For notational conciseness and to reinforce its use of an additional term in the log likelihood, we denote the LAC-IPWRA estimator by IPWRAL in lists and formulas.

The methods and formulas for the LAC-IPWRA estimator differ in three ways from those for the WAC-IPWRA estimator.

1. No censoring model is specified, so LAC-IPWRA does not perform a version of **step IPWRAR1** and it does not use the moment equations (14a).
2. The weights only depend on the treatment level and treatment assignment probabilities, not on the censoring.
3. The WML estimator for $\boldsymbol{\beta}_\tau$ includes a term for censored observations and censored observations are used. Recall that for the WAC-IPWRA estimator, the weights used in the WML estimator for $\boldsymbol{\beta}_\tau$ account for the censoring, and the censored observations are not used in the WML estimator.

The LAC-IPWRA estimators have the following logic.

IPWRAL1. Estimate by ML the parameters $\boldsymbol{\alpha}$ of a parametric model for the probability of treatment model $p(\mathbf{z}_i, \boldsymbol{\alpha})$.

IPWRAL2. For each treatment level $\tau \in \{0, 1\}$, estimate by WML the parameters $\boldsymbol{\beta}_\tau$ of a parametric model for the survival-time outcome t in which $F(t | \mathbf{x}, \tau, \boldsymbol{\beta}_\tau)$ is the distribution of t conditional on covariates \mathbf{x} and treatment level τ . The weights depend only on the treatment level and the treatment-assignment probabilities. For the ATE, the weights are those in (12a) and (12b). For the ATET, the weights are those in (13a) and (13b). We denote the estimates of $\boldsymbol{\beta}_\tau$ by $\hat{\boldsymbol{\beta}}_{\text{ipwral},\tau}$.

IPWRAL3. Use the estimated $\hat{\beta}_{\text{ipwral},\tau}$ and the functional form implied by $F(t|\mathbf{x}, \tau, \beta_\tau)$ to estimate the mean survival time, conditional on \mathbf{x} and treatment level τ , for each sample observation, denoted by $\hat{E}(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{\text{ipwral},\tau})$. Conditional independence of the treatment and the survival-time potential outcomes ensures that $E(t|\mathbf{x}, \tau, \beta_\tau) = E(t_\tau|\mathbf{x}, \beta_\tau)$, where t_τ is the potential survival-time outcome corresponding to treatment level τ . Under correct model specification, sample averages of $\hat{E}(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{\text{ipwral},\tau})$ consistently estimate the POM for treatment level τ , denoted by POM_τ .

The contribution of the i th observation to the log likelihood that is maximized in step IPWRAL1 is

$$L_{p,\text{ipwral}}(\tau_i, \mathbf{z}_i, \hat{\alpha}) = \varpi_i [(\tau_i == 1) \ln\{p(\mathbf{z}_i, \hat{\alpha})\} + \{1 - (\tau_i == 1)\} \ln\{1 - p(\mathbf{z}_i, \hat{\alpha})\}]$$

where $p(\mathbf{z}_i, \hat{\alpha})$ is the model for the probability that i gets treatment level 1.

The weights and the parameters in step IPWRAL2 used to estimate the ATE differ from those used to estimate the ATET. For the ATE, the contribution of the i th observation to the log likelihood that is maximized in step IPWRAL2 is

$$L_{\text{ipwral}}(t_i, \mathbf{x}_i, \tau, \hat{\beta}_{\text{ipwral,ate},\tau}) = (\tau_i == \tau) \varpi_i \omega_{i,\tau} \left\{ (1 - c_i) \ln\{f(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{\text{ipwral,ate},\tau})\} \right. \\ \left. c_i \ln\{1 - F(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{\text{ipwral,ate},\tau})\} \right\}$$

where $\omega_{i,1}$ is given in (12a), $\omega_{i,0}$ is given in (12b), and $f(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{\text{ipwral,ate},\tau})$ is the density corresponding to distribution $F(t_i|\mathbf{x}_i, \tau, \hat{\beta}_{\text{ipwral,ate},\tau})$. Unlike the WRA estimator, the censored observations are used, and there is a term in the likelihood function to account for censoring.

The LAC-IPWRA estimators for the POMs simultaneously solve estimating equations (16a) through (16e) for $\hat{\alpha}$, $\hat{\beta}_{\text{ipwral,ate},0}$, $\hat{\beta}_{\text{ipwral,ate},1}$, $\widehat{\text{POM}}_{\text{ipwral},0}$, and $\widehat{\text{POM}}_{\text{ipwral},1}$.

$$1/N \sum_{i=1}^N \mathbf{s}_{\text{ipwral}}(\tau_i, \mathbf{z}_i, \hat{\alpha}, p) = \mathbf{0} \quad (16a)$$

$$1/N \sum_{i=1}^N \mathbf{s}_{\text{ipwral}}(t_i, \mathbf{x}_i, 0, \hat{\beta}_{\text{ipwral,ate},0}, F) = \mathbf{0} \quad (16b)$$

$$1/N \sum_{i=1}^N \mathbf{s}_{\text{ipwral}}(t_i, \mathbf{x}_i, 1, \hat{\beta}_{\text{ipwral,ate},1}, F) = \mathbf{0} \quad (16c)$$

$$1/N \sum_{i=1}^N \varpi_i \left\{ \hat{E}(t_i|\mathbf{x}_i, \tau = 0, \hat{\beta}_{\text{ipwral,ate},0}) - \widehat{\text{POM}}_{\text{ipwral},0} \right\} = 0 \quad (16d)$$

$$1/N \sum_{i=1}^N \varpi_i \left\{ \hat{E}(t_i|\mathbf{x}_i, \tau = 1, \hat{\beta}_{\text{ipwral,ate},1}) - \widehat{\text{POM}}_{\text{ipwral},1} \right\} = 0 \quad (16e)$$

where

$\mathbf{s}_{\text{ipwral}}(\tau_i, \mathbf{z}_i, \hat{\alpha}, p) = \frac{\partial L_{p,\text{ipwral}}(\tau_i, \mathbf{z}_i, \hat{\alpha})}{\partial \hat{\alpha}}$ is the vector of score equations from the ML estimator for $\hat{\alpha}$ based on probability model p ,

$\mathbf{s}_{\text{ipwral}}(t_i, \mathbf{x}_i, 0, \widehat{\boldsymbol{\beta}}_{\text{ipwral,ate},0}, F) = \frac{\partial L_{\text{ipwral}}(t_i, \mathbf{x}_i, 0, \widehat{\boldsymbol{\beta}}_{\text{ipwral,ate},0})}{\partial \widehat{\boldsymbol{\beta}}_{\text{ipwral,ate},0}}$ is the vector of score equations from the WML estimator for $\widehat{\boldsymbol{\beta}}_{\text{ipwral,ate},0}$ based on survival-time model F ,

$\mathbf{s}_{\text{ipwral}}(t_i, \mathbf{x}_i, 1, \widehat{\boldsymbol{\beta}}_{\text{ipwral,ate},1}, F) = \frac{\partial L_{\text{ipwral}}(t_i, \mathbf{x}_i, 1, \widehat{\boldsymbol{\beta}}_{\text{ipwral,ate},1})}{\partial \widehat{\boldsymbol{\beta}}_{\text{ipwral,ate},1}}$ is the vector of score equations from the WML estimator for $\widehat{\boldsymbol{\beta}}_{\text{ipwral,ate},1}$ based on survival-time model F ,

$\widehat{E}(t_i | \mathbf{x}_i, \tau = 0, \widehat{\boldsymbol{\beta}}_{\text{ipwral,ate},0})$ is the predicted mean survival time assuming treatment level 0 for observation i conditional on \mathbf{x}_i , and

$\widehat{E}(t_i | \mathbf{x}_i, \tau = 1, \widehat{\boldsymbol{\beta}}_{\text{ipwral,ate},1})$ is the predicted mean survival time assuming treatment level 1 for observation i conditional on \mathbf{x}_i .

The ATE is estimated by replacing (16e) with

$$1/N \sum_{i=1}^N \varpi_i \left\{ \widehat{E}(t_i | \mathbf{x}_i, \tau = 1, \widehat{\boldsymbol{\beta}}_{\text{ipwral,ate},1}) - \widehat{\text{POM}}_{\text{ipwral},0} - \widehat{\text{ATE}}_{\text{ipwral}} \right\} = 0$$

For the ATET, the contribution of the i th observation to the WML function that is maximized in step IPWRAL2 is

$$\begin{aligned} L_{\text{ipwral}}(t_i, \mathbf{x}_i, \tau, \widehat{\boldsymbol{\beta}}_{\text{ipwral,atet},\tau}) &= (\tau_i == \tau) \varpi_i \omega_{i,\text{cot},\tau} \left\{ (1 - c_i) \ln \{f(t_i | \mathbf{x}_i, \tau, \widehat{\boldsymbol{\beta}}_{\text{ipwral,atet},\tau})\} \right. \\ &\quad \left. c_i \ln \{1 - F(t_i | \mathbf{x}_i, \tau, \widehat{\boldsymbol{\beta}}_{\text{ipwral,atet},\tau})\} \right\} \end{aligned}$$

where $\omega_{i,\text{cot},1}$ is given in (13a), $\omega_{i,\text{cot},0}$ is given in (13b), and $f(t_i | \mathbf{x}_i, \tau, \widehat{\boldsymbol{\beta}}_{\text{ipwral,atet},\tau})$ is the density corresponding to distribution $F(t_i | \mathbf{x}_i, \tau, \widehat{\boldsymbol{\beta}}_{\text{ipwral,atet},\tau})$. Again unlike the WRA, the censored observations are used, and there is a term in the likelihood function to account for censoring.

The LAC-IPWRA estimators for the conditional-on-treatment POMs simultaneously solve estimating equations (17a) through (17e) for $\widehat{\boldsymbol{\alpha}}$, $\widehat{\boldsymbol{\beta}}_{\text{ipwral,atet},0}$, $\widehat{\boldsymbol{\beta}}_{\text{ipwral,atet},1}$, $\widehat{\text{POM}}_{\text{ipwral,cot},0}$, and $\widehat{\text{POM}}_{\text{ipwral,cot},1}$.

$$1/N \sum_{i=1}^N \mathbf{s}_{\text{ipwral}}(\tau_i, \mathbf{z}_i, \widehat{\boldsymbol{\alpha}}, p) = \mathbf{0} \tag{17a}$$

$$1/N \sum_{i=1}^N \mathbf{s}_{\text{ipwral}}(t_i, \mathbf{x}_i, 0, \widehat{\boldsymbol{\beta}}_{\text{ipwral,atet},0}, F) = \mathbf{0} \tag{17b}$$

$$1/N \sum_{i=1}^N \mathbf{s}_{\text{ipwral}}(t_i, \mathbf{x}_i, 1, \widehat{\boldsymbol{\beta}}_{\text{ipwral,atet},1}, F) = \mathbf{0} \tag{17c}$$

$$1/N \sum_{i=1}^N \varpi_i \left\{ \widehat{E}(t_i | \mathbf{x}_i, \tau = 0, \widehat{\boldsymbol{\beta}}_{\text{ipwral,atet},0}) - \widehat{\text{POM}}_{\text{ipwral,cot},0} \right\} = 0 \tag{17d}$$

$$1/N \sum_{i=1}^N \varpi_i \left\{ \widehat{E}(t_i | \mathbf{x}_i, \tau = 1, \widehat{\boldsymbol{\beta}}_{\text{ipwral,atet},1}) - \widehat{\text{POM}}_{\text{ipwral,cot},1} \right\} = 0 \tag{17e}$$

where

$s_{\text{ipwral}}(\tau_i, \mathbf{z}_i, \hat{\boldsymbol{\alpha}}, p) = \frac{\partial L_{p,\text{ipwral}}(\tau_i, \mathbf{z}_i, \hat{\boldsymbol{\alpha}})}{\partial \hat{\boldsymbol{\alpha}}}$ is the vector of score equations from the ML estimator for $\hat{\boldsymbol{\alpha}}$ based on probability model p ,

$s_{\text{ipwral}}(t_i, \mathbf{x}_i, 0, \hat{\beta}_{\text{ipwral,atet},0}, F) = \frac{\partial L_{\text{ipwral}}(t_i, \mathbf{x}_i, 0, \hat{\beta}_{\text{ipwral,atet},0})}{\partial \hat{\beta}_{\text{ipwral,atet},0}}$ is the vector of score equations from the WML estimator for $\hat{\beta}_{\text{ipwral,atet},0}$ based on survival-time model F ,

$s_{\text{ipwral}}(t_i, \mathbf{x}_i, 1, \hat{\beta}_{\text{ipwral,atet},1}, F) = \frac{\partial L_{\text{ipwral}}(t_i, \mathbf{x}_i, 1, \hat{\beta}_{\text{ipwral,atet},1})}{\partial \hat{\beta}_{\text{ipwral,atet},1}}$ is the vector of score equations from the WML estimator for $\hat{\beta}_{\text{ipwral,atet},1}$ based on survival-time model F ,

$\hat{E}(t_i | \mathbf{x}_i, \tau = 0, \hat{\beta}_{\text{ipwral,atet},0})$ is the predicted mean survival time assuming treatment level 0 for observation i conditional on \mathbf{x}_i , and

$\hat{E}(t_i | \mathbf{x}_i, \tau = 1, \hat{\beta}_{\text{ipwral,atet},1})$ is the predicted mean survival time assuming treatment level 1 for observation i conditional on \mathbf{x}_i .

The ATET is estimated by replacing (17e) with

$$1/N \sum_{i=1}^N \varpi_i \left\{ \hat{E}(t_i | \mathbf{x}_i, \tau = 1, \hat{\beta}_{\text{ipwral,atet},1}) - \widehat{\text{POM}}_{\text{ipwral,cot},0} - \widehat{\text{ATET}}_{\text{ipwral}} \right\} = 0$$

Functional-form details

In this section, we specify the functional forms for the conditional distribution function used in the survival-time outcome model F , the conditional distribution function used in the survival-time censoring model F_c , and the conditional distribution used to model the treatment probabilities p .

You may choose among the same set of conditional distribution functions for either F or F_c : `exponential`, `weibull`, `lnormal`, or `gamma`.

Name	Cumulative	Density	Mean
exponential	$1 - \exp(-\lambda_i t_i)$	$\lambda_i \exp(-\lambda_i t_i)$	$1/\lambda_i$
Weibull	$1 - \exp\{-(\lambda_i t_i)^{s_i}\}$	$s_i t_i^{s_i-1} \lambda_i^{s_i} \exp\{-(\lambda_i t_i)^{s_i}\}$	$(1/\lambda_i) \Gamma\{(s_i + 1)/s_i\}$
log normal	$\Phi\{(\ln(t_i) - \lambda_i)/s_i\}$	$(1/(s_i t_i)) \phi\{(\ln(t_i) - \lambda_i)/s_i\}$	$\exp(\lambda_i + s_i^2/2)$
gamma	$\text{gammap}\{s_i, (s_i t_i / \lambda_i)\}$	$(s_i^{s_i} t_i^{s_i-1}) / \{\lambda_i^{s_i} \Gamma(s_i)\} \exp(-s_i t_i / \lambda_i)$	λ_i

where the following table specifies how λ_i and s_i are parameterized in terms of the covariates \mathbf{x}_i and the ancillary covariates $\tilde{\mathbf{x}}_i$, respectively.

Name	λ_i	s_i
exponential	$\exp(-\mathbf{x}_i \boldsymbol{\beta})$	
Weibull	$\exp(-\mathbf{x}_i \boldsymbol{\beta})$	$\exp(\tilde{\mathbf{x}}_i \tilde{\boldsymbol{\beta}})$
log normal	$\mathbf{x}_i \boldsymbol{\beta}$	$\exp(\tilde{\mathbf{x}}_i \tilde{\boldsymbol{\beta}})$
gamma	$\exp(\mathbf{x}_i \boldsymbol{\beta})$	$\exp(-2\tilde{\mathbf{x}}_i \tilde{\boldsymbol{\beta}})$

For the treatment-assignment models, the `probit` model uses the standard normal distribution, the `logit` uses the standard logistic distribution, the `hetprobit` model uses

$$\Phi\{\mathbf{z}_1\boldsymbol{\alpha}_1 / \exp(\mathbf{z}_2\boldsymbol{\alpha}_2)\}$$

and the multinomial logit uses

$$p(\mathbf{z}, t) = \exp(\mathbf{z}\boldsymbol{\alpha}_t) / \{1 + \sum_{k=1}^q \exp(\mathbf{z}\boldsymbol{\alpha}_k)\}$$

where the notation is defined below.

In the `hetprobit` model, \mathbf{z}_1 are the covariates specified in the treatment-assignment specification, \mathbf{z}_2 are the covariates specified in the `hetprobit()` option, and $\boldsymbol{\alpha}_1$ and $\boldsymbol{\alpha}_2$ are the corresponding coefficients.

In the multinomial logit model, \mathbf{z} are the covariates specified in the treatment-assignment specification and α_k are the coefficients; see [R] `mlogit` for further details.

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Also see

- [TE] **stteffects postestimation** — Postestimation tools for stteffects
- [TE] **stteffects intro** — Introduction to treatment effects for observational survival-time data
- [ST] **streg** — Parametric survival models
- [ST] **stset** — Declare data to be survival-time data
- [U] **20 Estimation and postestimation commands**

stteffects postestimation — Postestimation tools for stteffects

[Postestimation commands](#) [predict](#) [Remarks and examples](#) [References](#) [Also see](#)

Postestimation commands

The following postestimation commands are of special interest after **stteffects**:

Command	Description
<code>teffects overlap</code>	overlap plots
<code>tebalance</code>	check balance of covariates

The following standard postestimation commands are also available:

Command	Description
<code>estat summarize</code>	summary statistics for the estimation sample
<code>estat vce</code>	variance–covariance matrix of the estimators (VCE)
<code>estimates</code>	cataloging estimation results
<code>hausman</code>	Hausman’s specification test
<code>lincom</code>	point estimates, standard errors, testing, and inference for linear combinations of coefficients
<code>nlcom</code>	point estimates, standard errors, testing, and inference for nonlinear combinations of coefficients
<code>predict</code>	predictions, residuals, influence statistics, and other diagnostic measures
<code>predictnl</code>	point estimates, standard errors, testing, and inference for generalized predictions
<code>test</code>	Wald tests of simple and composite linear hypotheses
<code>testnl</code>	Wald tests of nonlinear hypotheses

predict

Description for predict

`predict` creates a new variable containing predictions such as treatment effects, conditional means, propensity scores, linear predictions, and log square roots of latent variances.

Menu for predict

Statistics > Postestimation

Syntaxes for predict

Syntaxes are presented under the following headings:

- [Syntax for predict after stteffects ipw](#)
- [Syntax for predict after stteffects ipwra](#)
- [Syntax for predict after stteffects ra](#)
- [Syntax for predict after stteffects wra](#)

Syntax for predict after stteffects ipw

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

<i>statistic</i>	Description
<hr/>	
Main	
<u>ps</u>	propensity score; the default
<u>censurv</u>	censored survival probability
<u>xb</u>	linear prediction for propensity score
<u>cxb</u>	linear prediction for censoring model
<u>lnsigma</u>	log square root of latent variance (for treatment model <code>hetprobit()</code>)
<u>clnshape</u>	log of conditional latent shape (for censoring distribution Weibull, log normal, or gamma)
<u>scores</u>	parameter-level or equation-level scores

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

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

You specify one or *t* new variables with `ps`, where *t* is the number of treatment levels.

You specify one or *t*–1 new variables with `xb` and `lnsigma`.

You specify one new variable with `censurv`, `cxb`, and `clnshape`.

Syntax for predict after stteffects ipwra

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

<i>statistic</i>	Description
Main	
<u>te</u>	treatment effect; the default
<u>cmean</u>	conditional mean at treatment level
<u>ps</u>	propensity score
<u>censurv</u>	censored survival probability
<u>xb</u>	linear prediction for outcome model
<u>cxb</u>	linear prediction for censoring model
<u>psxb</u>	linear prediction for propensity score
<u>lnshape</u>	log of conditional latent shape (for outcome distribution Weibull, log normal, or gamma) at treatment level
<u>clnshape</u>	log of conditional latent shape (for censoring distribution Weibull, log normal, or gamma)
<u>pslnsigma</u>	log square root of latent variance (for treatment model <code>hetprobit()</code> for propensity score
<u>scores</u>	parameter-level or equation-level scores

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, `cmean`, `ps`, `xb`, and `pslnsigma` assume `tlevel()` specifies the first treatment level.

You specify one or t new variables with `cmean`, `ps`, `xb`, and `lnshape`, where t is the number of treatment levels.

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

You specify one new variable with `censurv`, `cxb`, and `clnshape`.

Syntax for predict after stteffects ra

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

statistic	Description
<hr/>	
Main	
te	treatment effect; the default
cmean	conditional mean at treatment level
xb	linear prediction for outcome model
lnshape	log of conditional latent shape (for outcome distribution Weibull, log normal, or gamma) at treatment level
scores	parameter-level or equation-level scores

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

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

You specify one or t new variables with `cmean`, `xb`, and `lnshape`, where t is the number of treatment levels.

You specify one or $t-1$ new variables with `te`.

Syntax for predict after stteffects wra

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

statistic	Description
<hr/>	
Main	
te	treatment effect; the default
cmean	conditional mean at treatment level
censurv	censored survival probability
xb	linear prediction for outcome model
cxb	linear prediction for censoring model
lnshape	log of conditional latent shape (for outcome distribution Weibull, log normal, or gamma) at treatment level
clnshape	log of conditional latent shape (for censoring distribution Weibull, log normal, or gamma)
scores	parameter-level or equation-level scores

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

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

You specify one or t new variables with `cmean`, `xb`, and `lnshape`, where t is the number of treatment levels.

You specify one or $t-1$ new variables with `te`.

You specify one new variable with `censurv`, `cxb`, and `clnshape`.

Options for predict

Options are presented under the following headings:

- Options for predict after stteffects ipw*
- Options for predict after stteffects ipwra*
- Options for predict after stteffects ra*
- Options for predict after stteffects wra*

Options for predict after stteffects 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.

censurv calculates the survivor probability from the time-to-censoring model. (In other words, it calculates the probability that an outcome is not censored.) This option is allowed only if a censoring model is specified at estimation time. You need to specify only one new variable.

xb calculates the propensity score linear prediction 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).

cxb calculates the linear prediction of the censoring model. This option is allowed only if a censoring model is specified at estimation time. You need to specify only one new variable.

lnsigma calculates the log square root of the latent variance. This option is valid only when treatment model `hetprobit()` is used. You need to specify only one new variable.

clnshape calculates the log of the conditional latent shape parameter of the censoring distribution. This option is valid when censoring distribution Weibull, log normal, or gamma is used. You need to 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 censoring and 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 stteffects 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.

censurv calculates the survivor probability from the time-to-censoring model. (In other words, it calculates the probability that an outcome is not censored.) This option is allowed only if a censoring model is specified at estimation time. You need to specify only one new variable.

xb calculates the outcome model 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.

cxb calculates the linear prediction of the censoring model. This option is allowed only if a censoring model is specified at estimation time. You need to specify only one new variable.

psxb calculates the propensity score linear prediction 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).

lnshape calculates the log of the conditional latent shape parameter for each treatment level or the treatment level specified in `tlevel()`. This option is valid when outcome distribution Weibull, log normal, or gamma is 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.

clnshape calculates the log of the conditional latent shape parameter for the censoring distribution. This option is valid when censoring distribution Weibull, log normal, or gamma is used. You need to specify only one new variable.

pslnsigma calculates the log square root of the latent variance for the propensity score. This option is valid only when treatment model `hetprobit()` is used. You need to 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 outcome, censoring, and 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 stteffects 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 outcome model 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.

lnshape calculates the log of the conditional latent shape parameter for each treatment level or the treatment level specified in `tlevel()`. This option is valid when the outcome distribution Weibull, log normal, or gamma is 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.

`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 outcome 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 stteffects wra

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.

censurv calculates the survivor probability from the time-to-censoring model. (In other words, it calculates the probability that an outcome is not censored.) This option is allowed only if a censoring model is specified at estimation time. You need to specify only one new variable.

xb calculates the outcome model 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.

lnshape calculates the log of the conditional latent shape parameter for each treatment level or the treatment level specified in `tlevel()`. This option is valid when the outcome distribution Weibull, log normal, or gamma is 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.

clnshape calculates the log of the conditional latent shape parameter of the censoring distribution. This option is valid when the censoring distribution Weibull, log normal, or gamma is used. You need to 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 outcome and censoring 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 `stteffects 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 get too large and the estimators become unstable.

We estimate the average treatment effect of smoking on the time to a second heart attack by inverse-probability weighting; see example 1 of [TE] `stteffects ipw` for background.

Survival treatment-effects estimation						
		Number of obs = 2,000				
Estimator		inverse-probability weights				
Outcome model		weighted mean				
Treatment model:		logit				
Censoring model:		Weibull				
_t		Robust Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ATE						
smoke (Smoker vs Nonsmoker)		-2.22226	.6307573	-3.52	0.000	-3.458522 - .9859983
P0mean						
smoke Nonsmoker		4.235569	.5210937	8.13	0.000	3.214244 5.256894

Below, we compute the estimated probabilities of being a Nonsmoker and store them in `ps0`. Likewise, the estimated probabilities of being a Smoker are stored in `ps1`.

```
. predict ps0 ps1, ps
```

The overlap condition requires that each of these probabilities be sufficiently greater than 0 and less than 1 for every individual; see *Assumptions and trade-offs* under Remarks and examples in [TE] `stteffects intro`.

In practice, we know that weighting estimators perform poorly when the weights become too large. This approach requires that the probability of being a Nonsmoker not be too small among Nonsmokers and that the probability of being a Smoker not be too small among Smokers. Below, we summarize these probabilities.

```
. summarize ps0 if fail==1 & smoke==0
```

Variable	Obs	Mean	Std. Dev.	Min	Max
ps0	716	.6712529	.138754	.3872543	.9840293

```
. summarize ps1 if fail==1 & smoke==1
```

Variable	Obs	Mean	Std. Dev.	Min	Max
ps1	492	.4101277	.1101277	.0850604	.6125538

The minimum probability of being a **Nonsmoker** among **Nonsmokers** is 0.39. The minimum probability of being a **Smoker** among **Smokers** is 0.09. Neither minimum seems too small.

Estimating survival-time treatment effects also uses weights to adjust for censored outcomes; see [TE] **stteffects intro**. Thus we require that the probability of an uncensored failure also be sufficiently greater than 0. Below, we compute the estimated probabilities of failure and summarize them among those that fail.

```
. predict fprob2, censurv
. summarize fprob if fail==1
```

Variable	Obs	Mean	Std. Dev.	Min	Max
fprob2	1,208	.7246067	.2143543	.0364246	.9999086

The minimum probability of 0.04 does not appear too small.

□ Technical note

The previous discussion builds on the intuition that the weights used in a weighting estimator should not be too large.

This technical note goes a little further by explicitly computing the weights and using them to replicate the inverse-probability-weighted point estimate for the **Nonsmoker** potential-outcome mean.

We now compute the weights using the predicted probabilities computed in the examples above and then use **mean** to compute the weighted average that estimates the potential-outcome mean for **Nonsmokers**.

```
. generate double ipw0 = 1/(ps0*fprob)
. mean _t [pw=ipw0] if smoke==0 & fail==1
Mean estimation                               Number of obs     =      716

```

	Mean	Std. Err.	[95% Conf. Interval]
_t	4.235569	.5820212	3.092894 5.378244

The weights account for data lost to the **Smoker** potential outcome or to censoring by increasing the importance of observations that were observed to be **Nonsmoker** failure times even though they were not likely to be observed.

The point estimate matches that reported by **stteffects ipw**; the standard errors differ because **mean** takes the estimated weights as given. See *Inverse-probability-weighted estimators* under *Methods and formulas* in [TE] **stteffects ipwra**.



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Also see

- [TE] **tebalance** — Check balance after teffects or stteffects estimation
- [TE] **teffects overlap** — Overlap plots
- [TE] **stteffects ipw** — Survival-time inverse-probability weighting
- [TE] **stteffects ipwra** — Survival-time inverse-probability-weighted regression adjustment
- [TE] **stteffects ra** — Survival-time regression adjustment
- [TE] **stteffects wra** — Survival-time weighted regression adjustment
- [U] **20 Estimation and postestimation commands**

stteffects ra — Survival-time regression adjustment

Description	Quick start	Menu	Syntax
Options	Remarks and examples	Stored results	Methods and formulas
References	Also see		

Description

stteffects ra estimates the average treatment effect (ATE), the average treatment effect on the treated (ATET), and the potential-outcome means (POMs) from observational survival-time data by regression adjustment (RA). RA uses averages of treatment-specific predicted mean survival times to estimate mean survival times for each potential outcome. Contrasts of these predicted mean survival times estimate the treatment effects. **stteffects ra** offers several choices for the model used to predict mean survival time. Binary and multivalued treatments are accommodated.

See [TE] **stteffects intro** for an overview of estimating treatment effects from observational survival-time data.

Quick start

Specify `time` as observed failure time and `fail` as failure indicator

```
stset time, failure(fail)
```

ATE from a Weibull model for `time` on `x1` and `x2` with binary treatment `treat2`

```
stteffects ra (x1 x2) (treat2)
```

As above, but estimate the ATET

```
stteffects ra (x1 x2) (treat2), atet
```

As above, but estimate the potential-outcome means

```
stteffects ra (x1 x2) (treat2), pomeans
```

ATE of `treat2` using a gamma model for `time`

```
stteffects ra (x1 x2, gamma) (treat2)
```

ATE for each level of three-valued treatment `treat3`

```
stteffects ra (x1 x2) (treat3)
```

As above, and specify that `treat3 = 3` is the control level using the value label “MyControl” for 3

```
stteffects ra (x1 x2) (treat3), control("MyControl")
```

Menu

Statistics > Treatment effects > Survival outcomes > Regression adjustment

Syntax

```
stteffects ra (omvarlist [ , omoptions ]) (tvar) [if] [in] [ , stat options ]
```

omvarlist specifies the variables that predict the survival-time variable in the outcome model.
tvar must contain integer values representing the treatment levels.

<i>omoptions</i>	Description
Model	
<u>weibull</u>	Weibull; the default
<u>exponential</u>	exponential
<u>gamma</u>	two-parameter gamma
<u>lnormal</u>	lognormal
<u>ancillary</u> (<i>avarlist</i> [, <u>noconstant</u>])	specify variables used to model ancillary parameter
<u>noconstant</u>	suppress constant from outcome model
stat	
Stat	
<u>ate</u>	estimate average treatment effect in population; the default
<u>atet</u>	estimate average treatment effect on the treated
<u>pomeans</u>	estimate potential-outcome means
options	
SE/Robust	
<u>vce</u> (<i>vcetype</i>)	<i>vcetype</i> may be <u>robust</u> , <u>cluster</u> <i>clustvar</i> , <u>bootstrap</u> , or <u>jackknife</u>
Reporting	
<u>level</u> (#)	set confidence level; default is level(95)
<u>aequations</u>	display auxiliary-equation results
<u>noshow</u>	do not show st setting information
<u>display_options</u>	control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling
Maximization	
<u>maximize_options</u>	control the maximization process; seldom used
<u>iterinit</u> (#)	specify starting-value iterations; seldom used
Advanced	
<u>control</u> (# <i>label</i>)	specify the level of <i>tvar</i> that is the control
<u>tlevel</u> (# <i>label</i>)	specify the level of <i>tvar</i> that is the treatment
<u>coeflegend</u>	display legend instead of statistics

You must `stset` your data before using `stteffects`; see [ST] `stset`.

`omvarlist` and `avarlist` may contain factor variables; see [U] 11.4.3 Factor variables.

`bootstrap`, `by`, `jackknife`, and `statsby` are allowed; see [U] 11.1.10 Prefix commands.

Weights are not allowed with the `bootstrap` prefix; see [R] `bootstrap`.

`fweights`, `iweights`, and `pweights` may be specified using `stset`; see *Weights* under Remarks and examples in [ST] `stset`. However, weights may not be specified if you are using the `bootstrap` prefix.

`coeflegend` does not appear in the dialog box.

See [U] 20 Estimation and postestimation commands for more capabilities of estimation commands.

Options

Model

`ancillary(avarlist [, noconstant])` specifies the variables used to model the ancillary parameter.

By default, the ancillary parameter does not depend on covariates. Specifying `ancillary(avarlist, noconstant)` causes the constant to be suppressed in the model for the ancillary parameter.

`noconstant`; see [R] Estimation options.

Stat

`stat` is one of three statistics: `ate`, `atet`, or `pomeans`. `ate` is the default.

`ate` specifies that the average treatment effect be estimated.

`atet` specifies that the average treatment effect on the treated be estimated.

`pomeans` specifies that the potential-outcome means for each treatment level be estimated.

SE/Robust

`vce(vcetype)` specifies the type of standard error reported, which includes types that are robust to some kinds of misspecification (`robust`), that allow for intragroup correlation (`cluster clustvar`), and that use bootstrap or jackknife methods (`bootstrap`, `jackknife`); see [R] vce_option.

Reporting

`level(#)`; see [R] Estimation options.

`aequations` specifies that the results for the outcome-model or treatment-model parameters be displayed. By default, the results for these auxiliary parameters are not displayed.

`noshow` prevents `stteffects ra` from showing the key `st` variables. This option is rarely used because most people type `stset`, `show` or `stset, noshow` to permanently set whether they want to see these variables mentioned at the top of the output of every `st` command; see [ST] `stset`.

`display_options`: `noci`, `nopvalues`, `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `nofvlabel`, `fvwrap(#)`, `fvrapon(style)`, `cformat(%fmt)`, `pformat(%fmt)`, `sformat(%fmt)`, and `nolstretch`; see [R] Estimation options.

Maximization

`maximize_options`: `iterate(#)`, `[no]log`, and `from(init_specs)`; see [R] Maximize. These options are seldom used.

`init_specs` is one of

`matname [, skip copy]`

`# [, # ...] , copy`

`iterinit(#)` specifies the maximum number of iterations used to calculate the starting values. This option is seldom used.

Advanced

`control(#|label)` specifies the level of *tvar* that is the control. The default is the first treatment level. You may specify the numeric level # (a nonnegative integer) or the label associated with the numeric level. `control()` may not be specified with the statistic `pomeans`. `control()` and `tlevel()` may not specify the same treatment level.

`tlevel(#|label)` specifies the level of *tvar* that is the treatment for the statistic `atet`. The default is the second treatment level. You may specify the numeric level # (a nonnegative integer) or the label associated with the numeric level. `tlevel()` may only be specified with statistic `atet`. `tlevel()` and `control()` may not specify the same treatment level.

The following option is available with `stteffects` but is not shown in the dialog box:
`coeflegend`; see [R] **Estimation options**.

Remarks and examples

If you are not familiar with the framework for treatment-effects estimation from observational survival-time data, please see [TE] **stteffects intro**.

RA estimators use contrasts of the averages of treatment-specific predicted mean outcomes to estimate treatment effects. RA estimators use a two-step approach to estimating treatment effects:

1. For each treatment level, fit a model of the survival-time outcome on the same set of covariates.
2. Compute the averages of the predicted outcomes for each subject within each treatment level.

These averages estimate the potential-outcome means (POMs). Contrasts of these averages estimate the ATEs. By restricting the computations of the averages to the subset of treated subjects, we obtain estimates of the ATETs.

Here we note only a few entry points to the vast literature on RA estimators. [Imbens \(2004\)](#), [Imbens and Wooldridge \(2009\)](#), [Cameron and Trivedi \(2005, chap. 25\)](#), [Wooldridge \(2010, chap. 21\)](#), and [Vittinghoff et al. \(2012, chap. 9\)](#) provide excellent general introductions to estimating ATEs and to RA estimators in particular.

Like `streg` and other survival-time commands, `stteffects ra` uses the outcome variable and the failure indicator computed by, and optionally weights specified with, `stset`. `stteffects ra` is not appropriate for data with time-varying covariates, also known as multiple-record survival-time data, or for delayed-entry data.

► Example 1: Estimating the ATE

Suppose we wish to study the effect of smoking on the time to a second heart attack among women aged 45–55 years. In our fictional `sheart` dataset, `atime` is the observed time in years to a second heart attack or censoring, and `fail` is the 0/1 indicator that a second heart attack was observed. (When `fail` is 1, `atime` records the time to the second heart attack; when `fail` is 0, `atime` records a censored observation of the time to a second heart attack.) We previously `stset` these data; see [A quick tour of the estimators](#) in [TE] **stteffects intro**.

The treatment, smoking, is stored in the 0/1 indicator `smoke`. These data also contain age at the time of the first heart attack (`age`), and indices of the level of exercise (`exercise`), diet quality (`diet`), and education (`education`) prior to the first heart attack.

We can use `stteffects ra` to estimate the ATE by RA. We model the mean survival time using the default Weibull model, controlling for `age`, `exercise`, `diet`, and `education`, and we specify that `smoke` is the treatment variable.

```
. use https://www.stata-press.com/data/r16/sheart
(Time to second heart attack (fictional))
. stteffects ra (age exercise diet education) (smoke)
    failure _d: fail
    analysis time _t: atime
Iteration 0:  EE criterion =  1.006e-14
Iteration 1:  EE criterion =  2.305e-25
Survival treatment-effects estimation          Number of obs      =      2,000
Estimator       : regression adjustment
Outcome model   : Weibull
Treatment model: none
Censoring model: none
```

	<i>_t</i>	Robust				
		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ATE						
smoke (Smoker vs Nonsmoker)	-1.956657	.3331787	-5.87	0.000	-2.609676	-1.303639
P0mean						
smoke Nonsmoker	4.243974	.2620538	16.20	0.000	3.730358	4.75759

When every woman smoked in the population of women aged 45–55 years who have had a heart attack, the average time to a second heart attack is estimated to be 1.96 years less than when no women in the population of interest smoked. The estimated average time to a second heart attack when no women in the population of interest smoked is 4.24 years. In other words, if every woman in the population of interest smoked, then the average time to a second heart attack would fall by an estimated 46% relative to the case when no women smoked.



▷ Example 2: Changing the outcome model

Instead of a Weibull model for the outcome model, we could have used an exponential, a gamma, or a lognormal model. By way of comparison, we use a gamma model and the same covariates to estimate the ATE.

Survival treatment-effects estimation							Number of obs	=	2,000
Estimator : regression adjustment									
Outcome model : gamma									
Treatment model: none									
Censoring model: none									
	_t	Robust							
		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]			
ATE									
	smoke (Smoker vs Nonsmoker)	-1.801787	.2924388	-6.16	0.000	-2.374956	-1.228617		
P0mean									
	smoke Nonsmoker	3.994327	.2258257	17.69	0.000	3.551717	4.436937		

The estimated ATE of -1.80 and control-level POM of 3.99 are similar to those of -1.96 and 4.24 obtained from the Weibull model in [example 1](#). The ratio of the estimated ATE to the control-level POM indicates a 45% reduction instead of the 46% reduction obtained from the Weibull model.



▷ Example 3: Estimating the ratio of the ATE to the control-level POM

The ratio of the ATE to the control-level POM measures the importance of the effect. In [example 1](#), we computed the point estimate of this ratio from the output, but we were left without a confidence interval. In this example, we use `nlcom` to compute a point estimate and a confidence interval.

Below, we refit the model from [example 1](#), specifying the `coeflegend` option to learn the parameter names. We use the parameter names in `nlcom` to estimate the ratio of the ATE to the control-level POM.

```
. stteffects ra (age exercise diet education) (smoke), coeflegend
    failure _d: fail
    analysis time _t: atime
Iteration 0:   EE criterion =  1.006e-14
Iteration 1:   EE criterion =  2.305e-25
Survival treatment-effects estimation          Number of obs      =      2,000
Estimator       : regression adjustment
Outcome model   : Weibull
Treatment model: none
Censoring model: none

```

_t	Coef. Legend
ATE smoke (Smoker vs Non-smoker)	-1.956657 _b[ATE:r1vs0.smoke]
P0mean smoke Non-smoker	4.243974 _b[P0mean:0.smoke]
<pre>. nlcom _b[ATE:r1vs0.smoke] / _b[P0mean:0.smoke] _nl_1: _b[ATE:r1vs0.smoke] / _b[P0mean:0.smoke]</pre>	
_t	Coef. Std. Err. z P> z [95% Conf. Interval]
_nl_1	-.4610437 .0598709 -7.70 0.000 -.5783885 -.3436988

The output shows that when every woman smoked, the average time to a second heart attack falls by an estimated 46% relative to the case when no women smoked, as we computed earlier. We also obtain a 95% confidence interval of 34% to 58% for this estimate.



▷ Example 4: Estimating the ATET

Intuitively, the ATET measures the effect of the treatment on an at-risk subpopulation. Sometimes the subpopulation that gets the treatment defines such an at-risk subpopulation. The ATET has the added benefit that it can be estimated under weaker conditions than the ATE; see [Assumptions and trade-offs in \[TE\] stteffects intro](#).

Survival treatment-effects estimation							Number of obs	=	2,000
Estimator : regression adjustment									
Outcome model : Weibull									
Treatment model: none									
Censoring model: none									
	_t	Robust Coef.	Std. Err.	z	P> z	[95% Conf. Interval]			
ATET									
	smoke (Smoker vs Nonsmoker)	-1.527476	.2489203	-6.14	0.000	-2.015351	-1.039602		
POmean									
	smoke Nonsmoker	3.436937	.2217808	15.50	0.000	3.002255	3.87162		

When every woman in the subpopulation smoked, the average time to a second heart attack is estimated to be 1.53 years less than when no women in the subpopulation smoked. The estimated average time to a second heart attack when no women in the subpopulation smoked is 3.44 years.



▷ Example 5: Fixed or random censoring time

The time to censoring in survival-time data can be random or deterministic, although it must be independent of treatment assignment and the potential outcomes; see Kalbfleisch and Prentice (2002, chap. 3) for the standard case and see *The correct adjustment for censoring assumption* under *Assumptions and trade-offs* in [TE] **stteffects intro** for the treatment-effects case.

The RA estimator and the likelihood-adjusted-censoring version of the inverse-probability-weighted RA estimator can accommodate a fixed time to censoring; see *The correct adjustment for censoring assumption* in [TE] **stteffects intro**. (The estimators that handle censoring by weighting cannot accommodate a fixed time to censoring because the weights are not well defined with a fixed time to censoring.)

We have fictional data on the time to rearrest among men aged 25–35 who were previously in prison for a felony conviction (**rtime**). The time to censoring is fixed in these data because individuals were followed for a maximum of five years.

Some of the young men chose to enter a vocational training program before release from prison; **train** is 1 for participants and 0 for nonparticipants. The dataset also contains **fail** (which is 1 if the observed time is a failure time and 0 if it is time to censoring), age at the time of the first arrest (**age**), an index of the parents' socioeconomic level (**parental**), and the number of years behind in school at the time of the first arrest (**e deficit**).

We estimate the ATET because we wish to allow the gains from the training program to be related to an unobservable characteristic that affects who self-selects into the program; see *Average treatment effect on the treated* in [TE] **stteffects intro**.

We model the outcome as a function of age, parental, and eedeficit.

		Robust				
		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ATET						
train (Student vs Nonstudent)		2.440919	.4689057	5.21	0.000	1.52188 3.359957
P0mean						
train Nonstudent		2.062029	.1231492	16.74	0.000	1.820661 2.303397

When everyone who selected the training got the training, the average time to rearrest is 2.44 years later than the average rearrest time if none of those who selected the training got the training. The average rearrest time if none of those who selected the training got the training is 2.06 years. In other words, the average time to rearrest increases from about 2.06 years to about 4.50 years for the subpopulation of young men who self-selected into the prerelease vocational training program.



Stored results

stteffects ra stores the following in **e()**:

Scalars	
e(N)	number of observations
e(nj)	number of observations for treatment level <i>j</i>
e(N_clust)	number of clusters
e(k_eq)	number of equations in e(b)
e(k_levels)	number of levels in treatment variable
e(treated)	level of treatment variable defined as treated
e(control)	level of treatment variable defined as control
e(converged)	1 if converged, 0 otherwise
Macros	
e(cmd)	stteffects
e(cmdline)	command as typed
e(dead)	_d
e(depvar)	_t
e(tvar)	name of treatment variable
e(subcmd)	ra
e(omodel)	outcome model: weibull , exponential , gamma , or lognormal
e(stat)	statistic estimated: ate , atet , or pomeans

<code>e(wtype)</code>	weight type
<code>e(wexp)</code>	weight expression
<code>e(title)</code>	title in estimation output
<code>e(clustvar)</code>	name of cluster variable
<code>e(tlevels)</code>	levels of treatment variable
<code>e(vce)</code>	<i>vctype</i> specified in <code>vce()</code>
<code>e(vcetype)</code>	title used to label Std. Err.
<code>e(properties)</code>	<code>b V</code>
<code>e(estat_cmd)</code>	program used to implement <code>estat</code>
<code>e(predict)</code>	program used to implement <code>predict</code>
<code>e(marginsnotok)</code>	predictions disallowed by <code>margins</code>
<code>e(asbalanced)</code>	factor variables <code>fvset</code> as <code>asbalanced</code>
<code>e(asobserved)</code>	factor variables <code>fvset</code> as <code>asobserved</code>
Matrices	
<code>e(b)</code>	coefficient vector
<code>e(V)</code>	variance–covariance matrix of the estimators
Functions	
<code>e(sample)</code>	marks estimation sample

Methods and formulas

The methods and formulas for the RA estimators implemented in `stteffects ra` are given in *Methods and formulas* of [TE] `stteffects ipwra`.

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Also see

- [TE] **stteffects postestimation** — Postestimation tools for stteffects
- [TE] **stteffects intro** — Introduction to treatment effects for observational survival-time data
- [ST] **streg** — Parametric survival models
- [ST] **stset** — Declare data to be survival-time data
- [U] **20 Estimation and postestimation commands**

stteffects wra — Survival-time weighted regression adjustment

Description	Quick start	Menu	Syntax
Options	Remarks and examples	Stored results	Methods and formulas
References	Also see		

Description

stteffects wra estimates the average treatment effect (ATE), the average treatment effect on the treated (ATET), and the potential-outcome means (POMs) from observational survival-time data with random time to censoring. Estimation is by weighted regression adjustment (WRA). WRA estimators use inverse-probability-of-censoring adjusted regression coefficients to compute averages of treatment-level predicted outcomes. Contrasts of these averages estimate the treatment effects. WRA uses estimated weights from a time-to-censoring model to account for censored survival times instead of including a term in the likelihood function. **stteffects wra** offers several choices for the functional forms of the outcome model and the time-to-censoring model. Binary and multivalued treatments are accommodated.

See [TE] **stteffects intro** for an overview of estimating treatment effects from observational survival-time data.

Quick start

Specify `time` as observed failure time and `fail` as failure indicator

```
stset time, failure(fail)
```

ATE from a Weibull model for `time` on `x1` and `x2` with binary treatment `treat2` and a Weibull model on `x1` and `x2` for censoring

```
stteffects wra (x1 x2) (treat2) (x1 x2)
```

As above, but estimate the ATET

```
stteffects wra (x1 x2) (treat2) (x1 x2), atet
```

ATE of `treat2` using a gamma model for `time` and a gamma censoring model

```
stteffects wra (x1 x2, gamma) (treat2) (x1 x2, gamma)
```

ATE for each level of three-valued treatment `treat3`

```
stteffects wra (x1 x2) (treat3) (x1 x2)
```

As above, and specify that `treat3 = 3` is the control level using the value label "MyControl" for 3

```
stteffects wra (x1 x2) (treat3) (x1 x2), control("MyControl")
```

Menu

Statistics > Treatment effects > Survival outcomes > Weighted regression adjustment

Syntax

```
stteffects wra (omvarlist [ , omoptions ]) (tvar) (cmvarlist [ , cmoptions ])  
[ if ] [ in ] [ , stat options ]
```

omvarlist specifies the variables that predict the survival-time variable in the outcome model.

tvar must contain integer values representing the treatment levels.

cmvarlist specifies the variables that predict censoring in the censoring model.

<i>omoptions</i>	Description
Model	
<u>weibull</u>	Weibull; the default
<u>exponential</u>	exponential
<u>gamma</u>	two-parameter gamma
<u>lnormal</u>	lognormal
<u>ancillary</u> (avarlist [, <u>noconstant</u>])	specify variables used to model ancillary parameter
<u>noconstant</u>	suppress constant from outcome model
<i>cmoptions</i>	Description
Model	
<u>weibull</u>	Weibull; the default
<u>exponential</u>	exponential
<u>gamma</u>	two-parameter gamma
<u>lnormal</u>	lognormal
<u>ancillary</u> (avarlist [, <u>noconstant</u>])	specify variables used to model ancillary parameter
<u>noconstant</u>	suppress constant from censoring model
<i>stat</i>	Description
Stat	
<u>ate</u>	estimate average treatment effect in population; the default
<u>atet</u>	estimate average treatment effect on the treated
<u>pomeans</u>	estimate potential-outcome means

options	Description
SE/Robust	
<u>vce</u> (<i>vcetype</i>)	<i>vcetype</i> may be <u>robust</u> , <u>cluster</u> <i>clustvar</i> , <u>bootstrap</u> , or <u>jackknife</u>
Reporting	
<u>level</u> (#)	set confidence level; default is <u>level</u> (95)
<u>aequations</u>	display auxiliary-equation results
<u>noshow</u>	do not show st setting information
<u>display_options</u>	control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling
Maximization	
<u>maximize_options</u>	control the maximization process; seldom used
<u>iterinit</u> (#)	specify starting-value iterations; seldom used
Advanced	
<u>pstolerance</u> (#)	set the tolerance for the overlap assumption
<u>osample</u> (<i>newvar</i>)	identify observations that violate the overlap assumption
<u>control</u> (# <i>label</i>)	specify the level of <i>tvar</i> that is the control
<u>tlevel</u> (# <i>label</i>)	specify the level of <i>tvar</i> that is the treatment
<u>coeflegend</u>	display legend instead of statistics

You must **stset** your data before using **stteffects**; see [ST] **stset**.

omvarlist, *cmvarlist*, and *avarlist* may contain factor variables; see [U] **11.4.3 Factor variables**.

bootstrap, **by**, **jackknife**, and **statsby** are allowed; see [U] **11.1.10 Prefix commands**.

Weights are not allowed with the **bootstrap** prefix; see [R] **bootstrap**.

fweights, **iweights**, and **pweights** may be specified using **stset**; see **Weights** under Remarks and examples in [ST] **stset**. However, weights may not be specified if you are using the **bootstrap** prefix.

coeflegend does not appear in the dialog box.

See [U] **20 Estimation and postestimation commands** for more capabilities of estimation commands.

Options

Model

ancillary(*avarlist* [, **noconstant**]) specifies the variables used to model the ancillary parameter. By default, the ancillary parameter does not depend on covariates. Specifying **ancillary**(*avarlist*, **noconstant**) causes the constant to be suppressed in the model for the ancillary parameter. **ancillary()** may be specified for the model for survival-time outcome, for the model for the censoring variable, or for both. If **ancillary()** is specified for both, the varlist used for each model may be different.

noconstant; see [R] **Estimation options**.

Stat

stat is one of three statistics: **ate**, **atet**, or **pomeans**. **ate** is the default.

ate specifies that the average treatment effect be estimated.

atet specifies that the average treatment effect on the treated be estimated.

pomeans specifies that the potential-outcome means for each treatment level be estimated.

SE/Robust

vce(vcetype) specifies the type of standard error reported, which includes types that are robust to some kinds of misspecification (**robust**), that allow for intragroup correlation (**cluster clustvar**), and that use bootstrap or jackknife methods (**bootstrap**, **jackknife**); see [R] **vce_option**.

Reporting

level(#); see [R] **Estimation options**.

aequations specifies that the results for the outcome-model or treatment-model parameters be displayed. By default, the results for these auxiliary parameters are not displayed.

noshow prevents **stteffects wra** from showing the key st variables. This option is rarely used because most people type **stset**, **show** or **stset**, **noshow** to permanently set whether they want to see these variables mentioned at the top of the output of every st command; see [ST] **stset**.

display_options: **nocl**, **novalues**, **noomitted**, **vsquish**, **noemptycells**, **baselevels**, **allbaselevels**, **nofvlabel**, **fwrap(#)**, **fwrapon(style)**, **cformat(%fmt)**, **pformat(%fmt)**, **sformat(%fmt)**, and **nolstretch**; see [R] **Estimation options**.

Maximization

maximize_options: **iterate(#)**, [**no**] **log**, and **from(init_specs)**; see [R] **Maximize**. These options are seldom used.

init_specs is one of

matname [, **skip copy**]

[, # ...], **copy**

iterinit(#) specifies the maximum number of iterations used to calculate the starting values. This option is seldom used.

Advanced

pstolerance(#) specifies the tolerance used to check the overlap assumption. The default value is **pstolerance(1e-5)**. **stteffects** will exit with an error if an observation has an estimated propensity score smaller than that specified by **pstolerance()**.

osample(newvar) specifies that indicator variable *newvar* be created to identify observations that violate the overlap assumption.

control(#|label) specifies the level of *tvar* that is the control. The default is the first treatment level. You may specify the numeric level # (a nonnegative integer) or the label associated with the numeric level. **control()** may not be specified with the statistic **pomeans**. **control()** and **tlevel()** may not specify the same treatment level.

`tlevel(#|label)` specifies the level of `tvar` that is the treatment for the statistic `atet`. The default is the second treatment level. You may specify the numeric level # (a nonnegative integer) or the label associated with the numeric level. `tlevel()` may only be specified with statistic `atet`. `tlevel()` and `control()` may not specify the same treatment level.

The following option is available with `stteffects` but is not shown in the dialog box:
`coeflegend`; see [R] **Estimation options**.

Remarks and examples

If you are not familiar with the framework for treatment-effects estimation from observational survival-time data, please see [TE] **stteffects intro**.

Weighted regression-adjustment (WRA) estimators use estimated weights to account for censoring when estimating outcome-regression parameters. The estimated outcome-regression parameters are used to compute averages of treatment-level predicted outcomes. Contrasts of these averages estimate the treatment effects.

WRA estimators use a three-step approach to estimating treatment effects:

1. They estimate the parameters of a time-to-censoring model and compute inverse-probability-of-censoring weights.
2. Using the estimated inverse-probability-of-censoring weights, they use weighted maximum likelihood estimators for the outcome for each treatment level and obtain the treatment-specific predicted mean outcomes for each subject. The inverse-probability-of-censoring weights account for right-censored survival times.
3. They compute the means of the treatment-specific predicted mean outcomes. Contrasts of these averages provide the estimates of the ATEs. By restricting the computations of the means to the subset of treated subjects, we can obtain the ATETs.

WRA estimators differ from RA estimators in that WRA estimators use weights to account for observations lost to censoring while RA estimators use an additional term in the likelihood function. A model for the time to censoring is used to estimate the weights.

WRA estimators require more assumptions than RA estimators. Specifically, they require that the censoring time be random and that the time-to-censoring model be well specified. The implemented WRA estimators also require that the time-to-censoring process not vary by treatment level. The RA estimator and the likelihood-adjusted-censoring version of the inverse-probability-weighted RA estimator do not require these extra assumptions, because they use a likelihood term instead of weights to adjust for the data lost to censoring; see [TE] **stteffects ra** and [TE] **stteffects ipwra**.

Here we note only a few entry points to the vast literature on weighted estimators. [Imbens \(2004\)](#), [Imbens and Wooldridge \(2009\)](#), [Robins and Rotnitzky \(2006\)](#), [Wooldridge \(2002, 2007\)](#), [Cameron and Trivedi \(2005, chap. 25\)](#), [Wooldridge \(2010, chap. 21\)](#), and [Vittinghoff et al. \(2012, chap. 9\)](#) provide excellent general introductions to estimating ATEs and to WRA estimators in particular.

Like `streg` and other survival-time commands, `stteffects wra` uses the outcome variable and the failure indicator computed by, and optionally weights specified with, `stset`. `stteffects wra` is not appropriate for data with time-varying covariates, also known as multiple-record survival-time data, or for delayed-entry data.

► Example 1: Estimating the ATE

Suppose we wish to study the effect of smoking on the time to a second heart attack among women aged 45–55 years. In our fictional `sheart` dataset, `atime` is the observed time in years to a second heart attack or censoring, and `fail` is the 0/1 indicator that a second heart attack was observed. (When `fail` is 1, `atime` records the time to the second heart attack; when `fail` is 0, `atime` records a censored observation of the time to a second heart attack.) We previously `stset` these data; see [A quick tour of the estimators](#) in [TE] `stteffects intro`.

The treatment, smoking, is stored in the 0/1 indicator `smoke`. These data also contain age at the time of the first heart attack (`age`), and indices of the level of exercise (`exercise`), diet quality (`diet`), and education (`education`) prior to the first heart attack.

We can use `stteffects wra` to estimate the ATE by WRA. We model the mean survival time using the default Weibull outcome model with `age`, `exercise`, `diet`, and `education` as covariates, and we specify that `smoke` is the treatment variable. We also specify the default Weibull time-to-censoring model and include `age`, square of `age`, `exercise`, and `education`.

```
. use https://www.stata-press.com/data/r16/sheart
(Time to second heart attack (fictional))

. stteffects wra (age exercise diet education)
>           (smoke)
>           (age c.age#c.age exercise diet education)

failure _d: fail
analysis time _t: atime

Iteration 0:  EE criterion =  4.096e-18
Iteration 1:  EE criterion =  1.406e-29

Survival treatment-effects estimation          Number of obs      =      2,000
Estimator       : weighted regression adjustment
Outcome model   : Weibull
Treatment model: none
Censoring model: Weibull
```

	<code>_t</code>	Robust				
		Coef.	Std. Err.	<code>z</code>	<code>P> z </code>	[95% Conf. Interval]
ATE						
smoke (Smoker vs Nonsmoker)	-2.374174	.6017498	-3.95	0.000	-3.553582	-1.194766
P0mean						
smoke Nonsmoker	4.302131	.5528943	7.78	0.000	3.218478	5.385784

When every woman smoked in the population of women aged 45–55 years who have had a heart attack, the average time to a second heart attack is estimated to be 2.37 years less than when no women in the subpopulation of interest smoked. The estimated average time to a second heart attack when no women in the subpopulation of interest smoked is 4.30 years.



Stored results

`stteffects wra` stores the following in `e()`:

Scalars

<code>e(N)</code>	number of observations
<code>e(nj)</code>	number of observations for treatment level j
<code>e(N_clust)</code>	number of clusters
<code>e(k_eq)</code>	number of equations in <code>e(b)</code>
<code>e(k_levels)</code>	number of levels in treatment variable
<code>e(treated)</code>	level of treatment variable defined as treated
<code>e(control)</code>	level of treatment variable defined as control
<code>e(converged)</code>	1 if converged, 0 otherwise

Macros

<code>e(cmd)</code>	<code>stteffects</code>
<code>e(cmdline)</code>	command as typed
<code>e(dead)</code>	<code>_d</code>
<code>e(depvar)</code>	<code>_t</code>
<code>e(tvar)</code>	name of treatment variable
<code>e(subcmd)</code>	<code>wra</code>
<code>e(omodel)</code>	outcome model: <code>weibull</code> , <code>exponential</code> , <code>gamma</code> , or <code>lognormal</code>
<code>e(cmodel)</code>	censoring model: <code>weibull</code> , <code>exponential</code> , <code>gamma</code> , or <code>lognormal</code>
<code>e(stat)</code>	statistic estimated: <code>ate</code> , <code>atet</code> , or <code>pomeans</code>
<code>e(wtype)</code>	weight type
<code>e(wexp)</code>	weight expression
<code>e(title)</code>	title in estimation output
<code>e(clustvar)</code>	name of cluster variable
<code>e(tlevels)</code>	levels of treatment variable
<code>e(vce)</code>	<code>vcetype</code> specified in <code>vce()</code>
<code>e(vcetype)</code>	title used to label Std. Err.
<code>e(properties)</code>	<code>b V</code>
<code>e(estat_cmd)</code>	program used to implement <code>estat</code>
<code>e(predict)</code>	program used to implement <code>predict</code>
<code>e(marginsnotok)</code>	predictions disallowed by <code>margins</code>
<code>e(asbalanced)</code>	factor variables <code>fvset</code> as <code>asbalanced</code>
<code>e(asobserved)</code>	factor variables <code>fvset</code> as <code>asobserved</code>

Matrices

<code>e(b)</code>	coefficient vector
<code>e(V)</code>	variance–covariance matrix of the estimators

Functions

<code>e(sample)</code>	marks estimation sample
------------------------	-------------------------

Methods and formulas

The methods and formulas for the WRA estimators implemented in `stteffects wra` are given in *Methods and formulas* of [TE] `stteffects ipwra`.

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Also see

- [TE] **stteffects postestimation** — Postestimation tools for stteffects
- [TE] **stteffects intro** — Introduction to treatment effects for observational survival-time data
- [ST] **streg** — Parametric survival models
- [ST] **stset** — Declare data to be survival-time data
- [U] **20 Estimation and postestimation commands**

tebalance — Check balance after teffects or stteffects estimation
--

Description
References

Syntax
Also see

Remarks and examples

Methods and formulas

Description

The **tebalance** postestimation commands produce diagnostic statistics, test statistics, and diagnostic plots to assess whether a **teffects** or an **stteffects** command balanced the covariates over treatment levels.

Syntax

tebalance *subcommand* ... [, *options*]

<i>subcommand</i>	Description
summarize	compare means and variances in raw and balanced data
overid	overidentification test
density	kernel density plots for raw and balanced data
box	box plots for each treatment level for balanced data

Remarks and examples

This entry provides an overview of the commands in **tebalance**. We recommend that you read this entry before proceeding to **[TE] tebalance summarize**, **[TE] tebalance overid**, **[TE] tebalance density**, or **[TE] tebalance box** for command-specific syntax and details.

A covariate is said to be balanced when its distribution does not vary over treatment levels.

Covariates are balanced in experimental data because treatment assignment is independent of the covariates because of the study design. In contrast, covariates must be balanced by weighting or matching in observational data because treatment assignment is related to the covariates that also affect the outcome of interest.

The estimators implemented in **teffects** and **stteffects** use a model or matching method to make the outcome conditionally independent of the treatment by conditioning on covariates. If this model or matching method is well specified, it should balance the covariates. Balance diagnostic techniques and tests check the specification of the conditioning method used by a **teffects** or an **stteffects** estimator; see **[TE] teffects intro advanced** for an introduction to **teffects**, and **[TE] stteffects intro** for an introduction to **stteffects**.

tebalance implements four methods to check for balance after **teffects** and **stteffects**. Which **tebalance** methods are available depends on the **teffects** estimation method, as summarized in the table below.

tebalance		Works after teffects					Works after stteffects	
method	Description	ipw	aipw	ipwra	nnmatch	psmatch	ipw	ipwra
summarize	standardized differences and variance ratios	x	x	x	x	x	x	x
overid	chi-squared test for balance	x	x	x			x	x
density	diagnostic kernel-density plots	x	x	x	x	x	x	x
box	diagnostic box plots				x	x		

`tebalance overid` implements a formal test, while the other three methods are exploratory diagnostic techniques. There is no balance check after `teffects ra`, `stteffects ra`, or `stteffects wra`, because they use neither a treatment model nor a matching method.

Austin (2009, 2011) and Guo and Fraser (2015, sec. 5.52) provide introductions to covariate balance. Imai and Ratkovic (2014) derived a test for balance implemented in `tebalance overid`.

The remainder of this entry provides a quick introduction to using `tebalance` to check for balance after `teffects`. See [TE] `stteffects intro` for examples after `stteffects`.

▷ Example 1: Balance after estimators that use weighting

Inverse-probability-weighted (IPW) estimators use a model for the treatment to make the outcome conditionally independent of the treatment. If this model is well specified, it will also balance the covariates.

Using an extract from Cattaneo (2010), we use `teffects ipw` to estimate the effect of a mother's smoking behavior (`mbsmoke`) on the birthweight of her child (`bweight`), controlling for marital status (`mmarried`), the mother's age (`mage`), whether the mother had a prenatal doctor's visit in the baby's first trimester (`prenatal1`), and whether this baby is the mother's first child (`fbaby`).

. use https://www.stata-press.com/data/r16/cattaneo2 (Excerpt from Cattaneo (2010) Journal of Econometrics 155: 138–154)							
. teffects ipw (bweight) (mbsmoke mmarried mage prenatal1 fbaby)							
Iteration 0: EE criterion = 1.873e-22							
Iteration 1: EE criterion = 3.315e-26							
Treatment-effects estimation Number of obs = 4,642							
Estimator : inverse-probability weights							
Outcome model : weighted mean							
Treatment model: logit							
bweight	Robust						
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]		
ATE							
mbsmoke (smoker vs nonsmoker)	-236.1038	23.86187	-9.89	0.000	-282.8722	-189.3354	
P0mean							
mbsmoke nonsmoker	3402.552	9.539555	356.68	0.000	3383.855	3421.249	

Rubin (2008) recommends finding a model that balances the covariates before looking at results for the estimated treatment effect. Thus we do not interpret the above results, and we note that we could pay closer heed to Rubin's recommendation by preceding the `teffects` command with `quietly` to suppress the output.

Imai and Ratkovic (2014) derived a test for balance by viewing the restrictions imposed by balance as overidentifying conditions. This test is implemented in `tebalance overid`, and we use it to test whether the above treatment model balanced the covariates.

```
. tebalance overid

Iteration 0: criterion = .02146858
Iteration 1: criterion = .02159149 (backed up)
Iteration 2: criterion = .02177783
Iteration 3: criterion = .02260102
Iteration 4: criterion = .02267956
Iteration 5: criterion = .02292367
Iteration 6: criterion = .02431697
Iteration 7: criterion = .02457043
Iteration 8: criterion = .02488579
Iteration 9: criterion = .02529453
Iteration 10: criterion = .02545885
Iteration 11: criterion = .02550248
Iteration 12: criterion = .02552866
Iteration 13: criterion = .02554462
Iteration 14: criterion = .02554512
Iteration 15: criterion = .02554514

Overidentification test for covariate balance
H0: Covariates are balanced:
chi2(5)      =  38.1464
Prob > chi2  =  0.0000
```

We reject the null hypothesis that the treatment model balanced the covariates.

Let's use `tebalance summarize` to see where the problem lies. To get an idea of the extent to which the covariates are unbalanced, we begin by summarizing the covariates by group in the raw data by specifying the `baseline` option.

```
. tebalance summarize, baseline

Covariate balance summary

```

		Raw	Weighted
Number of obs	=	4,642	4,642.0
Treated obs	=	864	2,315.3
Control obs	=	3,778	2,326.7

	Means		Variances	
	Control	Treated	Control	Treated
mmarried	.7514558	.4733796	.1868194	.2495802
mage	26.81048	25.16667	31.87141	28.10429
prenatal1	.8268925	.6898148	.1431792	.2142183
fbaby	.4531498	.3715278	.2478707	.2337654

The output indicates that the covariates may not be balanced in the raw data. For example, the distribution of the mother's age may differ over the treatment groups. We can investigate the differences further with standardized differences and variance ratios. A perfectly balanced covariate has a standardized difference of zero and variance ratio of one. There are no standard errors on these

statistics, so inference is informal. Austin (2009) provides a recent introduction to these diagnostics, although they have been used at least since Rosenbaum and Rubin (1985).

By omitting the `baseline` option, we obtain these diagnostic statistics for the raw data and the weighted data.

```
. tebalance summarize
Covariate balance summary
```

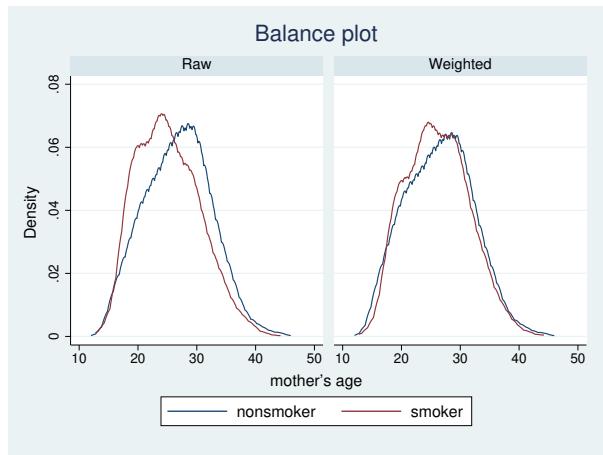
	Raw		Weighted	
	Standardized differences	Variance ratio	Raw	Weighted
	Raw	Weighted	Raw	Weighted
Number of obs =	4,642	4,642.0		
Treated obs =	864	2,315.3		
Control obs =	3,778	2,326.7		

	Standardized differences	Variance ratio	Raw	Weighted
	Raw	Weighted	Raw	Weighted
mmarried	-.5953009	-.0105562	1.335944	1.009079
mage	-.300179	-.0672115	.8818025	.8536401
prenatal1	-.3242695	-.0156339	1.496155	1.023424
fbaby	-.1663271	.0257705	.9430944	1.005698

Reviewing the output, we see that for `mmarried`, `prenatal1`, and `fbaby`, our model improved the level of balance. The weighted standardized differences are all close to zero and the variance ratios are all close to one. However, output indicates that `mage` may not be balanced by our model. The weighted standardized difference is close to zero, but the weighted variance ratio still appears to be considerably less than one.

Now, let's use `tebalance density` to look at how the densities of `mage` for treated and control groups differ.

```
. tebalance density mage
```



The plots also indicate a lack of balance in `mage` between the treatment groups.

To try to achieve better balance, we specify a richer model with interactions between `mage` and the other covariates and look at the resulting standardized differences.

```
. quietly teffects ipw (bweight) (mbsmoke mmarried mage prenatal1 fbaby
> c.mage#(c.mage i.mmarried prenatal1))
. tebalance summarize
```

Covariate balance summary

		Raw	Weighted
Number of obs =		4,642	4,642.0
Treated obs =		864	2,329.1
Control obs =		3,778	2,312.9

	Standardized differences	Variance ratio	
		Raw	Weighted
mmarried	-.5953009	.0053497	1.335944
mage	-.300179	.0410889	.8818025
prenatal1	-.3242695	.0009807	1.496155
fbaby	-.1663271	-.0130638	.9430944
			.9965406
mage#			
mage	-.3028275	.0477465	.8274389
			1.109134
mmarried#			
mage			
married	-.6329701	.0197209	1.157026
			1.034108
prenatal1#			
mage			
Yes	-.4053969	.0182109	1.226363
			1.032561

The standardized difference and variance ratio results for mage look closer to the expected values of zero and one, so we proceed to the formal test.

```
. tebalance overid
Iteration 0: criterion = .0602349
Iteration 1: criterion = .06172749 (backed up)
Iteration 2: criterion = .06428588 (backed up)
Iteration 3: criterion = .06489623 (backed up)
Iteration 4: criterion = .06527284 (backed up)
Iteration 5: criterion = .06643426
Iteration 6: criterion = .07120383
Iteration 7: criterion = .07647097
Iteration 8: criterion = .07674915
Iteration 9: criterion = .07684127
Iteration 10: criterion = .07703321
Iteration 11: criterion = .0776508
Iteration 12: criterion = .07771863
Iteration 13: criterion = .07773156
Iteration 14: criterion = .07773561
Iteration 15: criterion = .07774891
Iteration 16: criterion = .07775314
Iteration 17: criterion = .07775324
Iteration 18: criterion = .07775325
Iteration 19: criterion = .07775325
Iteration 20: criterion = .07775325
Iteration 21: criterion = .07775325
Iteration 22: criterion = .07775325

Overidentification test for covariate balance
H0: Covariates are balanced:
chi2(8)      = 11.8612
Prob > chi2  = 0.1575
```

We do not reject the null hypothesis that the specified treatment model balances the covariates. □



▷ Example 2: Balance after estimators that use matching

Instead of weighting, we might want to use a matching estimator. We can select **teffects nnmatch** or **teffects psmatch** for balance and estimation; in this example, we use **teffects nnmatch**.

		Treatment-effects estimation				Number of obs = 4,642	
		Estimator : nearest-neighbor matching				Matches: requested = 1	
		Outcome model : matching				min = 1	
		Distance metric: Mahalanobis				max = 139	
bweight		AI Robust				[95% Conf. Interval]	
	Coef.	Std. Err.	z	P> z			
ATE							
mbsmoke							
(smoker							
vs							
nonsmoker)	-240.4589	28.43008	-8.46	0.000	-296.1808	-184.7369	

Again we ignore the estimated effect and first check for balance. We begin by reviewing whether the summary statistics indicate good balance.

```
. tebalance summarize
note: refitting the model using the generate() option
```

Covariate balance summary

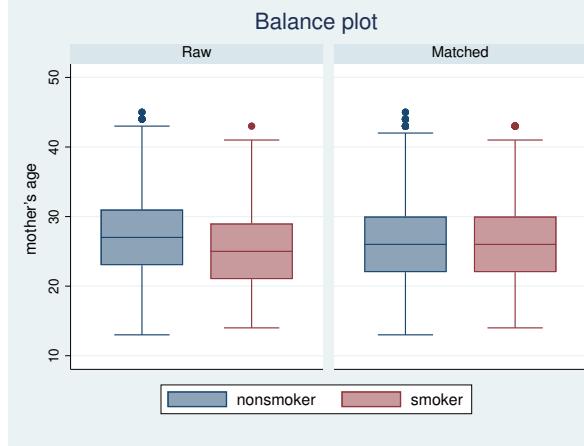
		Raw	Matched
Number of obs =		4,642	9,284
Treated obs =		864	4,642
Control obs =		3,778	4,642

	Standardized differences		Variance ratio	
	Raw	Matched	Raw	Matched
mmarried	-.5953009	-2.42e-16	1.335944	1
mage	-.300179	-.0040826	.8818025	.9815517
prenatal1	-.3242695	-2.78e-16	1.496155	1
fbaby	-.1663271	2.24e-16	.9430944	1

We do not have standard errors on these statistics, so we cannot make any formal conclusions, but the summary statistics appear to indicate much better balance than the IPW results. `tebalance summarize` has to refit the model to recover the matched sample because the `generate()` option was not specified on the `teffects nnmatch` command. The reestimation does not affect the results, although the computation takes longer; see [example 3](#) for details.

Because it is a matching estimator, and not an IPW estimator, we cannot use `tebalance overid` after `teffects nnmatch`. The matching estimators, however, provide diagnostic box plots using `tebalance box` that are not available after the IPW estimators.

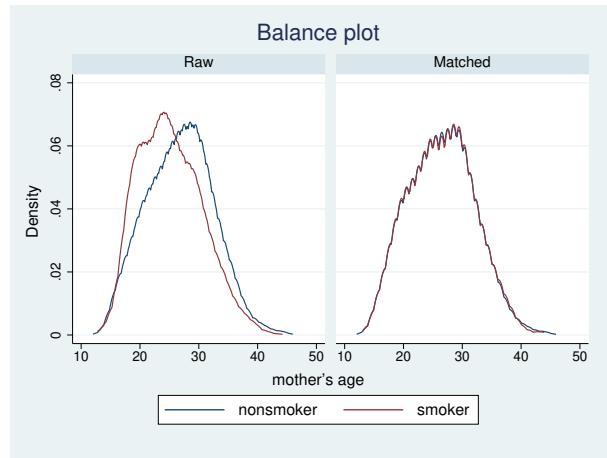
```
. tebalance box mage
note: refitting the model using the generate() option
```



The box plots of the matched data also indicate covariate balance.

Let's look at the kernel density plots using the matched data.

```
. tebalance density mage
note: refitting the model using the generate() option
```



The plots using the matched data appear to be balanced.



□ Technical note

`teffects` implements matching estimators, IPW estimators, regression-adjustment (RA) estimators, and estimators that combine IPW and RA. Matching estimators define a matched sample, and IPW estimators define a weighted sample, each of which can be used to compute covariate balance statistics. RA estimators do not define an adjusted sample that can be used to compute covariate balance statistics, and `tebalance` does not work after `teffects ra`. Only the IPW component of the estimators that combine RA and IPW defines a weighted sample that can be used to compute balance statistics. So, `tebalance` produces the same results after `teffects aipw` or `teffects ipwra` as it does after `teffects ipw`.



▷ Example 3: Faster results after a matching estimator

The `tebalance` commands run in [example 2](#) executed more slowly than necessary. `tebalance` issued the note

```
note: refitting the model using the generate() option
```

after the commands

```
. tebalance summarize
. tebalance box mage
```

and

```
. tebalance density mage
```

After `teffects nnmatch` or `teffects psmatch`, `tebalance` computes the balance statistics on the matched sample defined by the matching estimator. `teffects nnmatch` and `teffects psmatch` leave behind only variables that identify the matched sample when the `generate()` option is specified. Unless the `generate()` option is specified with `teffects nnmatch` or `teffects psmatch`, each `tebalance` command must rerun the estimation command to recover the matched sample.

Typing

```
. teffects nnmatch (bweight mmarried mage fbaby prenatal1)
> (mbsmoke), bias(mage) ematch(mmarried fbaby prenatal1)
> generate(matchv)
```

would generate variables that identify the matched sample that the `tebalance` commands could use. See *Remarks and examples* in [TE] **tebalance box**, [TE] **tebalance density**, and [TE] **tebalance summarize** for examples using the option `generate()` on `teffects psmatch` to speed up the postestimation computations.



Methods and formulas

Methods and formulas are presented under the following headings:

- [Introduction](#)
- [Matched samples](#)
- [IPW samples](#)
- [Testing the propensity-score model specification](#)

Introduction

For covariate z , we observe values $\{z_1, z_2, \dots, z_N\}$. Define a treatment indicator variable for J treatment levels as $t_i \in \{1, 2, \dots, J\}$, for $i = 1, \dots, N$, and frequency weights as $\{w_1, w_2, \dots, w_N\}$. The sample mean and variance of z for level t are

$$\begin{aligned}\hat{\mu}_z(t) &= \frac{\sum_i^N I(t_i = t) w_i z_i}{N_t} \quad \text{and} \\ \hat{\sigma}_z^2(t) &= \frac{\sum_i^N I(t_i = t) w_i \{z_i - \hat{\mu}_z(t)\}^2}{N_t - 1}\end{aligned}$$

where $N_t = \sum_i^N w_i I(t_i = t)$, and

$$I(t_i = t) = \begin{cases} 1 & \text{if } t_i = t \\ 0 & \text{otherwise} \end{cases}$$

As shown in Austin (2011), the standardized differences for covariate z between level t and the control t_0 are computed as

$$\delta_z(t) = \frac{\hat{\mu}_z(t) - \hat{\mu}_z(t_0)}{\sqrt{\frac{\hat{\sigma}_z^2(t) + \hat{\sigma}_z^2(t_0)}{2}}} \tag{1}$$

The variance ratio is $\rho_z(t) = \{\hat{\sigma}_z^2(t)\}/\{\hat{\sigma}_z^2(t_0)\}$.

Matched samples

We now turn our attention to the matched samples for the potential-outcome mean (POM), average treatment effect (ATE), and average treatment effect on the treated (ATET) estimators. We estimate the covariate for the counter-factual treatment by taking the mean of the matched observations

$$\dot{z}_i = \frac{\sum_{j \in \Omega(i)} w_j z_j}{\sum_{j \in \Omega(i)} w_j}$$

where $\Omega(i) = (k_1, k_2, \dots, k_{m_j})$ is the set of observation indices that are matched to observation i of the opposite treatment condition. The observed covariate and matched covariate pairs, (z_i, \dot{z}_i) , $i = 1, \dots, N$, are used in the box plot (see [G-2] **graph box**) and the kernel density plot (see [R] **kdensity**). The ATET sample is limited to those observations from the conditional treatment, \tilde{t} , and their matched covariate means.

In *Methods and formulas* of [TE] **teffects nnmatch**, we define $K_m(i)$ as the number of times observation i is used in a match with observation j of the opposite treatment condition, $i \in \Omega(j)$, weighted by the total number of matches for observation j . Specifically,

$$K_m(i) = \sum_{j=1}^N I\{i \in \Omega(j)\} \frac{w_j}{\sum_{k \in \Omega(j)} w_k}$$

These weights are used in the estimation of the mean and variance for the matched dataset. For the POM and ATE models, the estimated mean and variance are computed as

$$\begin{aligned} \hat{\mu}_{\dot{z}}(t) &= \frac{\sum_i^N I(t_i = t) w_i z_i \{1 + K_m(i)\}}{M_t} \quad \text{and} \\ \hat{\sigma}_{\dot{z}}^2(t) &= \frac{\sum_i^N I(t_i = t) w_i \{1 + K_m(i)\} \{z_i - \hat{\mu}_{\dot{z}}(t)\}^2}{M_t - 1} \end{aligned}$$

where $M_t = \sum_i^N I(t_i = t) w_i \{1 + K_m(i)\}$.

The standardized differences between the control level and all other levels for the matched covariate distribution are computed as in (1), but $\hat{\mu}_{\dot{z}}(t)$ is substituted for $\hat{\mu}_z(t)$ and $\hat{\sigma}_{\dot{z}}^2(t)$ for $\hat{\sigma}_z^2(t)$.

For the ATET model, there is no matched sample for the treatment levels other than the conditional treatment \tilde{t} . The covariate mean and variance for the conditional treatment are the same as that of the raw data, $\mu_z(\tilde{t})$ and $\sigma_z(\tilde{t})$. However, the covariate mean and variance for the sample matched to the conditional treatment, $t \neq \tilde{t}$, are computed as

$$\begin{aligned} \tilde{\mu}_{\dot{z}}(t) &= \frac{\sum_i^N I(t_i = t) w_i z_i K_m(i)}{M_t} \quad \text{and} \\ \tilde{\sigma}_{\dot{z}}^2(t) &= \frac{\sum_i^N I(t_i = t) w_i K_m(i) \{z_i - \tilde{\mu}_{\dot{z}}(t)\}^2}{M_t - 1} \end{aligned}$$

where $M_t = \sum_i^N I(t_i = t) w_i K_m(i)$.

IPW samples

Computation of the inverse-probability weights is discussed in [Methods and formulas of \[TE\] teffects aipw](#) and in [Methods and formulas of \[TE\] stteffects ipwra](#). For the POM and ATE estimators, we defined the normalized IPW weights as $\bar{d}_i(t) = N_t d_i(t) / \sum_i^N d_i(t)$, where $d_i(t) = I(t_i = t) / p(\mathbf{z}_i, t, \hat{\gamma})$ for treatment level t and individual i .

For the ATET estimator, we use the normalized weights $\bar{f}_i = N f_i / \sum_i^N f_i$, where $f_i = p(\mathbf{z}_i, \tilde{t}, \hat{\gamma}) / p(\mathbf{z}_i, t_i, \hat{\gamma})$ are the treatment-adjusted inverse-probability weights, and \tilde{t} is the conditional treatment.

We will simplify notation by defining a single weight

$$\bar{w}_i(t) = \begin{cases} \bar{d}_i(t) & \text{if model is ATE or POM} \\ \bar{f}_i(t) & \text{if model is ATET} \end{cases}$$

The covariate mean and variance for treatment level t are

$$\begin{aligned} \tilde{\mu}_{\hat{z}}(t) &= \frac{\sum_i^N I(t_i = t) w_i \bar{w}_i x_i}{M_t} \quad \text{and} \\ \tilde{\sigma}_{\hat{z}}^2(t) &= \frac{I(t_i = t) w_i \bar{w}_i \{z_i - \tilde{\mu}_{\hat{z}}(t)\}^2}{M_t - 1} \end{aligned}$$

where $M_t = \sum_i^N I(t_i = t) w_i \bar{w}_i$.

The kernel density is computed by [kdensity](#) for each covariate conditioned on each treatment level using the raw covariate with [iweights](#) equal to $w_i \bar{w}_i$.

Testing the propensity-score model specification

We estimate the probability of treatment conditioned on a set of covariates with a propensity-score model. [Imai and Ratkovic \(2014\)](#) derive a test for whether the estimated propensity score balances the covariates. The score equations for parameters of the propensity-score model define an exactly identified generalized method of moments (GMM) estimator. [Imai and Ratkovic \(2014\)](#) use the conditions imposed by mean balance as overidentifying conditions. A standard GMM test for the validity of the overidentifying conditions is then a test for covariate balance. See [\[R\] gmm](#) for a discussion of this overidentifying test, which is known as Hansen's J test in the econometrics literature.

Here are the details about the score equations and the overidentifying balance conditions. Recall from [Methods and formulas of \[TE\] teffects aipw](#) and [Methods and formulas of \[TE\] stteffects ipwra](#), we have the first-order condition of the treatment model

$$\frac{1}{N} \sum_{i=1}^N \mathbf{s}_{\text{tm},i}(\mathbf{z}_i, \hat{\gamma}) = 0$$

For a two-level treatment-effects model with conditional treatment \tilde{t} and control t_0 , the score is

$$\mathbf{s}_{\text{tm},i}(\mathbf{z}_i, \gamma) = \frac{I(t_i = \tilde{t})}{p(\mathbf{z}_i, \tilde{t}, \gamma)} \frac{\partial p(\mathbf{z}_i, t, \gamma)}{\partial \gamma} - \left\{ \frac{I(t_i = t_0)}{1 - p(\mathbf{z}_i, \tilde{t}, \gamma)} \right\} \frac{\partial p(\mathbf{z}_i, \tilde{t}, \gamma)}{\partial \gamma} \Big|_{\gamma=\hat{\gamma}}$$

The score reduces to

$$\mathbf{s}_{\text{tm},i}(\mathbf{z}_i, \tilde{\gamma}) = \left[\frac{I(t_i = \tilde{t}) - p(\mathbf{z}_i, \tilde{t}, \gamma)}{p(\mathbf{z}_i, \tilde{t}, \gamma) \{1 - p(\mathbf{z}_i, \tilde{t}, \gamma)\}} \right] \frac{\partial p(\mathbf{z}_i, \tilde{t}, \gamma)}{\partial \gamma'} \Big|_{\gamma=\tilde{\gamma}}$$

The corresponding covariate balancing moment conditions are

$$\mathbf{w}_{\text{tm},i}(\mathbf{z}_i, \gamma) = \left[\frac{I(t_i = \tilde{t}) - p(\mathbf{z}_i, \tilde{t}, \gamma)}{p(\mathbf{z}_i, \tilde{t}, \gamma) \{1 - p(\mathbf{z}_i, \tilde{t}, \gamma)\}} \right] \mathbf{z}_i$$

for the POM and ATE models. For the ATET model with conditional treatment \tilde{t} , we multiply by $p(\mathbf{z}_i, \tilde{t}, \gamma)$ and scale by $N/N_{\tilde{t}}$:

$$\mathbf{w}_{\text{tm},i}(\mathbf{z}_i, \gamma) = \frac{N}{N_{\tilde{t}}} \left\{ \frac{I(t_i = \tilde{t}) - p(\mathbf{z}_i, \tilde{t}, \gamma)}{1 - p(\mathbf{z}_i, \tilde{t}, \gamma)} \right\} \mathbf{z}_i$$

We stack the moment conditions

$$\begin{aligned} \mathbf{g}_{\text{tm}}(\mathbf{Z}, \gamma) &= \frac{1}{N} \sum_{i=1}^N \left\{ \begin{array}{l} \mathbf{s}_{\text{tm},i}(\mathbf{z}_i, \gamma) \\ \mathbf{w}_{\text{tm},i}(\mathbf{z}_i, \gamma) \end{array} \right\} \\ &= \frac{1}{N} \sum_{i=1}^N \mathbf{g}_{\text{tm},i}(\mathbf{z}_i, \gamma) \end{aligned}$$

The overidentified GMM estimator is then

$$\tilde{\gamma} = \operatorname{argmin}_{\gamma} N \mathbf{g}_{\text{tm}}(\mathbf{Z}, \gamma)' \mathbf{W}_{\text{tm}}(\mathbf{Z}, \gamma)^{-1} \mathbf{g}_{\text{tm}}(\mathbf{Z}, \gamma) \quad (2)$$

where

$$\mathbf{W}_{\text{tm}}(\mathbf{Z}, \gamma) = \frac{1}{N} \sum_{i=1}^N E_T \{ \mathbf{g}_{\text{tm},i}(\mathbf{z}, \gamma) \mathbf{g}_{\text{tm},i}(\mathbf{z}, \gamma)' \}$$

and the expectation is taken with respect to treatment distribution. The weight matrix $\mathbf{W}_{\text{tm}}(\mathbf{Z}, \gamma)$ is computed explicitly (Imai and Ratkovic 2014), and (2), written as a maximization problem, is solved using `ml`.

Finally, Hansen's J statistic is evaluated at its minimum,

$$J = N \mathbf{g}_{\text{tm}}(\mathbf{Z}, \tilde{\gamma})' \mathbf{W}_{\text{tm}}(\mathbf{Z}, \tilde{\gamma})^{-1} \mathbf{g}_{\text{tm}}(\mathbf{Z}, \tilde{\gamma})$$

and is asymptotically distributed chi-squared with degrees of freedom d ,

$$d = \operatorname{rank} \{ \mathbf{W}_{\text{tm}}(\mathbf{Z}, \tilde{\gamma}) \} - \operatorname{rank} \left[\frac{1}{N} \sum_{i=1}^N E_T \{ \mathbf{s}_{\text{tm},i}(\mathbf{z}_i, \tilde{\gamma}) \mathbf{s}_{\text{tm},i}(\mathbf{z}_i, \tilde{\gamma})' \} \right]$$

References

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- . 2011. An introduction to propensity score methods for reducing the effects of confounding in observational studies. *Multivariate Behavioral Research* 46: 399–424.
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- Imai, K., and M. Ratkovic. 2014. Covariate balancing propensity score. *Journal of the Royal Statistical Society, Series B* 76: 243–263.
- Rosenbaum, P. R., and D. B. Rubin. 1985. Constructing a control group using multivariate matched sampling methods that incorporate the propensity score. *American Statistician* 39: 33–38.
- Rubin, D. B. 2008. For objective causal inference, design trumps analysis. *Annals of Applied Statistics* 2: 808–840.

Also see

- [TE] [stteffects intro](#) — Introduction to treatment effects for observational survival-time data
- [TE] [tebalance box](#) — Covariate balance box
- [TE] [tebalance density](#) — Covariate balance density
- [TE] [tebalance overid](#) — Test for covariate balance
- [TE] [tebalance summarize](#) — Covariate-balance summary statistics
- [TE] [teffects](#) — Treatment-effects estimation for observational data

tebalance box — Covariate balance box

Description
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Also see

Description

`tebalance box` produces box plots that are used to check for balance in matched samples after `teffects nnmatch` and `teffects psmatch`.

Quick start

Box plot of the propensity score from the last `teffects psmatch` command
`tebalance box`

Box plot of values of `x1` in the treatment and control groups from raw data and the matched sample from the last `teffects nnmatch` or `teffects psmatch` command

`tebalance box x1`

Menu

Statistics > Treatment effects > Balance > Graphs

Syntax

Box plots for the propensity score

```
tebalance box [ , options ]
```

Box plots for a covariate

```
tebalance box varname [ , options ]
```

<i>options</i>	Description
Main	
<i>boxlook_options</i>	graph box options controlling how the box looks
<i>legending_options</i>	graph box options controlling how the variables are labeled
<i>axis_options</i>	graph box options controlling how numerical <i>y</i> axis is labeled
<i>title_and_other_options</i>	graph box options controlling titles, added text, aspect ratio, etc.
<i>by_options</i>	suboptions inside by() controlling plots by raw and matched samples

Options

Main

boxlook_options are any of the options documented in *boxlook_options* in [G-2] **graph box**.

legending_options are any of the options documented in *legending_options* in [G-2] **graph box**.

axis_options are any of the options documented in *axis_options* in [G-2] **graph box**.

title_and_other_options are any of the options, except by(), documented in *title_and_other_options* in [G-2] **graph box**. tebalance box uses by() to differentiate between raw and matched samples, and some *twoway_options* will be repeated for by graph and might be better specified as *byopts()*.

by_options are any of the *byopts* documented in [G-3] **by_option**. *byopts()* generally affects the entire graph, and some *by_options* may be better specified as *twoway_options*; see [G-3] **twoway_options**.

Remarks and examples

When the distribution of a covariate does not vary over the treatment levels, the covariate is said to be balanced. tebalance box produces box plots of a covariate over treatment levels for the raw data and for the matched sample produced by teffects. If the matched-sample box plots are the same over the treatment levels, the covariate is balanced in the matched sample.

After teffects nnmatch and teffects psmatch,

```
. tebalance box varname [ , options ]
```

produces box plots to check whether *varname* is balanced.

After **teffects psmatch**,

. **tebalance box** [, *options*]

produces box plots to check whether the propensity score estimated by **teffects** is balanced.

We recommend that you read [**TE**] **tebalance** before proceeding; it provides an introduction to covariate balance and an overview of the implemented methods.

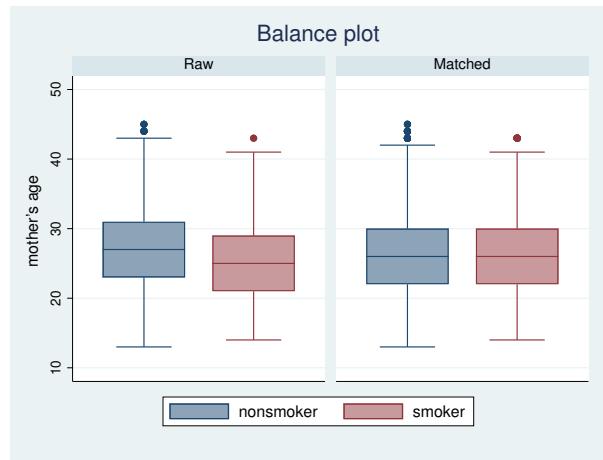
▷ Example 1: Checking covariate balance after psmatch

Using an extract from the data used by Cattaneo (2010), we use **teffects psmatch** to estimate the effect of a mother's smoking behavior (**mbsmoke**) on the birthweight of her child (**bweight**), controlling for marital status (**mmarried**), the mother's age (**mage**), whether the mother had a prenatal doctor's visit in the baby's first trimester (**prenatal1**), and whether this baby is the mother's first child (**fbaby**).

<pre>. use https://www.stata-press.com/data/r16/cattaneo2 (Excerpt from Cattaneo (2010) Journal of Econometrics 155: 138-154) . teffects psmatch (bweight) (mbsmoke mmarried mage prenatal1 fbaby), > generate(matchv)</pre>																																								
Treatment-effects estimation Estimator : propensity-score matching Outcome model : matching Treatment model: logit																																								
Number of obs = 4,642 Matches: requested = 1 min = 1 max = 139																																								
<table border="1"> <thead> <tr> <th></th> <th colspan="5">AI Robust</th> <th></th> </tr> <tr> <th></th> <th>Coef.</th> <th>Std. Err.</th> <th>z</th> <th>P> z </th> <th>[95% Conf. Interval]</th> <th></th> </tr> </thead> <tbody> <tr> <td>bweight</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td>ATE</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> </tr> <tr> <td> mbsmoke (smoker vs nonsmoker)</td> <td>-235.1714</td> <td>27.74409</td> <td>-8.48</td> <td>0.000</td> <td>-289.5488</td> <td>-180.794</td> </tr> </tbody> </table>							AI Robust							Coef.	Std. Err.	z	P> z	[95% Conf. Interval]		bweight							ATE							mbsmoke (smoker vs nonsmoker)	-235.1714	27.74409	-8.48	0.000	-289.5488	-180.794
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We specified the option **generate(matchv)** to speed up the postestimation command that produces density plots, as discussed in [example 3](#) under *Remarks and examples* of [**TE**] **tebalance**. We do not interpret the estimated effect produced by this preliminary model but rather check the specification. Now we look at the box plots.

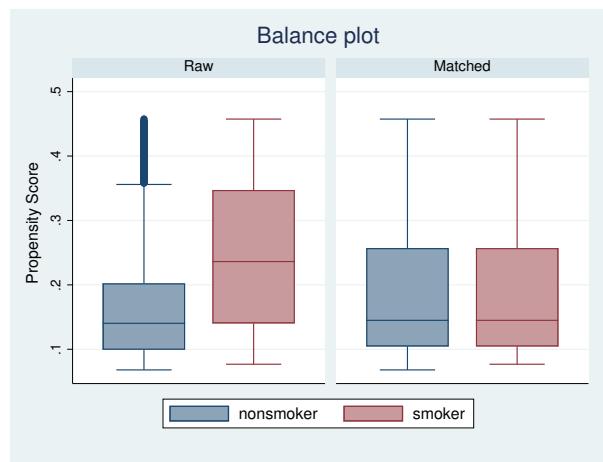
```
. tebalance box mage
```



The box plots for the matched sample are very similar. The medians, the 25th percentiles, and the 75th percentiles appear to be the same, although there may be some differences in the tails, the upper adjacent values, the lower adjacent values, and the outliers. Matching on the estimated propensity score appears to have balanced `mage`, except for the tails.

To get an idea of whether `teffects psmatch` balanced all the covariates, we look at the box plots for the estimated propensity score.

```
. tebalance box
```



The box plots indicate that `teffects psmatch` balanced the estimated propensity scores.



Reference

Cattaneo, M. D. 2010. Efficient semiparametric estimation of multi-valued treatment effects under ignorability. *Journal of Econometrics* 155: 138–154.

Also see

[TE] **tebalance** — Check balance after teffects or stteffects estimation

[TE] **teffects nnmatch** — Nearest-neighbor matching

[TE] **teffects overlap** — Overlap plots

[TE] **teffects psmatch** — Propensity-score matching

tebalance density — Covariate balance density[Description](#)[Options](#)[Also see](#)[Quick start](#)[Remarks and examples](#)[Menu](#)[Stored results](#)[Syntax](#)[Reference](#)

Description

`tebalance density` produces kernel density plots that are used to check for covariate balance after estimation by a `teffects` inverse-probability-weighted estimator, a `teffects` matching estimator, or an `stteffects` inverse-probability-weighted estimator.

Quick start

Kernel density plot of the propensity score after `teffects psmatch`
`tebalance density`

Kernel density plot of `x1` after a `teffects` command or an `stteffects` command
`tebalance density x1`

As above, but rescale the kernel bandwidth by a factor of 2
`tebalance density x1, bwidth(*2)`

Menu

Statistics > Treatment effects > Balance > Graphs

Syntax

Density plots for the propensity score

tebalance density [, *options*]

Density plots for a covariate

tebalance density *varname* [, *options*]

<i>Options</i>	Description
Main	
kernel (<i>kernel</i>)	specify the kernel function; default is <code>kernel(epanechnikov)</code>
bwidth (*#)	rescale default bandwidth
line#opts (<i>line_options</i>)	twoway line options for density line number #
twoway_options	any options other than <code>by()</code> documented in [G-3] twoway_options
byopts (<i>byopts</i>)	how subgraphs are combined, labeled, etc.

<i>kernel</i>	Description
triangle	triangle kernel function; the default
epanechnikov	Epanechnikov kernel function
epan2	alternative Epanechnikov kernel function
biweight	biweight kernel function
cosine	cosine trace kernel function
gaussian	Gaussian kernel function
parzen	Parzen kernel function
rectangle	rectangle kernel function

Options

Main

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

bwidth(*#) specifies the factor by which the default bandwidths are to be rescaled. A bandwidth is the half-width of the kernel, the width of the density window around each point. Each kernel density plot has its own bandwidth, and by default, each kernel density plot uses its own optimal bandwidth; see [R] **kdensity**. **bwidth()** rescales each plot's optimal bandwidth by the specified amount.

line#opts(*line_options*) specifies the line pattern, width, color, and overall style of density line number #. The line numbers are in the same order as the treatment levels specified in `e(tlevels)`.

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**). **tebalance density** uses `by()` to differentiate between raw and weighted or matched samples, and some **twoway_options** will be repeated for `by graph` and might be better specified as `byopts()`.

`byopts(by_option)` is as documented in [G-3] *by_option*. `byopts()` affects how the subgraphs are combined, labeled, etc. `byopts()` generally affects the entire graph, and some *by_option* may be better specified as *two-way-options*; see [G-3] **two-way-options**.

Remarks and examples

When the distribution of a covariate does not vary over the treatment levels, the covariate is said to be balanced. `tebalance density` produces kernel density plots of a covariate over treatment levels for the raw data and the weighted or matched sample produced by `teffects` or `stteffects`. If the weighted-sample or matched-sample kernel density plots of the covariate are the same over the treatment levels, the covariate is balanced in the weighted or matched sample.

After all `teffects` commands except `teffects ra`, `stteffects ipw`, and `stteffects ipwra`,

```
. tebalance density varname [, options]
```

produces kernel density plots to check whether *varname* is balanced.

After all `teffects` commands except `teffects ra`, `teffects nnmatch`, `stteffects ipw`, and `stteffects ipwra`,

```
. tebalance density [, options]
```

produces kernel density plots to check whether the propensity score estimated by `teffects` or `stteffects` is balanced. Our discussion of the use of `tebalance density` and interpretation of its results for a covariate below also apply to a propensity score.

We recommend that you read [TE] **tebalance** before proceeding; it provides an introduction to covariate balance and an overview of the implemented methods. See [TE] **stteffects intro** for a discussion of survival-time features.

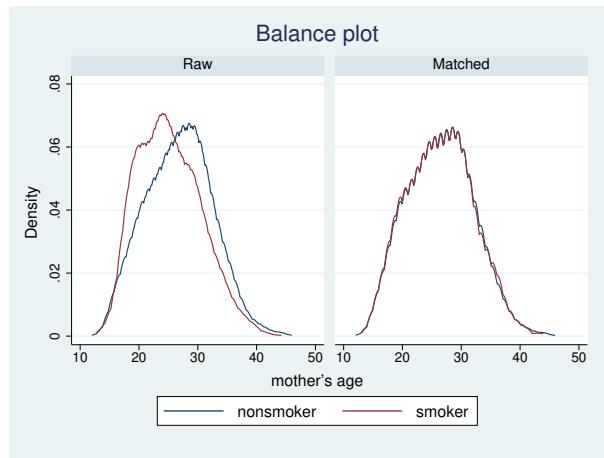
▷ Example 1: Checking covariate balance after psmatch

Using an extract from the data used by Cattaneo (2010), we use `teffects psmatch` to estimate the effect of a mother's smoking behavior (`mbsmoke`) on the birthweight of her child (`bweight`), controlling for marital status (`mmarried`), the mother's age (`mage`), whether the mother had a prenatal doctor's visit in the baby's first trimester (`prenatal1`), and whether this baby is the mother's first child (`fbaby`).

Treatment-effects estimation						
Estimator		Number of obs = 4,642				
Outcome model		Matches: requested = 1				
Treatment model:		min = 1				
		max = 139				
		Coef.	AI Robust Std. Err.	z	P> z	[95% Conf. Interval]
ATE	mbsmoke (smoker vs nonsmoker)	-235.1714	27.74409	-8.48	0.000	-289.5488 -180.794

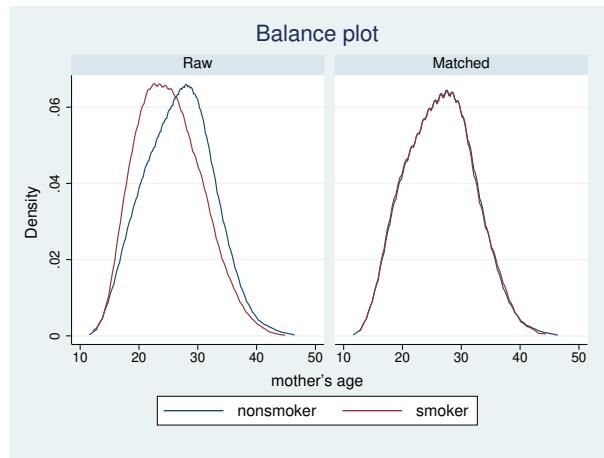
We specified the option `generate(matchv)` to speed up the postestimation command that produces density plots, as discussed in [example 3](#) under *Remarks and examples* in [TE] **tebalance** entry. We do not interpret the estimated effect produced by this preliminary model but rather check the specification. We begin by looking at the default density plots.

```
. tebalance density mage
```



The density plots for the matched sample are nearly indistinguishable, implying that matching on the estimated propensity score balanced the covariates. The density plots are too jagged for presentation, so we oversmooth them by scaling up the bandwidth used for each plot.

```
. tebalance density mage, bwidth(*1.5)
```



Option `bwidth()` rescales the default optimal bandwidths by the specified scale factor. Each of the four density plots has its own sample size and optimal bandwidth. Rescaling each of the four bandwidths by 1.5 produces smoother plots.



Stored results

After `teffects` or `stteffects` fits a binary treatment, `tebalance density` stores the following in `r()`:

Scalars

<code>r(bwc_adj)</code>	bandwidth for control in weighted or matched-adjusted sample
<code>r(Nc_adj)</code>	observations on control in weighted or matched-adjusted sample
<code>r(bwt_adj)</code>	bandwidth for treated in weighted or matched-adjusted sample
<code>r(Nt_adj)</code>	observations on treated in weighted or matched-adjusted sample
<code>r(bwc_raw)</code>	bandwidth for control in raw sample
<code>r(Nc_raw)</code>	observations on control in raw sample
<code>r(bwt_raw)</code>	bandwidth for treated in raw sample
<code>r(Nt_raw)</code>	observations on treated in raw sample

Macros

<code>r(kernel)</code>	name of kernel
------------------------	----------------

After `teffects` or `stteffects` fits a multivalued treatment, `tebalance density` stores the following in `r()`:

Scalars

<code>r(bw#_adj)</code>	bandwidth for treatment level # in weighted or matched-adjusted sample
<code>r(N#_adj)</code>	observations on treatment level # in weighted or matched-adjusted sample
<code>r(bw#_raw)</code>	bandwidth for treatment level # in raw sample
<code>r(N#_raw)</code>	observations on treatment level # in raw sample

Macros

<code>r(kernel)</code>	name of kernel
------------------------	----------------

Reference

Cattaneo, M. D. 2010. Efficient semiparametric estimation of multi-valued treatment effects under ignorability. *Journal of Econometrics* 155: 138–154.

Also see

- [TE] **stteffects intro** — Introduction to treatment effects for observational survival-time data
- [TE] **tebalance** — Check balance after `teffects` or `stteffects` estimation
- [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 overlap** — Overlap plots
- [TE] **teffects psmatch** — Propensity-score matching

tebalance overid — Test for covariate balance

Description
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Syntax
References

Description

`tebalance overid` performs a test for covariate balance after estimation by a `teffects` inverse-probability-weighted (IPW) estimator or an `stteffects` IPW estimator.

Quick start

Test for covariate balance after a `teffects` or an `stteffects` IPW estimator

`tebalance overid`

As above, but test for balance only in base covariates and exclude interaction terms

`tebalance overid, bconly`

Menu

Statistics > Treatment effects > Balance > Overidentification test

Syntax

```
tebalance overid [ , bconly nolog iterate(#) ]
```

Options

Main

bconly specifies that only the base covariates be included in the test for balance. By default, the powers and interactions specified by factor-variable notation in the **teffects** or **stteffects** model are also included in the test for balance.

nolog suppresses the display of the optimization search log.

iterate(#) sets the maximum number of iterations to # in the generalized method of moments estimator used to compute the test statistic.

Remarks and examples

When the distribution of a covariate is the same for all treatment levels, the covariate is said to be balanced. **tebalance overid** performs a test to see whether the covariates are balanced after **teffects** or **stteffects**. **tebalance overid** can be executed after **teffects ipw**, **teffects aipw**, **teffects ipwra**, **stteffects ipw**, or **stteffects ipwra**, which use the inverse-probability weights predicted by a treatment model to account for how treatment assignment depends on observed covariates. If the treatment model is well specified, IPW functions of the covariates from the model are balanced.

We recommend that you read [TE] **tebalance** before proceeding; it provides an introduction to covariate balance and an overview of the implemented methods. See [TE] **stteffects intro** for survival-time discussion and examples.

▷ Example 1: Base covariates and interactions

This example illustrates the interpretation of the **bconly** option, which excludes powers and interactions when factor variables are included in the propensity-score model.

We frequently use factor variables to include powers of, and interactions between, base covariates in our specification of the propensity-score model. In [example 1](#) under *Remarks and examples in [TE] tebalance*, we rejected the null hypothesis of balance in a model using only base covariates but not in the richer model that included power and interaction terms. By default, **tebalance overid** tests whether the model balances the base covariates and the power-and-interaction covariates. When option **bconly** is specified, **tebalance overid** tests whether the model balances the base covariates only.

Using an extract from the data used by [Cattaneo \(2010\)](#), we use **teffects ipw** to estimate the effect of a mother's smoking behavior (**mbsmoke**) on the birthweight of her child (**bweight**), controlling for marital status (**mmarried**), the mother's age (**mage**), whether the mother had a prenatal doctor's visit in the baby's first trimester (**prenatal1**), and whether this baby is the mother's first child (**fbaby**). In addition to the base covariates, we include the square of **mage**, an interaction between **mage** and **mmarried**, and an interaction between **mage** and **prenatal1** in the model for the propensity score.

Treatment-effects estimation						
	Number of obs = 4,642					
Estimator	inverse-probability weights					
Outcome model	weighted mean					
Treatment model	logit					
	Robust					
bweight	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
ATE						
mbsmoke (smoker vs nonsmoker)	-239.6875	26.43427	-9.07	0.000	-291.4977	-187.8773
P0mean						
mbsmoke nonsmoker	3403.638	9.56792	355.73	0.000	3384.885	3422.39
TME1						
mmarried	.8522468	.462536	1.84	0.065	-.0543072	1.758801
mage	.1742823	.0651039	2.68	0.007	.0466811	.3018836
prenatal1	.4018114	.4341762	0.93	0.355	-.4491584	1.252781
fbaby	-.4824413	.0868982	-5.55	0.000	-.6527587	-.3121239
c.mage# c.mage	-.002515	.0012585	-2.00	0.046	-.0049817	-.0000483
mmarried# c.mage	-.0787984	.0175508	-4.49	0.000	-.1131973	-.0443996
married						
prenatal1# c.mage						
Yes	-.0286228	.0176391	-1.62	0.105	-.0631948	.0059492
_cons	-2.928851	.8409119	-3.48	0.000	-4.577008	-1.280694

We specified option `aequations` to see the parameter estimates for the coefficients in the propensity-score model. There are eight coefficients, five on the base covariates (`mmarried`, `mage`, `fbaby`, `prenatal1`, and `_cons`) and three on the power-and-interaction covariates (`c.mage#c.mage`, `c.mage#1.mmarried`, and `c.mage#1.prenatal1`). Below we test whether the model balances all eight covariates.

```
. tebalance overid
Iteration 0: criterion = .0602349
Iteration 1: criterion = .06172749 (backed up)
Iteration 2: criterion = .06428588 (backed up)
Iteration 3: criterion = .06489623 (backed up)
Iteration 4: criterion = .06527284 (backed up)
Iteration 5: criterion = .06643426
Iteration 6: criterion = .07120383
Iteration 7: criterion = .07647097
Iteration 8: criterion = .07674915
Iteration 9: criterion = .07684127
Iteration 10: criterion = .07703321
Iteration 11: criterion = .0776508
Iteration 12: criterion = .07771863
Iteration 13: criterion = .07773156
Iteration 14: criterion = .07773561
Iteration 15: criterion = .07774891
Iteration 16: criterion = .07775314
Iteration 17: criterion = .07775324
Iteration 18: criterion = .07775325
Iteration 19: criterion = .07775325
Iteration 20: criterion = .07775325
Iteration 21: criterion = .07775325
Iteration 22: criterion = .07775325

Overidentification test for covariate balance
      H0: Covariates are balanced:
      chi2(8)      = 11.8612
      Prob > chi2  = 0.1575
```

We cannot reject the null hypothesis that the IPW model balanced all eight covariates.

Below we specify option bconly to test whether the IPW model balanced the five base covariates only.

```
. tebalance overid, bconly
Iteration 0: criterion = .1079977
Iteration 1: criterion = .10800825 (backed up)
Iteration 2: criterion = .10844177 (backed up)
Iteration 3: criterion = .10851228 (backed up)
Iteration 4: criterion = .10860856 (backed up)
Iteration 5: criterion = .10907494
Iteration 6: criterion = .11009793
Iteration 7: criterion = .11164037
Iteration 8: criterion = .11260665
Iteration 9: criterion = .11286445
Iteration 10: criterion = .11331466
Iteration 11: criterion = .11333969
Iteration 12: criterion = .11335601
Iteration 13: criterion = .11335696
Iteration 14: criterion = .11335696
Iteration 15: criterion = .11335696

Overidentification test for covariate balance
      H0: Covariates are balanced:
      chi2(5)      = 7.82169
      Prob > chi2  = 0.1663
```

We cannot reject the null hypothesis that the IPW model balanced the five base covariates.

Each test has a justification.

In a model-based approach, the Imai and Ratkovic (2014) test checks whether the propensity score is correctly specified. We include all eight covariates because they must all be balanced, if the propensity-score model is correctly specified.

A conditional-independence approach can be used to justify only including the base covariates in the test. In this approach, the propensity-score model need only balance the base covariates. Powers and interactions of the base covariates are included to get a propensity-score model that balances the base covariates, but balance of these higher-order terms is more than what needs to be checked.

In large samples, both tests should have nominal coverage under the null hypothesis that the propensity-score model is correctly specified. Under the alternative that the propensity-score model is misspecified, including all the covariates should yield a test with higher power.

The test that includes all the covariates is the default.



Stored results

`tebalance overid` stores the following in `r()`:

Scalars

<code>r(p)</code>	<i>p</i> -value
<code>r(df)</code>	overidentifying constraints, test degrees of freedom
<code>r(chi2)</code>	chi-squared statistic

References

- Cattaneo, M. D. 2010. Efficient semiparametric estimation of multi-valued treatment effects under ignorability. *Journal of Econometrics* 155: 138–154.
- Imai, K., and M. Ratkovic. 2014. Covariate balancing propensity score. *Journal of the Royal Statistical Society, Series B* 76: 243–263.

Also see

- [TE] **stteffects intro** — Introduction to treatment effects for observational survival-time data
- [TE] **tebalance** — Check balance after teffects or stteffects estimation
- [TE] **teffects aipw** — Augmented inverse-probability weighting
- [TE] **teffects ipw** — Inverse-probability weighting
- [TE] **teffects ipwra** — Inverse-probability-weighted regression adjustment
- [TE] **teffects overlap** — Overlap plots

tebalance summarize — Covariate-balance summary statistics[Description](#)[Option](#)[Also see](#)[Quick start](#)[Remarks and examples](#)[Menu](#)[Stored results](#)[Syntax](#)[Reference](#)

Description

`tebalance summarize` reports diagnostic statistics that are used to check for covariate balance over treatment groups after estimation by a `teffects` inverse-probability-weighted (IPW) estimator, a `teffects` matching estimator, or an `stteffects` IPW estimator.

Quick start

Raw and weighted standardized differences and variance ratios of all covariates from the most recently estimated `teffects` model or `stteffects` model

```
tebalance summarize
```

As above, but report statistics only for covariates `x1` and `x2`

```
tebalance summarize x1 x2
```

Baseline means and variances for treated and control groups

```
tebalance summarize, baseline
```

Menu

Statistics > Treatment effects > Balance > Summaries

Syntax

```
tebalance summarize [varlist] [, baseline]
```

varlist may contain factor variables; see [U] 11.4.3 Factor variables.

Option

Main

baseline specifies that **tebalance summarize** report means and variances by treatment level.

Remarks and examples

When the distribution of a covariate is the same for all treatment levels, the covariate is said to be balanced. **tebalance summarize** reports diagnostic statistics to check for covariate balance after **teffects** or **stteffects**. **tebalance summarize** can be executed after all **teffects** estimators with the exception of **teffects ra** and executed after **stteffects ipw** and **stteffects ipwra**.

We recommend that you read [TE] **tebalance** before proceeding; it provides an introduction to covariate balance and an overview of the implemented methods. See [TE] **stteffects intro** for survival-time discussion and examples.

▷ Example 1: Checking covariate balance after psmatch

Using an extract from the data used by Cattaneo (2010), we use **teffects psmatch** to estimate the effect of a mother's smoking behavior (*mbsmoke*) on the birthweight of her child (*bweight*), controlling for marital status (*mmarried*), the mother's age (*mage*), whether the mother had a prenatal doctor's visit in the baby's first trimester (*prenatal1*), and whether this baby is the mother's first child (*fbaby*).

```
. use https://www.stata-press.com/data/r16/cattaneo2
(Excerpt from Cattaneo (2010) Journal of Econometrics 155: 138-154)
. teffects psmatch (bweight) (mbsmoke mmarried mage prenatal1 fbaby),
> generate(matchv)
Treatment-effects estimation
Estimator      : propensity-score matching
Outcome model  : matching
Treatment model: logit
Number of obs      =      4,642
Matches: requested =          1
                           min =          1
                           max =      139
```

	AI Robust				
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ATE					
mbsmoke					
(smoker					
vs					
nonsmoker)	-235.1714	27.74409	-8.48	0.000	-289.5488 -180.794

We specified the option `generate(matchv)` to speed up the postestimation commands that compute balance statistics, as discussed in [example 3](#) under *Remarks and examples* in [TE] `tebalance`. We do not interpret the estimated effect produced by this preliminary model but rather check the specification.

We begin by looking at the standardized differences and variance ratios for the raw data and the matched sample.

```
. tebalance summarize
```

Covariate balance summary

	Standardized differences		Variance ratio	
	Raw	Matched	Raw	Matched
Number of obs =		4,642		9,284
Treated obs =		864		4,642
Control obs =		3,778		4,642

	Means		Variances	
	Control	Treated	Control	Treated
mmarried	.7514558	.4733796	.1868194	.2495802
mage	26.81048	25.16667	31.87141	28.10429
prenatal1	.8268925	.6898148	.1431792	.2142183
fbaby	.4531498	.3715278	.2478707	.2337654

The matched sample results indicate that matching on the estimated propensity score balanced the covariates. The standardized differences are all close to zero, and the variance ratios are all close to one. This inference is informal because we do not have standard errors for these statistics.

We may also wish to see the baseline summary statistics.

```
. tebalance summarize, baseline
```

Covariate balance summary

	Means		Variances	
	Control	Treated	Control	Treated
Number of obs =		4,642		9,284
Treated obs =		864		4,642
Control obs =		3,778		4,642

	Means		Variances	
	Control	Treated	Control	Treated
mmarried	.7514558	.4733796	.1868194	.2495802
mage	26.81048	25.16667	31.87141	28.10429
prenatal1	.8268925	.6898148	.1431792	.2142183
fbaby	.4531498	.3715278	.2478707	.2337654

While we rely on the standardized differences for conclusions about balance in the unmatched sample from this output, the baseline means and variances give us some idea of the scale of the differences.



▷ Example 2: Multivalued treatments

In the multivalued-treatment case, `tebalance summarize` produces output grouped by treatment level. In the [Cattaneo \(2010\)](#) extract, the variable `msmoke` is an ordered categorical variable specifying the number of cigarettes smoked. We begin by tabulating `msmoke`.

cigarettes smoked during pregnancy	Freq.	Percent	Cum.
0 daily	3,778	81.39	81.39
1-5 daily	200	4.31	85.70
6-10 daily	337	7.26	92.96
11+ daily	327	7.04	100.00
Total	4,642	100.00	

All the treatment groups have significantly smaller numbers of observations than the control group of not smoking. Still, each group has at least 200 observations. We continue by quietly fitting a candidate IPW model and reporting the baseline summaries.

```
. quietly teffects ipw (bweight) (msmoke mmarried mage prenatal1 fbaby)
. tebalance summarize, baseline
```

Covariate balance summary

Treatment	Observations	
	Raw	Weighted
0 daily =	3,778	1,164.8
1-5 daily =	200	1,164.4
6-10 daily =	337	1,157.9
11+ daily =	327	1,154.9
Total =	4,642	4,642.0

	Means		Variances	
	Control	Treated	Control	Treated
1-5 daily	.7514558	.455	.1868194	.2492211
	26.81048	24.64	31.87141	31.44764
	.8268925	.695	.1431792	.2130402
	.4531498	.48	.2478707	.2508543
6-10 daily	.7514558	.4480712	.1868194	.2480394
	26.81048	25.06231	31.87141	27.07051
	.8268925	.6795252	.1431792	.2184188
	.4531498	.3827893	.2478707	.2369648
11+ daily	.7514558	.5107034	.1868194	.250652
	26.81048	25.59633	31.87141	26.93471
	.8268925	.6972477	.1431792	.2117409
	.4531498	.293578	.2478707	.2080261

The results for the control level of 0 daily are repeated for the treatment group. These results give a sense of the scale of imbalance in the raw data. Now we compute the balance statistics.

```
. tebalance summarize
Covariate balance summary
```

	Treatment	Observations	
		Raw	Weighted
0 daily	=	3,778	1,164.8
1-5 daily	=	200	1,164.4
6-10 daily	=	337	1,157.9
11+ daily	=	327	1,154.9
Total	=	4,642	4,642.0

	Standardized differences		Variance ratio	
	Raw	Weighted	Raw	Weighted
1-5 daily				
mmarried	-.634909	-.0016208	1.334021	1.001406
mage	-.3857482	-.0219656	.9867038	.9905584
prenatal1	-.312519	-.0012611	1.487927	1.001898
fbaby	.053769	.0422102	1.012037	1.008631
6-10 daily				
mmarried	-.6506304	-.0108454	1.327696	1.009331
mage	-.3220222	-.0836571	.8493666	.7984901
prenatal1	-.3465797	-.0100232	1.525493	1.015051
fbaby	-.1429048	.0268118	.9560018	1.005899
11+ daily				
mmarried	-.5147672	-.0212969	1.34168	1.018136
mage	-.2239116	-.0636951	.8451058	.8468934
prenatal1	-.3077549	-.0380744	1.478852	1.056645
fbaby	-.3342243	.0155427	.8392526	1.003598

These results indicate that the IPW estimator probably did not fully balance the covariates (the variance ratios for `mage` at the daily levels of 6–10 cigarettes and 11-plus cigarettes are not close to 1). At this point, we would use a richer model and see whether it balanced the covariates.

Note that we cannot use `tebalance overid`, because it has not been implemented for multivalued treatments.



Stored results

`tebalance summarize` stores the following in `r()`:

Matrices

<code>r(size)</code>	number of observations in the raw and matched or weighted samples
<code>r(table)</code>	table of covariate statistics

Reference

Cattaneo, M. D. 2010. Efficient semiparametric estimation of multi-valued treatment effects under ignorability. *Journal of Econometrics* 155: 138–154.

Also see

- [TE] **stteffects intro** — Introduction to treatment effects for observational survival-time data
- [TE] **stteffects ipw** — Survival-time inverse-probability weighting
- [TE] **stteffects ipwra** — Survival-time inverse-probability-weighted regression adjustment
- [TE] **tebalance** — Check balance after teffects or stteffects estimation
- [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 overlap** — Overlap plots
- [TE] **teffects psmatch** — Propensity-score matching

teffects — Treatment-effects estimation for observational data[Description](#) [Syntax](#) [Also see](#)

Description

teffects estimates potential-outcome means (POMs), average treatment effects (ATEs), and average treatment effects on the treated (ATETs) using observational data. Regression-adjustment, inverse-probability-weighting, and matching estimators are provided, as are doubly robust methods that combine regression adjustment and inverse-probability weighting. **teffects overlap** plots the estimated densities of the probability of getting each treatment level.

The outcomes can be continuous, binary, count, fractional, or nonnegative. The treatment model can be binary, or it can be multinomial, allowing for multivalued treatments.

For a brief description and example of each estimator, see *Remarks and examples* in [TE] **teffects intro**.

Syntax

teffects *subcommand* ... [, *options*]

<i>subcommand</i>	Description
aipw	augmented inverse-probability weighting
ipw	inverse-probability weighting
ipwra	inverse-probability-weighted regression adjustment
nnmatch	nearest-neighbor matching
overlap	overlap plots
psmatch	propensity-score matching
ra	regression adjustment

Also see

[TE] **teffects intro** — Introduction to treatment effects for observational data

[TE] **teffects intro advanced** — Advanced introduction to treatment effects for observational data

[TE] **teffects multivalued** — Multivalued treatment effects

Description

This entry provides a nontechnical introduction to treatment-effects estimators and the **teffects** command in Stata. Advanced users may want to instead read [TE] **teffects intro advanced** or skip to the individual commands' entries.

The **teffects** command estimates average treatment effects (ATEs), average treatment effects among treated subjects (ATETs), and potential-outcome means (POMs) using observational data.

Treatment effects can be estimated using regression adjustment (RA), inverse-probability weights (IPW), and “doubly robust” methods, including inverse-probability-weighted regression adjustment (IPWRA) and augmented inverse-probability weights (AIPW), and via matching on the propensity score or nearest neighbors.

The outcome can be continuous, binary, count, fractional, or nonnegative. Treatments can be binary or multivalued.

Remarks and examples

This entry presents a nontechnical overview of treatment-effects estimators for those who are new to the subject of treatment-effects estimation or are at least new to Stata's facilities for estimating treatment effects. More advanced users may want to instead read [TE] **teffects intro advanced** or skip to the individual commands' entries.

Remarks are presented under the following headings:

- Introduction*
- Defining treatment effects*
- Estimating treatment effects*
 - Regression adjustment*
 - Inverse-probability weighting*
 - Doubly robust combinations of RA and IPW*
 - Matching*
- Caveats and assumptions*
- A quick tour of the estimators*
 - RA*
 - IPW*
 - IPWRA*
 - AIPW*
 - Nearest-neighbor matching*
 - Propensity-score matching*
- Video examples*

Introduction

Suppose we have observed a sample of subjects, some of whom received a treatment and the rest of whom did not. As the name suggests, in most applications, the “subjects” are indeed people. A “treatment” could indeed be a medical treatment such as a new drug regimen or surgical procedure. In social science applications, a treatment could be participation in a job-training program or inclusion in a classroom or school in which a new pedagogical method is being used. However, not all applications use individuals as the subjects. For example, a policy analyst might be interested in examining the impact of an experimental program in which a national agency held a lottery to award only some local governments the resources needed to implement the program. Here the subjects are the local governments, and treatment refers to whether a local government received the resources needed to implement the program.

We would like to know if a treatment has an effect on an outcome Y . The outcome could be the cholesterol level of a patient taking either an existing statin or a new experimental drug, or the outcome could be the wage offered to a person who either did or did not participate in a job-training program. In an ideal world, we would observe Y when a subject is treated (which we denote as Y_1), and we would observe Y when the same subject is not treated (which we denote as Y_0). We would be careful to make both observations under identical conditions so that the only difference is the presence or absence of the treatment. We could then average the difference between Y_1 and Y_0 across all the subjects in our dataset to obtain a measure of the average impact of the treatment.

Unfortunately, this ideal experiment is almost never available in observational data because it is not possible to observe a specific subject having received the treatment and having not received the treatment. When the outcome is the birthweight of a specific baby and the treatment is the mother smoking while pregnant, it is impossible to observe the baby’s birthweight under both treatments of the mother smoking and the mother not smoking.

A classic solution to this problem is to randomize the treatment. High costs or ethical issues rule out this solution in many observational datasets. For example, we could not ask a random selection of pregnant women to smoke.

The defining characteristic of observational data is that treatment status is not randomized. Moreover, that implies that the outcome and treatment are not necessarily independent. The goal of the estimators implemented by `teffects` is to utilize covariates to make treatment and outcome independent once we condition on those covariates.

The treatment-effect estimators implemented by `teffects` allow us to estimate the efficacy of treatments using observational data. The rest of this entry discusses these treatment-effect estimators at an introductory level. For a more technical introduction, see [\[TE\] teffects intro advanced](#).

Defining treatment effects

We introduce treatment effects more formally by using the potential-outcomes framework, which is also known as the counterfactual framework. What is a potential outcome? Consider a subject that did not receive treatment so that we observe Y_0 . What would Y_1 be for that same subject if it were exposed to treatment? We call Y_1 the potential outcome or counterfactual for that subject. For a subject that did receive treatment, we observe Y_1 , so Y_0 would be the counterfactual outcome for that subject. We can view this as a missing-data problem, and treatment-effect methods can account for that problem.

Treatment-effect estimators allow us to estimate three parameters. The potential-outcome means (POMs) are the means of Y_1 and Y_0 in the population. The average treatment effect (ATE) is the mean of the difference ($Y_1 - Y_0$). Finally, the average treatment effect on the treated (ATET) is the mean of the difference ($Y_1 - Y_0$) among the subjects that actually receive the treatment.

To develop our intuition, suppose we have observed a sample of patients, some of whom received a medication to reduce their blood pressure. Figure 1 plots each of our patient's systolic blood pressures as a function of weight. We use the color green to indicate patients who did not receive the drug and blue to indicate patients who did receive the drug.

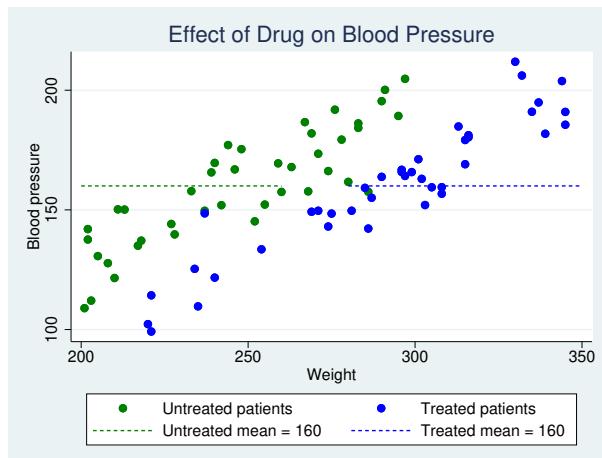


Figure 1

A remarkable feature of our data is that the average blood pressure of patients not taking the drug is 160, and the average blood pressure of patients taking the drug is also 160. Can we therefore conclude that taking the drug has no impact on blood pressure? The answer is no.

Because this is observational data, we could not randomly assign who would receive the drug and who would not. As a result, treatment status could be related to covariates that also affect blood pressure. Heavier patients were more likely to be prescribed the medication, and blood pressure is correlated with weight. The difference in sample means does not estimate the true average treatment effect, because blood pressure depends on weight and weight is correlated with the treatment.

Suppose that we did in fact observe both potential outcomes for all patients. In figure 2, we continue to use solid dots for our observed data points, and we introduce hollow dots to represent the counterfactual outcomes. That is, the green hollow dots represent the blood pressures we would measure if only our treated patients had not taken the drug, and the blue hollow dots represent the blood pressures we would measure if only our untreated patients had taken the drug. The green and blue dashed lines represent the untreated and treated POMs, respectively. That is, the green line represents the mean of all the green dots, and the blue line represents the mean of all the blue dots.

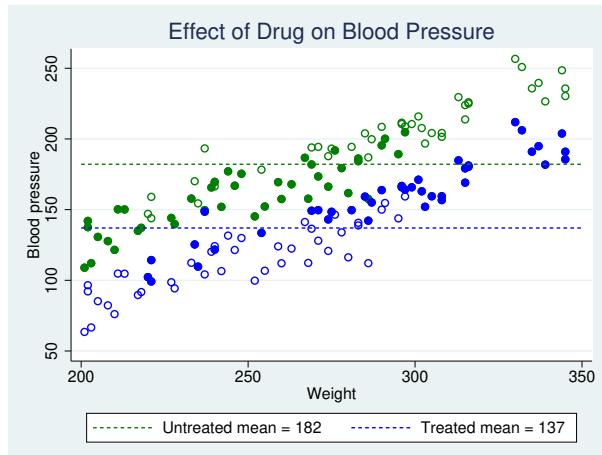


Figure 2

If we did have the data represented by the hollow dots, then we could say that the average treatment effect is the difference between the mean of all the green dots and the mean of all the blue dots. In this ideal scenario, there are no missing data on the other potential outcome, and we have all the data we need to use the difference in means to estimate the ATE.

Looking at figure 2, we can see why a difference in means using only the solid dots does not estimate the ATE. Using only the solid green dots underestimates the average blood pressure for untreated individuals, and using only the solid blue dots overestimates the average blood pressure for treated individuals.

Estimating an ATE is essentially a missing-data problem. When covariates that affect the potential outcomes are related to treatment, we cannot use a difference in sample means, because the missing data are informative.

The treatment-effect estimators implemented in `teffects` allow for covariates like weight to be related to the potential outcomes and the treatment. Essentially, the estimators implemented by `teffects` utilize covariates to fill in the hollow circles or otherwise account for how the missing data depend on covariates that affect the potential outcomes.

Estimating treatment effects

We cannot estimate the ATE by simply taking the difference between the sample means for the treated and untreated subjects, because there are covariates that are related to the potential outcomes and the treatment. The estimators implemented by `teffects` require us to specify enough of these covariates so that after we condition on these covariates, any remaining influences on the treatment are not related to the potential outcomes. `teffects` implements several different estimators to accomplish this, including regression adjustment (RA), inverse-probability weighting (IPW), “doubly robust” methods that combine elements of RA and IPW, and matching methods. Here we introduce the methods by using intuition and simple examples.

See [TE] `teffects intro advanced` for a more technical introduction, and see the individual commands’ entries for estimator-specific details.

Regression adjustment

The RA method extends the idea of using sample means to estimate treatment effects by using a regression model to predict potential outcomes adjusted for covariates. In the examples here, we use linear regression, but the **teffects ra** command provides you with the flexibility to use logistic, probit, and heteroskedastic probit regression models for binary outcomes as well as Poisson regression for nonnegative outcomes; see [TE] **teffects ra** for more information.

`bweightex.dta` is a hypothetical dataset based on Cattaneo (2010) that we have created to illustrate treatment-effects estimators using graphs. The subjects in this dataset are women who were pregnant, some of whom smoked during the pregnancy. The outcome variable is the birthweight of the baby, and we want to know whether smoking during pregnancy affects the birthweight. The dataset also contains other demographic variables that we will use later.

Figure 3 illustrates the relationship between birthweight and smoking status as a function of the mother's age:

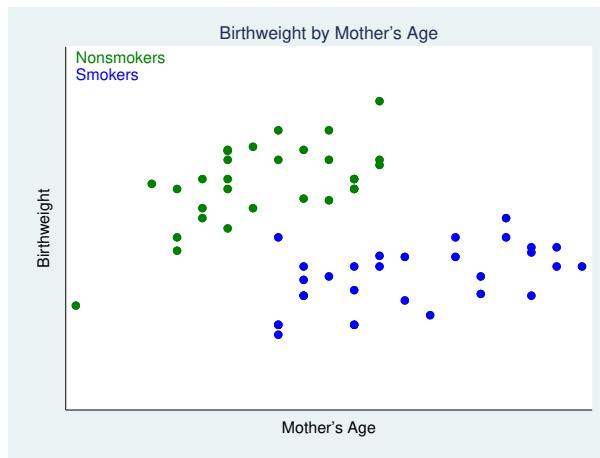


Figure 3

We see that smokers tend to be older than nonsmokers and that birthweight depends on smoking. Therefore, the difference between the sample means of birthweights of babies born to smokers and nonsmokers will not estimate the true average treatment effect.

We also still have the same problem as in the previous section: we do not observe the counterfactual birthweights of babies. Suppose, however, that we did. In figure 4, we use solid points to represent observed birthweights and the colors green to represent nonsmokers and blue to represent smokers. The hollow points represent the counterfactual birthweights. The hollow blue points represent the birthweights of babies that we would observe if only our young nonsmoking mothers had instead smoked during their pregnancies. Similarly, the hollow green points represent the birthweights of babies that we would observe if only our older smoking mothers had instead not smoked during their pregnancies.

Figure 4 suggests a way to estimate the potential outcomes for each mother:

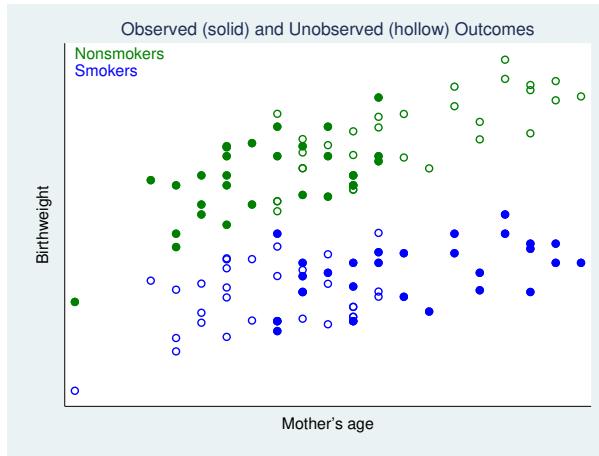


Figure 4

We could fit a linear regression of birthweight on mother's age by using the observed birthweights for nonsmokers, and we could do likewise for smokers. The following graph includes these two regression lines:

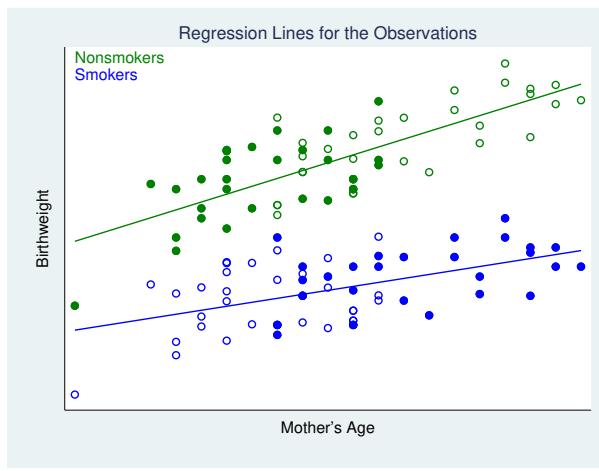


Figure 5

Figure 5 illustrates the principle behind the RA method. We use the green regression line to predict each baby's birthweight assuming the mother did not smoke, and we use the blue regression line to predict each baby's birthweight assuming the mother did smoke. The treatment effect of smoking for a mother of a particular age is the vertical difference between the green and blue regression lines.

The three parameters we mentioned in the introduction are now easy to estimate. For each mother, we obtain two values, say, bw_0 and bw_1 , representing our predictions of her baby's birthweight assuming the mother did not or did smoke, respectively. The means of these variables represent the untreated and treated POMs. The ATE is the sample mean of the difference ($bw_1 - bw_0$), and the ATET is the sample mean of that difference computed using only the mothers who in fact did smoke during pregnancy.

Adding the circles highlights the fact that the average age is higher for smokers than for nonsmokers. Even though the blue and green lines have different slopes, if the average age was the same for smokers and nonsmokers, a difference in the sample means of birthweights could still estimate the true ATE.

Figure 5 lets us address one more issue. Users who are versed in regression analysis may be inclined to estimate the effect of smoking using a regression model for birthweight as a function of smoking and the mother's age. We clearly see in figure 5 that regression lines for smokers and nonsmokers have different slopes—the effect of age on birthweight is not the same for smokers and nonsmokers. In regression analysis, we would therefore include an interaction term between smoking and age. The RA method fits separate regression lines for smokers and nonsmokers, which also handles these differential effects of age on smoking.

Inverse-probability weighting

As we remarked in our discussion of the RA method, we cannot simply use the sample mean birthweights of babies born to smokers and nonsmokers to estimate the effect of smoking. If we did that, we would conflate the negative effect of smoking with the positive effect of age and the positive relationship between age and smoking. IPW is a treatment-effects estimator that uses weighted means rather than simple unweighted means to disentangle the effects of treatment and other confounders like age.

The concept underlying IPW can be gleaned from figure 2, where, as you will recall, the hollow points represent counterfactual outcomes. As we demonstrated in *Defining treatment effects*, we could estimate the average treatment effect if we knew the means of all the nonsmoking outcomes and the means of all the smoking outcomes. In the context of figure 4, we need the mean of all the green points, both solid and hollow, and the mean of all the blue.

If we could observe all of these points, then the ATE would be the difference between those two means. However, the outcomes illustrated by the hollow circles are unobserved. IPW estimators view the hollow circles as missing data and use weights to correct the estimates of the treated and untreated sample means for the missing data. If we calculate the mean nonsmoking birthweight using just the solid green points, that mean is biased downward because we are ignoring the hollow green points, which correspond to higher birthweights.

In IPW, we apply more weight to the solid green points corresponding to older mothers and less weight to those corresponding to younger mothers. Using this weighting scheme will pull up the estimated mean birthweight of babies born to nonsmoking mothers to estimate the true mean of all nonsmoking outcomes. The method for obtaining the mean smoking birthweight is virtually the same: we need to apply more weight to the younger smoking mothers than to the older smoking mothers to better approximate the true mean of all smoking outcomes.

Where do these weights for the weighted means come from? As the name implies, IPW uses the inverse (reciprocal) of the probability of being in the observed treatment group. These probabilities are obtained by modeling the observed treatment as a function of subject characteristics that determine treatment group. In our exposition of the RA method, we focused solely on the mother's age and smoking status as determinants of each baby's birthweight. To make the results comparable, we will use the same model in this example.

We first fit a logistic model of the mother's smoking status, `mbsmoke`, as a function of the mother's age (`mage`):

```
. use https://www.stata-press.com/data/r16/bweightex
(Hypothetical birthweight data)

. logistic mbsmoke mage
Logistic regression                                         Number of obs      =       60
                                                               LR chi2(1)      =     30.45
                                                               Prob > chi2    =     0.0000
                                                               Pseudo R2      =     0.3661

Log likelihood = -26.362201



| mbsmoke            | Odds Ratio | Std. Err. | z     | P> z  | [95% Conf. Interval] |
|--------------------|------------|-----------|-------|-------|----------------------|
| <code>mage</code>  | 1.631606   | .21316    | 3.75  | 0.000 | 1.263022 2.107754    |
| <code>_cons</code> | 7.76e-06   | .0000243  | -3.76 | 0.000 | 1.69e-08 .0035718    |


```

Note: `_cons` estimates baseline odds.

Next, we compute the inverse-probability weights, which we will store in a variable called `ps`. In the IPW method, for subjects who did receive treatment, the weight is equal to the reciprocal of the predicted probability of treatment. For subjects who did not receive treatment, the weight is equal to the reciprocal of the predicted probability of not receiving treatment; the probability of not receiving treatment is just one minus the probability of receiving treatment:

```
. predict ps
(option pr assumed; Pr(mbsmoke))
. replace ps = 1/ps if mbsmoke==1
(30 real changes made)
. replace ps = 1/(1-ps) if mbsmoke==0
(30 real changes made)
```

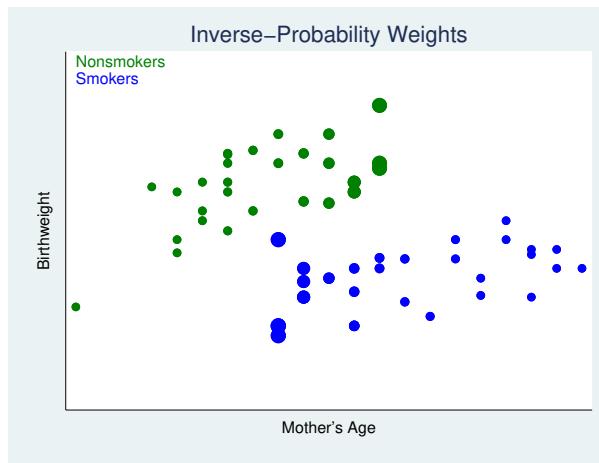


Figure 6

Figure 6 replicates figure 3 with one twist. Rather than making all the points the same size, we have made the size of the points proportional to the IPW variable `ps`. Notice that the largest blue points correspond to the youngest smoking mothers in our sample, so they will receive the most weight when we compute the weighted mean birthweight of babies born to smoking mothers, just as we explained we wanted to do. Similarly, the green points corresponding to older nonsmoking mothers are larger, representing larger weights.

There is a caveat to the IPW estimator. When we fit our logistic or probit model to obtain the predicted probabilities, it is possible that some of the predictions will be close to zero. Because the IPW is the reciprocal of that probability, the weight becomes arbitrarily large as the probability goes to zero. In those cases, the IPW can become unstable. We can improve the estimated IPW by developing a more accurate treatment model. For example, in our dataset, we have other variables such as marital status and the education level of the baby's father that may also help predict whether the mother smoked during pregnancy. We excluded these variables for simplicity, but in a real analysis, we would want to use all relevant data.

This phenomenon of unstable IPWs is related to the concept of overlap, which means that every subject must have a strictly positive probability of obtaining treatment. We remarked that in our sample, we had few young mothers who smoked. As should be clear from [figure 6](#), the overlap assumption is likely to be violated—young mothers do not appear to have a positive probability of being smokers. We would want to check this assumption before proceeding with an IPW analysis. See [\[TE\] teffects overlap](#) and [\[TE\] teffects intro advanced](#) for more information about overlap.

Another limitation of the IPW estimator is that we are using weighted means to estimate the POMs and ATE. Thus, unlike the RA estimator, we cannot obtain subject-level predictions of the treatment effects or potential outcomes, because we do not have the two regression lines that we can use to predict outcomes for each subject.

Doubly robust combinations of RA and IPW

You may have noticed a clear distinction between the RA and IPW estimators. In the case of RA, we built linear regression models to predict the outcomes (birthweights) of each subject but said nothing about how treatment (smoking) arises. In the case of IPW, we built a logistic regression model to predict treatment status but did not build a formal model of the outcome. Doubly robust estimators combine the outcome modeling strategy of RA and the treatment modeling strategy of IPW. These estimators have a remarkable property: although they require us to build two models, we only need to specify one of the two models correctly. If we misspecify the treatment model but correctly specify the outcome model, we still obtain correct estimates of the treatment effect. If we correctly specify the treatment model but misspecify the outcome model, we again will obtain correct estimates of the treatment effect.

Stata's `teffects` command implements two doubly robust estimators, the augmented inverse-probability-weighted (AIPW) estimator and the inverse-probability-weighted regression-adjustment (IPWRA) estimator. These estimators combine elements of RA and IPW to be more robust to misspecification.

The AIPW estimator is an IPW estimator that includes an augmentation term that corrects the estimator when the treatment model is misspecified. When the treatment model is correctly specified, the augmentation term vanishes as the sample size becomes large. Like the IPW, the AIPW does not perform well when the predicted treatment probabilities are too close to zero or one.

The IPWRA estimator is an RA estimator that uses estimated inverse-probability weights to correct the estimator when the regression function is misspecified. When the regression function is correctly specified, the weights do not affect the consistency of the estimator.

Matching

Matching estimators are based on the idea of comparing the outcomes of subjects that are as similar as possible with the sole exception of their treatment status. In our birthweight and smoking example, we could select a mother who smokes and select a mother of the same age who does not smoke and compare the birthweights of their infants. The data of each mother serve as the potential outcome for the other mother.

For a single covariate such as age, identifying a pair of comparable mothers is not difficult. If we have a second covariate that is categorical, such as race, we might still be able to identify pairs of mothers who are the same age and of the same race assuming our dataset is large enough. However, once we consider covariates that are measured on continuous scales or allow for more than a few discrete ones, then finding identical matches is a challenge. The solution is to use what is called a similarity measure, which is a statistic that measures how “close” two observations are. `teffects` offers two methods to find comparable observations based on similarity measures: nearest-neighbor matching and propensity-score matching.

Nearest-neighbor matching (NNM) is accomplished by calculating the “distance” between pairs of observations with regard to a set of covariates and then “matching” each subject to comparable observations that are closest to it. For example, suppose we have a variable that records each subject’s annual income to the penny. Say one subject who received treatment had an income of \$69,234.21. The likelihood that our dataset has an untreated subject who also earned \$69,234.21 is nil. However, we can determine the difference between each untreated subject’s income and our treated subject’s income, then match our treated subject with the untreated subjects whose income differences are smallest. Measuring the distance between subjects when we have multiple covariates is no challenge. By default, `teffects` uses what is known as the Mahalanobis distance, which is really nothing more than the Pythagorean theorem adapted to handle the fact that covariates may be correlated and measured on different scales.

NNM does not use a formal model for either the outcome or the treatment status, but this flexibility comes at a price. When matching on more than one continuous covariate, the NNM estimator must be augmented with a bias-correction term. `teffects nnmatch` uses a linear function of the covariates specified in the `biasadj()` option to remove the large-sample bias.

Propensity-score matching (PSM) is an alternative to NNM. PSM matches on the estimated predicted probabilities of treatment, known as the propensity scores. PSM does not require bias correction, because it uses a model for the treatment. If the treatment model is reasonably well specified, PSM will perform at least as well as NNM; see [TE] [teffects intro advanced](#).

Caveats and assumptions

To use the estimators implemented in `teffects`, we must make several assumptions about the process that generated our data. Different estimators and statistics may require slightly more or slightly less restrictive assumptions and may exhibit varying degrees of robustness to departures from these assumptions, but in general, all the estimators require some form of the following three assumptions.

The independent and identically distributed (i.i.d.) sampling assumption ensures that the outcome and treatment status of each individual are unrelated to the outcome and treatment status of all the other individuals in the population. Correlated data arising from hierarchical or longitudinal study designs do not meet this assumption.

The conditional-independence (CI) assumption means once we control for all observable variables, the potential outcomes are independent of treatment assignment. The easiest way to understand the CI assumption is to understand when it is violated. In our birthweight example, suppose mothers

who did not smoke were more health conscious and consumed better prenatal diets than those who did smoke. Unless we explicitly controlled for health awareness or diet, our model would violate the CI assumption: the mother's decision to smoke or not smoke would not be independent of the baby's birthweight. If we did not control for health awareness, we would overstate the negative impact of smoking on birthweight. Babies born to mothers who smoke weigh less than babies born to nonsmoking mothers not just because of the effects of cigarettes but also because of poorer prenatal diets.

In a study examining the effect of a job-training program, the CI assumption requires that there not be any unobserved factors such as ambition or work ethic that influence both whether a person enrolls in the program and the wage received upon completion. To use the methods implemented by the **teffects** estimators, we must have variables in our dataset that allow us to control for those types of factors.

We mentioned the third assumption, overlap, in our discussions of IPW. More formally, the overlap assumption states that each individual have a positive probability of receiving treatment. In our birthweight example, we noted that there were no observations on young smokers and older nonsmokers. Perhaps we just have an unlucky sample, but to accurately assess the impact of treatment using these methods, we must have overlap to accurately estimate the counterfactual birthweights. In the context of matching estimators, overlap essentially means that we can actually match treated subjects with similar nontreated subjects.

A quick tour of the estimators

The **teffects** command implements six estimators of treatment effects. We introduce each one by showing the basic syntax one would use to apply them to our birthweight example. See each command's entry for more information.

RA

teffects ra implements the RA estimator. We estimate the effect of a mother's smoking behavior (**mbsmoke**) on the birthweight of her child (**bweight**), controlling for marital status (**mmarried**), the mother's age (**mage**), whether the mother had a prenatal doctor's visit in the baby's first trimester (**prenatal1**), and whether this baby is the mother's first child (**fbaby**). We use linear regression (the default) to model **bweight**:

```
. use https://www.stata-press.com/data/r16/cattaneo2  
. teffects ra (bweight mmarried mage prenatal1 fbaby) (mbsmoke)
```

IPW

teffects ipw implements the IPW estimator. Here we estimate the effect of smoking by using a probit model to predict the mother's smoking behavior as a function of marital status, the mother's age, and indicators for first-trimester doctor's visits and firstborn status:

```
. teffects ipw (bweight) (mbsmoke mmarried mage prenatal1 fbaby, probit)
```

IPWRA

`teffects ipwra` implements the IPWRA estimator. We model the outcome, birthweight, as a linear function of marital status, the mother's age, and indicators for first-trimester doctor's visits and firstborn status. We use a logistic model (the default) to predict the mother's smoking behavior, using the same covariates as explanatory variables:

```
. teffects ipwra (bweight mmarried mage prenatal1 fbaby) ///
    (mbsmoke mmarried mage prenatal1 fbaby)
```

AIPW

`teffects aipw` implements the AIPW estimator. Here we use the same outcome- and treatment-model specifications as we did with the IPWRA estimator:

```
. teffects aipw (bweight mmarried mage prenatal1 fbaby) ///
    (mbsmoke mmarried mage prenatal1 fbaby)
```

Nearest-neighbor matching

`teffects nnmatch` implements the NNM estimator. In this example, we match treated and untreated subjects based on marital status, the mother's age, the father's age, and indicators for first-trimester doctor's visits and firstborn status. We use the Mahalanobis distance based on the mother's and father's ages to find matches. We use exact matching on the other three variables to enforce the requirement that treated subjects are matched with untreated subjects who have the same marital status and indicators for first-trimester doctor's visits and firstborn statuses. Because we are matching on two continuous covariates, we request that `teffects nnmatch` include a bias-correction term based on those two covariates:

```
. teffects nnmatch (bweight mage fage) (mbsmoke),           ///
    ematch(prenatal1 mmarried fbaby) biasadj(mage fage)      //
```

Propensity-score matching

`teffects psmatch` implements the PSM estimator. Here we model the propensity score using a probit model, incorporating marital status, the mother's age, and indicators for first-trimester doctor's visits and firstborn status as covariates:

```
. teffects psmatch (bweight) (mbsmoke mmarried mage prenatal1 fbaby, probit)
```

Video examples

[Introduction to treatment effects in Stata, part 1](#)

[Introduction to treatment effects in Stata, part 2](#)

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Also see

[TE] **teffects** — Treatment-effects estimation for observational data

[TE] **teffects intro advanced** — Advanced introduction to treatment effects for observational data

[TE] **teffects multivalued** — Multivalued treatment effects

Description
Also see

Remarks and examples

Acknowledgments

References

Description

This entry provides a technical overview of treatment-effects estimators and their implementation in Stata. Those who are new to treatment-effects estimation may want to instead see [TE] [teffects intro](#).

The `teffects` command estimates average treatment effects (ATEs), average treatment effects among treated subjects (ATETs), and potential-outcome means (POMs) using observational data.

Treatment effects can be estimated using regression adjustment (RA), inverse-probability weights (IPW), and “doubly robust” methods, including inverse-probability-weighted regression adjustment (IPWRA) and augmented inverse-probability weights (AIPW), and via matching on the propensity score or nearest neighbors.

The outcome can be continuous, binary, count, fractional, or nonnegative. Treatments can be binary or multivalued.

Remarks and examples

This entry presents a technical overview of treatment-effects estimators and their implementation in Stata. Users who are new to treatment-effects estimators for observational data should instead read [TE] [teffects intro](#).

Remarks are presented under the following headings:

Introduction
Defining treatment effects
The potential-outcome model
Assumptions needed for estimation
 The CI assumption
 The overlap assumption
 The i.i.d. assumption
Comparing the ATE and ATET
Overview of treatment-effect estimators
RA estimators
IPW estimators
AIPW estimators
IPWRA estimators
Nearest-neighbor matching estimators
Propensity-score matching estimators
Choosing among estimators
Model choice

Introduction

The `teffects` commands estimate treatment effects from observed data. A treatment effect is the change in an outcome caused by a subject, often an individual, getting one treatment instead of another. We cannot estimate individual-level treatment effects, because we only observe each individual getting one or another treatment.

Potential-outcome models provide a solution to this missing-data problem and allow us to estimate the distribution of individual-level treatment effects. A potential-outcome model specifies the potential outcomes that each individual would obtain under each treatment level, the treatment assignment process, and the dependence of the potential outcomes on the treatment assignment process.

When the potential outcomes do not depend on the treatment levels, after conditioning on covariates, regression estimators, inverse-probability-weighted estimators, and matching estimators are commonly used.

What we call the potential-outcome model is also known as the Rubin causal model and the counterfactual model. See Rubin (1974); Holland (1986); Robins (1986); Heckman (1997); Heckman and Navarro-Lozano (2004); Imbens (2004); Cameron and Trivedi (2005, chap. 2.7); Imbens and Wooldridge (2009); and Wooldridge (2010, chap. 21) for more detailed discussions.

For a discussion related to health econometrics, see Deb, Norton, and Manning (2017).

Defining treatment effects

Three parameters are often used to measure treatment effects: the average treatment effect (ATE), the average treatment effect on the treated (ATET), and the potential-outcome means (POMs). In this section, we define each of these terms and introduce the notation and parameters used in the rest of our discussion.

In the binary-treatment case, the two potential outcomes for each individual are y_{0i} and y_{1i} ; y_{0i} is the outcome that would be obtained if i does not get the treatment, and y_{1i} is the outcome that would be obtained if i gets the treatment. y_{0i} and y_{1i} are realizations of the random variables y_0 and y_1 . Throughout this entry, i subscripts denote realizations of the corresponding unsubscripted random variables. We do not discuss multivalued treatments here, because doing so only increases the number of parameters and notation required and detracts from the essential points; see [TE] `teffects multivalued` for information about multivalued treatments.

The parameters of interest summarize the distribution of the unobservable individual-level treatment effect $y_1 - y_0$. In defining the parameters, t denotes a random treatment, t_i denotes the treatment received by individual i , $t = 1$ is the treatment level, and $t = 0$ is the control level. Given this notation, we can now define our parameters of interest.

ATE The ATE is the average effect of the treatment in the population:

$$\text{ATE} = E(y_1 - y_0)$$

POM The POM for treatment level t is the average potential outcome for that treatment level:

$$\text{POM}_t = E(y_t)$$

ATET The ATET is the average treatment effect among those that receive the treatment:

$$\text{ATET} = E(y_1 - y_0 | t = 1)$$

For an illustration of these concepts, see *Defining treatment effects* in [TE] `teffects intro`.

The potential-outcome model

Next we specify a potential-outcome model that serves as a touchstone for the rest of our discussion. The model described here generates data in which y_i is the observed outcome variable, t_i is the treatment variable, \mathbf{x}_i is a vector of covariates that affect the outcome, and \mathbf{w}_i is a vector of covariates that affect the treatment assignment. \mathbf{x}_i and \mathbf{w}_i may have elements in common.

This potential-outcome model specifies that the observed outcome variable y is y_0 when $t = 0$ and that y is y_1 when $t = 1$. Algebraically, we say that

$$y = (1 - t)y_0 + ty_1$$

The functional forms for y_0 and y_1 are

$$y_0 = \mathbf{x}'\beta_0 + \epsilon_0 \quad (1)$$

$$y_1 = \mathbf{x}'\beta_1 + \epsilon_1 \quad (2)$$

where β_0 and β_1 are coefficients to be estimated, and ϵ_0 and ϵ_1 are error terms that are not related to \mathbf{x} or \mathbf{w} . This potential-outcome model separates each potential outcome into a predictable component, $\mathbf{x}\beta_t$, and an unobservable error term, ϵ_t .

The treatment assignment process is

$$t = \begin{cases} 1 & \text{if } \mathbf{w}'\gamma + \eta > 0 \\ 0 & \text{otherwise} \end{cases} \quad (3)$$

where γ is a coefficient vector, and η is an unobservable error term that is not related to either \mathbf{x} or \mathbf{w} . The treatment assignment process is also separated into a predictable component, $\mathbf{w}'\gamma$, and an unobservable error term, η .

We emphasize six points about this model:

1. The observed data from this model contain y_i , t_i , \mathbf{w}_i , and \mathbf{x}_i . The data do not reveal both y_{0i} and y_{1i} for any given i .
2. The model for t determines how the data on y_0 and y_1 are missing.
3. The model separates the potential outcomes and treatment assignment into observable and unobservable components.
4. Whether η is independent of the vector (ϵ_0, ϵ_1) is essential in specifying the set of available estimators.
5. The coefficient vectors β_0 , β_1 , and γ are auxiliary parameters. We use estimates of these coefficient vectors to estimate the ATE, the POMs, and the ATET.
6. For notational simplicity, we represented y_0 and y_1 as linear functions. In practice, we can use other functional forms.

In specifying this potential-outcome model, we explicitly showed the functional forms for the potential outcomes and the treatment assignment process. To ease subsequent discussions, we refer to the set of functional forms for the potential outcomes as the “outcome model”, and we refer to the treatment assignment process as the “treatment model”.

Assumptions needed for estimation

As with any type of estimator, we must make some assumptions to use treatment-effects estimators. The particular assumptions we need for each estimator implemented by `teffects` and for each effect parameter vary, but some version of each of the following is required.

CI The conditional-independence CI assumption restricts the dependence between the treatment model and the potential outcomes.

Overlap The overlap assumption ensures that each individual could receive any treatment level.

i.i.d. The independent and identically distributed (i.i.d.) sampling assumption ensures that the potential outcomes and the treatment status of each individual are unrelated to the potential outcomes and treatment statuses of all other individuals in the population.

We now discuss each assumption in detail.

The CI assumption

After conditioning on covariates, when no unobservable variable affects both treatment assignment and the potential outcomes, the potential outcomes are conditionally independent of the treatment. In epidemiological jargon, there are no unmeasured confounders. In econometric jargon, we have selection on observables. If we observe enough covariates, the potential outcomes may indeed be conditionally independent of the treatment.

Intuitively, the CI assumption says that only the covariates \mathbf{x} affect both the treatment and the potential outcomes. Any other factors that affect the treatment must be independent of the potential outcomes, and any other factors that affect the potential outcomes must be independent of the treatment. Formally, the CI assumption states that, conditional on covariates \mathbf{x} , the treatment t is independent of the vector of potential outcomes $(y_0, y_1)'$.

The CI assumption allows us to estimate the effects by regression-adjustment (RA) methods, inverse-probability-weighting (IPW) methods, methods that combine RA and IPW concepts, and matching methods. The data only reveal information about $E(y_0|\mathbf{x}, \mathbf{w}, t = 0)$ and $E(y_1|\mathbf{x}, \mathbf{w}, t = 1)$, but we are interested in an average of $E(y_0|\mathbf{x}, \mathbf{w})$ and $E(y_1|\mathbf{x}, \mathbf{w})$, where \mathbf{x} represents the outcome covariates and \mathbf{w} the treatment-assignment covariates. The CI assumption allows us to estimate $E(y_0|\mathbf{x}, \mathbf{w})$ and $E(y_1|\mathbf{x}, \mathbf{w})$ directly from the observations for which $E(y_0|\mathbf{x}, \mathbf{w}, t = 0)$ and $E(y_1|\mathbf{x}, \mathbf{w}, t = 1)$, respectively.

For our potential-outcome model presented in (1) through (3), the CI assumption can be viewed as a set of restrictions on the covariance matrix of the error terms. Suppose that the vector of unobservables $(\epsilon_0, \epsilon_1, \eta)$ is normally distributed

$$\begin{pmatrix} \epsilon_0 \\ \epsilon_1 \\ \eta \end{pmatrix} \sim N \left\{ \begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_0^2 & \rho_{01}\sigma_0\sigma_1 & \rho_{\eta 0}\sigma_0 \\ \rho_{01}\sigma_0\sigma_1 & \sigma_1^2 & \rho_{\eta 1}\sigma_1 \\ \rho_{\eta 0}\sigma_0 & \rho_{\eta 1}\sigma_1 & 1 \end{pmatrix} \right\} \quad (4)$$

where σ_0 is the standard deviation of ϵ_0 , ρ_{01} is the correlation between ϵ_0 and ϵ_1 , σ_1 is the standard deviation of ϵ_1 , $\rho_{\eta 0}$ is the correlation between η and ϵ_0 , and $\rho_{\eta 1}$ is the correlation between η and ϵ_1 . As is standard in the normally distributed latent-variable specification of a binary-dependent variable, we normalize the variance of η to 1.

CI specifies that $\rho_{\eta 0} = \rho_{\eta 1} = 0$ so that we can write (4) as

$$\begin{pmatrix} \epsilon_0 \\ \epsilon_1 \\ \eta \end{pmatrix} \sim N \left\{ \begin{pmatrix} 0 \\ 0 \\ 0 \end{pmatrix}, \begin{pmatrix} \sigma_0^2 & \rho_{01}\sigma_0\sigma_1 & 0 \\ \rho_{01}\sigma_0\sigma_1 & \sigma_1^2 & 0 \\ 0 & 0 & 1 \end{pmatrix} \right\}$$

Writing the covariance matrix this way makes clear what we mean by conditional independence: unobserved shocks that affect whether a subject is treated do not have any effect on the potential outcomes, and unobserved shocks that affect a potential outcome do not affect treatment.

The command `teffects` implements estimators that require the CI assumption. See [TE] `etregress` and [TE] `etpoisson` for commands that handle two cases in which the CI assumption is replaced by precise specifications of the joint dependence among the unobservables. Brown and Mergoupi (2011) discuss the `itreatreg` command that extends [TE] `etregress`.

The CI assumption is also known as unconfoundedness and selection-on-observables in the literature. See Rosenbaum and Rubin (1983); Heckman (1997); Heckman and Navarro-Lozano (2004); Cameron and Trivedi (2005, sec. 25.2.1); Tsiatis (2006, sec. 13.3); Angrist and Pischke (2009, chap. 3); Imbens and Wooldridge (2009); and Wooldridge (2010, sec. 21.3). Some discussions with Stata commands can be found in Becker and Caliendo (2007), Nichols (2007), and Daniel, De Stavola, and Cousens (2011).

□ Technical note

In fact, full CI is stronger than what we need to estimate the ATE, the ATET, or the POMs. For the estimators implemented in `teffects`, we only need a conditional mean independence (CMI) assumption. Intuitively, the CMI assumption says that after accounting for the covariates \mathbf{x}_i , the treatment does not affect the conditional mean of each potential outcome. Formally, the CMI requires that $E(y_0|\mathbf{x}, t) = E(y_0|\mathbf{x})$ and that $E(y_1|\mathbf{x}, t) = E(y_1|\mathbf{x})$. The CMI assumption allows the conditional variance to depend on the treatment, while the CI assumption does not.

The CI assumption implies the CMI assumption, but not vice versa.

See Wooldridge (2010, sec. 21.2 and 21.3) for an excellent introduction to this topic, and see Cattaneo, Drukker, and Holland (2013) for some discussion of the multiple treatment case.

□

The overlap assumption

The overlap assumption requires that each individual have a positive probability of receiving each treatment level. Formally, the overlap assumption requires that for each possible \mathbf{x} in the population and each treatment level \tilde{t} , $0 < \Pr(t = \tilde{t}|\mathbf{x}) < 1$. Rosenbaum and Rubin (1983) call the combination of the CI and overlap assumptions strong ignorability; see also Abadie and Imbens (2006, 237–238) and Imbens and Wooldridge (2009).

The i.i.d. assumption

The third of the three assumptions listed above is the i.i.d. assumption; it is the standard assumption of having an i.i.d. sample from the population. In potential-outcome models, i.i.d. sampling implies that the potential outcomes and treatment status of each individual are unrelated to the potential outcomes and treatment statuses of all the other individuals in the population. I.i.d. sampling rules out interactions among the individuals. For instance, models of vaccinations in epidemiology and general

equilibrium effects in economics violate the independence assumption. This third assumption is a part of what is known as the stable unit treatment value assumption (SUTVA); see [Wooldridge \(2010, 905\)](#) and [Imbens and Wooldridge \(2009\)](#).

Comparing the ATE and ATET

When comparing the ATE and the ATET, two points should be mentioned.

First, the assumptions required to estimate the ATET are less restrictive than the assumptions required to estimate the ATE. Estimating the ATET requires a weaker form of the CI assumption and a weaker version of the overlap assumption.

To estimate the ATE under CI, we require that the unobservables in the treatment model be conditionally independent of the unobservables in both potential outcomes. In contrast, we can estimate the ATET under CI when the unobservables in the treatment model are conditionally independent of just the control-level potential outcome; see [Wooldridge \(2010, 906–912\)](#).

Although the ATE version of overlap requires that all covariate patterns have a positive probability of being allocated to each treatment state, we can estimate the ATET when only the covariate patterns for which someone is treated have a positive probability of being allocated to each treatment state. This weaker overlap assumption can be important in some studies. For example, [Heckman \(1997\)](#) discusses how the ATET makes sense in job-training programs for which many types of individuals have zero chance of signing up. See also [Wooldridge \(2010, 911–913\)](#).

Second, the ATET reduces to the ATE when the mean of the covariates among the treated is the same as the mean of the covariates in the population and when the average contribution from the unobservables for the participants is zero.

Overview of treatment-effect estimators

We can classify the estimators implemented by `teffects` into five categories: 1) estimators based on a model for the outcome variable; 2) estimators based on a model for treatment assignment; 3) estimators based on models for both the outcome variable and the treatment assignment; 4) estimators that match on covariates; and 5) estimators that match on predicted probabilities of treatment. Within each category of estimator, there is a variety of choices about the functional forms for the models.

Because there are several categories of estimators, the user must decide whether to model the outcomes, the probability of treatment, or both. Under correct model specification, using an outcome model and a model for the probability of treatment will produce more efficient estimates. Surprisingly, some of the estimators that use both models only require that one of the two be correctly specified to consistently estimate the effects of interest, a property known as the double-robust property.

With the exception of using a matching estimator with a single continuous covariate, some choice of functional forms is required. There are two aspects one must consider when choosing the functional form for the outcome or treatment assignment. First, one must select the functional form for the conditional mean or conditional probability; depending on the variable being modeled, a linear, a binary choice, or an exponential model may be appropriate. Second, one must determine the appropriate polynomials of the covariates to include in the model. `teffects` offers a wide variety of options to specify different functional form choices for the conditional mean and conditional probability models. The factor variable notation in Stata allows us to easily specify the desired polynomial in the covariates.

We now provide some intuition behind each type of estimator.

RA estimators

RA estimators use means of predicted outcomes for each treatment level to estimate each POM. ATEs and ATETs are differences in estimated POMs.

The CI assumption implies that we can estimate $E(y_0|\mathbf{x})$ and $E(y_1|\mathbf{x})$ directly from the observations for which $t = 0$ and $t = 1$, respectively. Regression adjustment fits separate regressions for each treatment level and uses averages of the predicted outcomes over all the data to estimate the POMs. The estimated ATEs are differences in the estimated POMs. The estimated ATETs are averages of the predicted outcomes over the treated observations.

RA is a venerable estimator. See [Lane and Nelder \(1982\)](#); [Cameron and Trivedi \(2005, chap. 25\)](#); [Wooldridge \(2010, chap. 21\)](#); and [Vittinghoff et al. \(2012, chap. 9\)](#). The usefulness of RA has been periodically questioned in the literature because it relies on specifying functional forms for the conditional means and because it requires having sufficient observations of each covariate pattern in each treatment level; see [Rubin \(1973\)](#) for an early salvo. Our experience is that RA is an exceptionally useful base-case estimator. We describe its relative advantages and disadvantages in the course of covering other estimators.

IPW estimators

IPW estimators use weighted averages of the observed outcome variable to estimate means of the potential outcomes. The weights account for the missing data inherent in the potential-outcome framework. Each weight is the inverse of the estimated probability that an individual receives a treatment level. Outcomes of individuals who receive a likely treatment get a weight close to one. Outcomes of individuals who receive an unlikely treatment get a weight larger than one, potentially much larger.

IPW estimators model the probability of treatment without any assumptions about the functional form for the outcome model. In contrast, RA estimators model the outcome without any assumptions about the functional form for the probability of treatment model.

IPW estimators become extremely unstable as the overlap assumption gets close to being violated. When the overlap assumption is nearly violated, some of the inverse-probability weights become very large, IPW estimators produce erratic estimates, and the large-sample distribution provides a poor approximation to the finite-sample distribution of IPW estimators. This instability occurs even though the functional form for the treatment model is correctly specified.

In contrast, when the overlap assumption is nearly violated, there are very few observations in a treatment level for some covariate patterns, so RA estimators use the model to predict in regions in which there are very little data. If the model is well specified and there are “enough” observations, an RA estimator will not become unstable as quickly as an IPW estimator, and the large-sample distribution of the RA estimator still provides a good approximation to the finite-sample distribution. However, in real situations in which “all models are approximate”, relying on a correctly specified outcome model with little data is extremely risky.

IPW estimators are a general approach to missing-data problems that obey some CI assumptions. While IPW is an old idea in statistics that dates back to [Horvitz and Thompson \(1952\)](#), biostatisticians and econometricians have been actively working on extending it to handle modern problems and estimation methods. See [Robins and Rotnitzky \(1995\)](#); [Robins, Rotnitzky, and Zhao \(1994, 1995\)](#); and [Wooldridge \(2002, 2007\)](#). IPW has been used extensively in the modern treatment-effect estimation literature. See [Imbens \(2000\)](#); [Hirano, Imbens, and Ridder \(2003\)](#); [Tan \(2010\)](#); [Wooldridge \(2010, chap. 19\)](#); [van der Laan and Robins \(2003\)](#); and [Tsiatis \(2006, chap. 6\)](#).

To see the intuition behind IPW, consider a study with observed outcome variable y , treatment variable $t \in \{0, 1\}$, and potential outcomes y_0 and y_1 . As part of this process, we need to estimate

the POM for treatment $t = 1$, $E(y_1)$. Using the observed data, $y_i t_i$ is y_{1i} when $t = 1$, but y_{1i} is unobserved when $t = 0$. An IPW estimator for $E(y_1)$ is $1/N \sum_{i=1}^N y_i t_i / p(\mathbf{x}_i)$, where $p(\mathbf{x}_i)$ is the probability that $t_i = 1$ and is a function of the covariates \mathbf{x}_i . If y_{1i} were always observed, the weights would all equal 1. This IPW estimator places a larger weight on those observations for which y_{1i} is observed even though its observation was not likely.

AIPW estimators

Instead of modeling either the outcome, like RA, or the treatment probability, like IPW, augmented inverse-probability-weighted (AIPW) estimators model both the outcome and the treatment probability. A surprising fact is that only one of the two models must be correctly specified to consistently estimate the treatment effects, a property of the AIPW estimators known as being “doubly robust”. Given that two models instead of one are used, it is less surprising that the AIPW estimators can be more efficient than either the RA or the IPW estimators, though deriving this result is rather technical and relies on the theory of semiparametric estimators.

Intuitively, the AIPW estimator is an IPW that includes an augmentation term that corrects the estimator when the treatment model is misspecified. When the treatment is correctly specified, the augmentation term vanishes as the sample size becomes large. Like the IPW, the AIPW does not perform well when the predicted treatment probabilities are too close to zero or one.

AIPW estimators emerge naturally from a technique of producing more efficient estimators from estimators that have a few main parameters of interest and some auxiliary, or nuisance, parameters used in estimating the few main parameters. This method constructs efficient estimating equations for the main parameters that are orthogonal to the auxiliary parameters. The estimators produced by this method are known as efficient-influence function (EIF) estimators.

To gain some intuition, consider finding an EIF estimator from an IPW estimator for two POMs. Note that we only care about the two POM parameters and not about the many auxiliary parameters used to estimate the treatment probabilities. EIF estimators project the equations that yield the POM parameters onto the equations that yield the auxiliary treatment-model parameters and then use the residuals from this projection to estimate the POM parameters.

We refer to these estimators as “AIPW estimators” instead of “EIF estimators” because the former is commonly used in the biostatistical literature for some of the binary-treatment estimators and because the term “augmented inverse-probability-weighted” tells more about how these estimators relate to the other implemented estimators; see [Tsiatis \(2006\)](#) and [Tan \(2010\)](#). The estimators implemented in `teffects aipw` with the `wnls` option are based on those of [Rubin and van der Laan \(2008\)](#), which did well in simulations reported by [Tan \(2010\)](#), and denoted as $\tilde{\alpha}_{RV}(\hat{\pi})$ in [Tan \(2010, 663\)](#).

When either the outcome model or the treatment model is well specified, the AIPW estimators implemented in `teffects aipw` are more robust than either the RA or the IPW estimators because the AIPW estimators are doubly robust but the RA and IPW estimators are not. When both the outcome and the treatment model are misspecified, which estimator is more robust is a matter of debate in the literature; see [Kang and Schafer \(2007\)](#) and [Robins et al. \(2007\)](#) for some debate, and see [Tan \(2010\)](#) for a more recent discussion.

To the best of our knowledge, there is no general solution to the question of which estimator performs best when both the outcome and the treatment models are misspecified. We suspect that the answer depends on the true models, the implemented specifications, and the polynomials in the covariates used. To help users through this process, the estimators implemented in `teffects` offer many functional forms to approximate either the outcome process or the treatment process. In addition, Stata’s factor-variable notation makes it easy to include polynomials in the covariates. Both of these approximation methods rely on having enough data. `teffects` also makes it easy to compare the results produced by different estimators.

The literature on these methods is vast and growing. For double-robust results and explanations, see [Robins and Rotnitzky \(1995\)](#); [Robins, Rotnitzky, and Zhao \(1995\)](#); [van der Laan and Robins \(2003, chap. 6\)](#); [Bang and Robins \(2005\)](#); [Tsiatis \(2006, chap. 13\)](#); [Wooldridge \(2007; 2010, sec. 21.3.4\)](#); and [Tan \(2010\)](#).

IPWRA estimators

Like AIPW estimators, inverse-probability-weighted regression-adjustment (IPWRA) estimators combine models for the outcome and treatment status; also like AIPW estimators, IPWRA estimators are doubly robust. IPWRA estimators emerge naturally from a robust approach to missing-data methods. IPWRA estimators use the inverse of the estimated treatment-probability weights to estimate missing-data-corrected regression coefficients that are subsequently used to compute the POMs.

As far as we know, there is no literature that compares the relative efficiency of AIPW estimators, which emerge from a general approach to creating efficient estimators, and the IPWRA estimators, which emerge from a robust-correction approach to missing-data analysis.

The IPWRA estimators are also known as “Wooldridge’s double-robust” estimators because they were derived in [Wooldridge \(2007\)](#) and discussed at length in [Wooldridge \(2010, section 21.3.4\)](#).

Nearest-neighbor matching estimators

Matching estimators use an average of the outcomes of the nearest individuals to impute the missing potential outcome for each sampled individual. The difference between the observed outcome and the imputed potential outcome is an estimate of the individual-level treatment effect. These estimated individual-level treatment effects are averaged to estimate the ATE or the ATET.

`teffects nnmatch` determines the “nearest” by using a weighted function of the covariates for each observation. This type of matching is known as nearest-neighbor matching (NNM). `teffects psmatch` determines the “nearest” by using the estimated treatment probabilities, which are known as the propensity scores. This second type of matching is known as propensity-score matching (PSM).

NNM is nonparametric in that no explicit functional form for either the outcome model or the treatment model is specified. This flexibility comes at a price; the estimator needs more data to get to the true value than an estimator that imposes a functional form. More formally, the NNM estimator converges to the true value at a rate slower than the parametric rate, which is the square root of the sample size, when matching on more than one continuous covariate. `teffects nnmatch` uses bias correction to fix this problem. PSM provides an alternative to bias correction because it matches on a single continuous covariate, the estimated treatment probabilities.

[Abadie and Imbens \(2006, 2011\)](#) derived the rate of convergence of the NNM estimator and the bias-corrected NNM estimator and the large-sample distributions of the NNM and the bias-corrected NNM estimators. These articles provided the formal results that built on methods suggested in [Rubin \(1973, 1977\)](#).

`teffects nnmatch` is based on the results in [Abadie and Imbens \(2006, 2011\)](#) and a previous implementation in [Abadie et al. \(2004\)](#).

Propensity-score matching estimators

Instead of performing bias correction to handle the case of more than one continuous covariate, a common solution is to combine all the covariate information into estimated treatment probabilities, known as propensity scores, and use this single continuous covariate as the matching variable.

The term “propensity score” is widely used, but we continue to refer to it as the “treatment probability” to be consistent with the other estimators. We call the estimator that matches on the estimated treatment probabilities the “propensity-score matching (PSM) estimator” because the latter term is ubiquitous.

In effect, the PSM estimator parameterizes the bias-correction term in the treatment probability model. One advantage of matching on the estimated treatment probabilities over the bias-correction method is that one can explore the fit of different treatment probability models using standard methods before performing the nonparametric matching. For example, one can select the treatment model by minimizing an information criterion under i.i.d. sampling. We know of no counterpart for selecting the proper order of the bias-correction term for the NNM estimator.

Matching on estimated treatment probability models has been very popular since [Rosenbaum and Rubin \(1983\)](#) showed that if adjusting for covariates x_i is sufficient to estimate the effects, then one can use the probability of treatment to perform the adjustment. [Abadie and Imbens \(2012\)](#) derived a method to estimate the standard errors of the estimator that matches on estimated treatment probabilities, and this method is implemented in `teffects psmatch`.

Choosing among estimators

There is no definitive way to select one of the estimators implemented in `teffects` over the others. We offer three observations about the tradeoffs among the estimators.

First, if the outcome model is correctly specified, the RA estimator will break down more slowly than the IPW, AIPW, IPWRA, or PSM estimators as the overlap assumption begins to fail. This result depends critically on the ability of the RA estimator to predict into regions in which there are little data.

Second, if the overlap assumption holds, the AIPW and IPWRA estimators have the double-robust property for some functional form combinations. The double-robust property says that if either the outcome model or the treatment model is correctly specified, we can consistently estimate the effects. The properties of double-robust estimators when both models are misspecified are not known, although there is some discussion in the literature about the properties of the AIPW estimators; see [Kang and Schafer \(2007\)](#), [Robins et al. \(2007\)](#), and [Tan \(2010\)](#).

Third, all the estimators require the same assumptions, so if each is correctly specified, they should all produce similar results. Of course, just because they produce similar results does not mean that they are correctly specified; it is possible that they are just behaving similarly in response to some underlying problem.

Model choice

`teffects` offers a broad selection of functional form combinations so that you can choose a combination that fits your data. Picking a functional form that respects the values of the observed outcomes is usually best. Select `linear` for continuous outcomes over the real line; `logit`, `probit`, or `hetprobit` for binary outcomes; and `poisson` for counts or nonnegative outcomes.

For binary treatments, you can select among `logit`, `probit`, or `hetprobit` models. For multivalued treatments, only the multinomial logit is available to model the treatment probabilities.

Selecting a functional form of a given set of covariates is a famously difficult problem in statistics. In the treatment-effects context, Cattaneo, Drukker, and Holland (2013) found that model selection by minimizing an information criterion worked well. Cattaneo, Drukker, and Holland (2013) discuss a method and a community-contributed command to facilitate the process.

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Also see

[TE] **teffects** — Treatment-effects estimation for observational data

[TE] **teffects intro** — Introduction to treatment effects for observational data

[TE] **teffects multivalued** — Multivalued treatment effects

teffects aipw — Augmented inverse-probability weighting

Description	Quick start	Menu	Syntax
Options	Remarks and examples	Stored results	Methods and formulas
References	Also see		

Description

teffects aipw estimates the average treatment effect (ATE) and the potential-outcome means (POMs) from observational data by augmented inverse-probability weighting (AIPW). AIPW estimators combine aspects of regression-adjustment and inverse-probability-weighted methods. AIPW estimators have the double-robust property. **teffects aipw** accepts a continuous, binary, count, fractional, or nonnegative outcome and allows a multivalued treatment.

See [TE] **teffects intro** or [TE] **teffects intro advanced** for more information about estimating treatment effects from observational data.

Quick start

ATE of binary treatment `treat2` by AIPW using a linear model for outcome `y1` on `x1` and `x2` and a logistic model for `treat2` on `x1` and `w`

```
teffects aipw (y1 x1 x2) (treat2 x1 w)
```

As above, but use a fractional logistic model for fractional outcome `y2`

```
teffects aipw (y2 x1 x2, flogit) (treat2 x1 w)
```

As above, but use a heteroskedastic probit model for binary outcome `y3` and a probit model for `treat2`

```
teffects aipw (y3 x1 x2, hetprobit(x1 x2)) (treat2 x1 w, probit)
```

ATE for each level of three-valued treatment `treat3` on `y1`

```
teffects aipw (y1 x1 x2) (treat3 x1 w)
```

As above, and specify that `treat3 = 3` is the control level

```
teffects aipw (y1 x1 x2) (treat3 x1 w), control(3)
```

Same as above, specified using the label “MyControl” corresponding to `treat3 = 3`

```
teffects aipw (y1 x1 x2) (treat3 x1 w), control(MyControl)
```

Menu

Statistics > Treatment effects > Continuous outcomes > Augmented inverse-probability weighting

Statistics > Treatment effects > Binary outcomes > Augmented inverse-probability weighting

Statistics > Treatment effects > Count outcomes > Augmented inverse-probability weighting

Statistics > Treatment effects > Fractional outcomes > Augmented inverse-probability weighting

Statistics > Treatment effects > Nonnegative outcomes > Augmented inverse-probability weighting

Syntax

```
teffects aipw (ovar omvarlist [ , omodel noconstant ] )
    (tvar tmvarlist [ , tmodel noconstant ] ) [if] [in] [weight]
    [ , stat options ]
```

ovar is a binary, count, continuous, fractional, or nonnegative outcome of interest.

omvarlist specifies the covariates in the outcome model.

tvar must contain integer values representing the treatment levels.

tmvarlist specifies the covariates in the treatment-assignment model.

<i>omodel</i>	Description
---------------	-------------

Model

<code>linear</code>	linear outcome model; the default
<code>logit</code>	logistic outcome model
<code>probit</code>	probit outcome model
<code>hetprobit</code> (<i>varlist</i>)	heteroskedastic probit outcome model
<code>poisson</code>	exponential outcome model
<code>flogit</code>	fractional logistic outcome model
<code>fprobit</code>	fractional probit outcome model
<code>fhetprobit</code> (<i>varlist</i>)	fractional heteroskedastic probit outcome model

omodel specifies the model for the outcome variable.

<i>tmodel</i>	Description
---------------	-------------

Model

<code>logit</code>	logistic treatment model; the default
<code>probit</code>	probit treatment model
<code>hetprobit</code> (<i>varlist</i>)	heteroskedastic probit treatment model

tmodel specifies the model for the treatment variable.

For multivalued treatments, only `logit` is available and multinomial logit is used.

<i>stat</i>	Description
-------------	-------------

Stat

<code>ate</code>	estimate average treatment effect in population; the default
<code>pomeans</code>	estimate potential-outcome means

<i>options</i>	Description
Model	
nls	estimate conditional means by nonlinear least squares
wnls	estimate conditional means by weighted nonlinear least squares
SE/Robust	
vce (<i>vcetype</i>)	<i>vcetype</i> may be robust , cluster <i>clustvar</i> , bootstrap , or jackknife
Reporting	
level (#)	set confidence level; default is level(95)
aequations	display auxiliary-equation results
display_options	control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling
Maximization	
maximize_options	control the maximization process; seldom used
Advanced	
pstolerance (#)	set tolerance for overlap assumption
osample (<i>newvar</i>)	<i>newvar</i> identifies observations that violate the overlap assumption
control (# <i>label</i>)	specify the level of <i>tvar</i> that is the control
coeflegend	display legend instead of statistics

omvarlist and *tmvarlist* may contain factor variables; see [U] 11.4.3 Factor variables.

bootstrap, **by**, **jackknife**, and **statsby** are allowed; see [U] 11.1.10 Prefix commands.

Weights are not allowed with the **bootstrap** prefix; see [R] **bootstrap**.

fweights and **iweights** are allowed; see [U] 11.1.6 weight.

coeflegend does not appear in the dialog box.

See [U] 20 Estimation and postestimation commands for more capabilities of estimation commands.

Options

Model

noconstant; see [R] **Estimation options**.

nls specifies that the parameters of the outcome model be estimated by nonlinear least squares instead of the default maximum likelihood.

wnls specifies that the parameters of the outcome model be estimated by weighted nonlinear least squares instead of the default maximum likelihood. The weights make the estimator of the effect parameters more robust to a misspecified outcome model.

Stat

stat is one of two statistics: **ate** or **pomeans**. **ate** is the default.

ate specifies that the average treatment effect be estimated.

pomeans specifies that the potential-outcome means for each treatment level be estimated.

SE/Robust

`vce(vcetype)` specifies the type of standard error reported, which includes types that are robust to some kinds of misspecification (`robust`), that allow for intragroup correlation (`cluster clustvar`), and that use bootstrap or jackknife methods (`bootstrap`, `jackknife`); see [R] [vce_option](#).

Reporting

`level(#)`; see [R] [Estimation options](#).

`aequations` specifies that the results for the outcome-model or the treatment-model parameters be displayed. By default, the results for these auxiliary parameters are not displayed.

`display_options`: `noci`, `nopvalues`, `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `nofvlabel`, `fwwrap(#)`, `fwrapon(style)`, `cformat(%fmt)`, `pformat(%fmt)`, `sformat(%fmt)`, and `nolstretch`; see [R] [Estimation options](#).

Maximization

`maximize_options`: `iterate(#)`, `[no]log`, and `from(init_specs)`; see [R] [Maximize](#). These options are seldom used.

`init_specs` is one of

```
matname [, skip copy]
# [, # ...], copy
```

Advanced

`pstolerance(#)` specifies the tolerance used to check the overlap assumption. The default value is `pstolerance(1e-5)`. `teffects` will exit with an error if an observation has an estimated propensity score smaller than that specified by `pstolerance()`.

`osample(newvar)` specifies that indicator variable `newvar` be created to identify observations that violate the overlap assumption.

`control(#|label)` specifies the level of `tvar` that is the control. The default is the first treatment level. You may specify the numeric level `#` (a nonnegative integer) or the label associated with the numeric level. `control()` may not be specified with statistic `pomeans`.

The following option is available with `teffects aipw` but is not shown in the dialog box: `coeflegend`; see [R] [Estimation options](#).

Remarks and examples

Remarks are presented under the following headings:

[Overview](#)

[Video example](#)

Overview

AIPW estimators use inverse-probability weights to correct for the missing-data problem arising from the fact that each subject is observed in only one of the potential outcomes; these estimators also use an augmentation term in the outcome model to correct the estimator in case the treatment model is misspecified. If the treatment model is correctly specified, the augmentation term goes to zero in large samples.

AIPW estimators compute averages of the augmented inverse-probability-weighted outcomes for each treatment level. Contrasts of these averages provide estimates of the treatment effects.

AIPW estimators use a model to predict treatment status, and they use another model to predict outcomes. Because of the double-robust property, only one of these two models must be correctly specified for the AIPW estimator to be consistent.

AIPW estimators use a three-step approach to estimating treatment effects:

1. They estimate the parameters of the treatment model and compute inverse-probability weights.
2. They estimate separate regression models of the outcome for each treatment level and obtain the treatment-specific predicted outcomes for each subject.
3. They compute the weighted means of the treatment-specific predicted outcomes, where the weights are the inverse-probability weights computed in step 1. The contrasts of these weighted averages provide the estimates of the ATEs.

These steps produce consistent estimates of the effect parameters because the treatment is assumed to be independent of the potential outcomes after conditioning on the covariates. The overlap assumption ensures that predicted inverse-probability weights do not get too large. The standard errors reported by **teffects aipw** correct for the three-step process. See [TE] **teffects intro** or [TE] **teffects intro advanced** for more information about this estimator.

We will illustrate the use of **teffects aipw** by using data from a study of the effect of a mother's smoking status during pregnancy (**mbsmoke**) on infant birthweight (**bweight**) as reported by Cattaneo (2010). This dataset also contains information about each mother's age (**mage**), education level (**medu**), marital status (**mmarried**), whether the first prenatal exam occurred in the first trimester (**prenatal1**), and whether this baby was the mother's first birth (**fbaby**).

▷ Example 1: Estimating the ATE

We begin by using **teffects aipw** to estimate the average treatment effect of **mbsmoke** on **bweight**. We use a probit model to predict treatment status as a function of **mmarried**, **mage**, and **fbaby**; to maximize the predictive power of this model, we use factor-variable notation to incorporate quadratic effects of the mother's age, the only continuous covariate in our model. We use linear regression to model birthweight, using **prenatal1**, **mmarried**, **mage**, and **fbaby** as explanatory variables. We type

<pre>. use https://www.stata-press.com/data/r16/cattaneo2 (Excerpt from Cattaneo (2010) Journal of Econometrics 155: 138-154) . teffects aipw (bweight prenatal1 mmarried mage fbaby) > (mbsmoke mmarried c.mage##c.mage fbaby medu, probit) Iteration 0: EE criterion = 4.629e-21 Iteration 1: EE criterion = 1.944e-25 Treatment-effects estimation Number of obs = 4,642 Estimator : augmented IPW Outcome model : linear by ML Treatment model: probit</pre>						
<hr/>						
bweight	Robust Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
ATE mbsmoke (smoker vs nonsmoker)	-230.9892	26.21056	-8.81	0.000	-282.361	-179.6174
P0mean mbsmoke nonsmoker	3403.355	9.568472	355.68	0.000	3384.601	3422.109

The average birthweight if all mothers were to smoke would be 231 grams less than the average of 3,403 grams that would occur if none of the mothers had smoked.

□

By default, `teffects aipw` reports the ATE and the POM for the base (untreated) subjects. The `pomeans` option allows us to view the treated subjects' POM as well; the `aequations` option displays the regression model coefficients used to predict the POMs as well as the coefficients from the model used to predict treatment.

▷ Example 2: Displaying the POMs and equations

Here we use the `pomeans` and `aequations` options to obtain estimates of both POMs and view all the fitted equations underlying our estimates:

```
. teffects aipw (bweight prenatal1 mmarried mage fbaby)
> (mbsmoke mmarried c.mage##c.mage fbaby medu, probit), pomeans aequations
Iteration 0: EE criterion = 4.629e-21
Iteration 1: EE criterion = 6.856e-26
Treatment-effects estimation
Number of obs      = 4,642
Estimator          : augmented IPW
Outcome model      : linear by ML
Treatment model: probit
```

bweight	Robust	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
P0means						
mbsmoke						
nonsmoker	3403.355	9.568472	355.68	0.000	3384.601	3422.109
smoker	3172.366	24.42456	129.88	0.000	3124.495	3220.237
OME0						
prenatal1	64.40859	27.52699	2.34	0.019	10.45669	118.3605
mmarried	160.9513	26.6162	6.05	0.000	108.7845	213.1181
mage	2.546828	2.084324	1.22	0.222	-1.538373	6.632028
fbaby	-71.3286	19.64701	-3.63	0.000	-109.836	-32.82117
_cons	3202.746	54.01082	59.30	0.000	3096.886	3308.605
OME1						
prenatal1	25.11133	40.37541	0.62	0.534	-54.02302	104.2457
mmarried	133.6617	40.86443	3.27	0.001	53.5689	213.7545
mage	-7.370881	4.21817	-1.75	0.081	-15.63834	.8965804
fbaby	41.43991	39.70712	1.04	0.297	-36.38461	119.2644
_cons	3227.169	104.4059	30.91	0.000	3022.537	3431.801
TME1						
mmarried	-.6484821	.0554173	-11.70	0.000	-.757098	-.5398663
mage	.1744327	.0363718	4.80	0.000	.1031452	.2457202
c.mage#						
c.mage	-.0032559	.0006678	-4.88	0.000	-.0045647	-.0019471
fbaby	-.2175962	.0495604	-4.39	0.000	-.3147328	-.1204595
medu	-.0863631	.0100148	-8.62	0.000	-.1059917	-.0667345
_cons	-1.558255	.4639691	-3.36	0.001	-2.467618	-.6488926

The coefficient table indicates that the treated POM is 3,172 grams, 231 grams less than the untreated POM. The sections of the table labeled OME0 and OME1 represent the linear regression coefficients for the untreated and treated potential-outcome equations, respectively. The coefficients of the TME1 equation are used in the probit model to predict treatment status. □

As is well known, the standard probit model assumes that the error terms in the latent-utility framework are homoskedastic; the model is not robust to departures from this assumption. An alternative is to use the heteroskedastic probit model, which explicitly models the error variance as a function of a set of variables.

► Example 3: Heteroskedastic probit treatment model

Here we refit our model as in the previous examples, but we instead use heteroskedastic probit to model the treatment variable. We posit that the heteroskedasticity is a function of the mother's age. We type

```
. teffects aipw (bweight prenatal1 mmarried fbaby)
> (mbsmoke mmarried c.mage##c.mage fbaby medu, hetprobit(c.mage)), aequations
Iteration 0:  EE criterion =  1.746e-19
Iteration 1:  EE criterion =  1.746e-19  (backed up)

Treatment-effects estimation                               Number of obs      =     4,642
Estimator        : augmented IPW
Outcome model   : linear by ML
Treatment model: heteroskedastic probit
```

bweight	Robust					
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
ATE						
mbsmoke (smoker vs nonsmoker)	-230.2699	27.49461	-8.38	0.000	-284.1584	-176.3815
P0mean						
mbsmoke nonsmoker	3403.657	9.540713	356.75	0.000	3384.957	3422.356
OME0						
prenatal1	69.5048	27.04642	2.57	0.010	16.49479	122.5148
mmarried	173.74	24.63865	7.05	0.000	125.4491	222.0308
fbaby	-79.19473	18.62584	-4.25	0.000	-115.7007	-42.68875
_cons	3260.768	28.29282	115.25	0.000	3205.315	3316.221
OME1						
prenatal1	12.86437	39.83916	0.32	0.747	-65.21894	90.94768
mmarried	113.3491	39.47422	2.87	0.004	35.9811	190.7172
fbaby	64.22326	38.42042	1.67	0.095	-11.07939	139.5259
_cons	3051.268	37.30413	81.79	0.000	2978.153	3124.383
TME1						
mmarried	-.3551755	.1044199	-3.40	0.001	-.5598347	-.1505162
mage	.0831898	.0349088	2.38	0.017	.0147699	.1516097
c.mage# c.mage	-.0013458	.0006659	-2.02	0.043	-.002651	-.0000406
fbaby	-.1170697	.044998	-2.60	0.009	-.2052643	-.0288752
medu	-.0435057	.0147852	-2.94	0.003	-.0724842	-.0145272
_cons	-.8757021	.347814	-2.52	0.012	-1.557405	-.1939993
TME1_lnsigma						
mage	-.0236336	.0107134	-2.21	0.027	-.0446315	-.0026357

The equation labeled TME1_lnsigma represents the heteroskedasticity function used to model the logarithm of the variance. Because the coefficient on the single variable we specified is significant below the 5% level, we conclude that allowing for heteroskedasticity was indeed necessary. ◁

Rather than using maximum likelihood to fit the outcome model, you can instruct `teffects aipw` to use a weighted nonlinear least-squares (WNLS) estimator instead. The WNLS estimator may be more robust to outcome model misspecification.

► Example 4: Using the WNLS estimator

Here we use WNLS to fit our outcome model:

Treatment-effects estimation							Number of obs	=	4,642
	bweight	Coef.	Robust Std. Err.	z	P> z	[95% Conf. Interval]			
ATE									
ATE	mbsmoke (smoker vs nonsmoker)	-227.1956	27.34794	-8.31	0.000	-280.7966	-173.5946		
P0mean									
P0mean	mbsmoke nonsmoker	3403.251	9.596622	354.63	0.000	3384.442	3422.06		

The ATE of -227 is slightly greater than the ATE of -231 estimated in [example 1](#). The estimated POMs are nearly indistinguishable.



Video example

Treatment effects: Augmented inverse-probability weighting

Stored results

`teffects aipw` stores the following in `e()`:

Scalars

<code>e(N)</code>	number of observations
<code>e(nj)</code>	number of observations for treatment level j
<code>e(N_clust)</code>	number of clusters
<code>e(k_eq)</code>	number of equations in <code>e(b)</code>
<code>e(k_levels)</code>	number of levels in treatment variable
<code>e(treated)</code>	level of treatment variable defined as treated
<code>e(control)</code>	level of treatment variable defined as control
<code>e(converged)</code>	1 if converged, 0 otherwise

Macros

<code>e(cmd)</code>	<code>teffects</code>
<code>e(cmdline)</code>	command as typed
<code>e(depvar)</code>	name of outcome variable
<code>e(tvar)</code>	name of treatment variable
<code>e(subcmd)</code>	<code>aipw</code>
<code>e(tmodel)</code>	<code>logit, probit, or hetprobit</code>
<code>e(omodel)</code>	<code>linear, logit, probit, hetprobit, poisson, flogit, fprobit, or fhetprobit</code>
<code>e(stat)</code>	statistic estimated, <code>ate</code> or <code>pomeans</code>
<code>e(wtype)</code>	weight type
<code>e(wexp)</code>	weight expression
<code>e(title)</code>	title in estimation output
<code>e(clustvar)</code>	name of cluster variable
<code>e(tlevels)</code>	levels of treatment variable
<code>e(cme)</code>	<code>ml, nls, or wnl</code>
<code>e(vce)</code>	<code>vcetype</code> specified in <code>vce()</code>
<code>e(vcetype)</code>	title used to label Std. Err.
<code>e(properties)</code>	<code>b V</code>
<code>e(estat_cmd)</code>	program used to implement <code>estat</code>
<code>e(predict)</code>	program used to implement <code>predict</code>
<code>e(marginsnotok)</code>	predictions disallowed by <code>margins</code>
<code>e(asbalanced)</code>	factor variables <code>fvset</code> as <code>asbalanced</code>
<code>e(asobserved)</code>	factor variables <code>fvset</code> as <code>asobserved</code>

Matrices

<code>e(b)</code>	coefficient vector
<code>e(V)</code>	variance–covariance matrix of the estimators

Functions

<code>e(sample)</code>	marks estimation sample
------------------------	-------------------------

Methods and formulas

The methods and formulas presented here provide the technical details underlying the estimators implemented in `teffects ra`, `teffects ipw`, `teffects aipw`, and `teffects ipwra`. See [Methods and formulas](#) of [TE] `teffects nnmatch` for the methods and formulas used by `teffects nnmatch` and `teffects psmatch`.

Methods and formulas are presented under the following headings:

Parameters and notation
Overview of EE estimators
VCE for EE estimators
TM and OM estimating functions
 TM estimating functions
 OM estimating functions
Effect estimating functions
 RA estimators
 IPW estimators
 AIPW estimators
 IPWRA estimators

Parameters and notation

We begin by reviewing the effect parameters estimated by `teffects` and some essential notation.

The potential outcome that an individual would obtain if given treatment level $t \in \{0, 1, \dots, q\}$ is y_t . Each y_t is a random variable, the realizations of which are y_{ti} . Throughout this document, i subscripts denote realizations of the corresponding, unsubscripted random variables.

The three parameters of interest are

1. the potential-outcome mean (POM) $\alpha_t = E(y_t)$;
2. the average treatment effect (ATE) $\tau_t = E(y_t - y_0)$; and
3. the average treatment effect on the treated (ATET) $\delta_t = E(y_t - y_0 | t = \tilde{t})$.

The no-treatment level is 0.

The estimators implemented in `teffects` use three assumptions to justify the equations used for estimation and inference about the effect parameters of interest:

1. Conditional mean independence (CMI) allows us to estimate potential-outcome means from the observed outcomes in the sample.
2. Overlap ensures that we have data on each type of individual in each treatment level.
3. Independent observations ensure that the outcome and treatment for one individual has no effect on the outcome or treatment for any other individual.

`teffects ra` implements some regression-adjustment (RA) estimators; `teffects ipw` implements some inverse-probability-weighted (IPW) estimators; `teffects ipwra` implements some inverse-probability-weighted regression-adjustment (IPWRA) estimators; and `teffects aipw` implements some augmented inverse-probability-weighted (AIPW) estimators. All are implemented as estimating-equation (EE) estimators. The estimators are consistent and asymptotically normally distributed under the CMI, overlap, and independence assumptions.

Overview of EE estimators

EE estimators compute estimates by solving sample estimating equations. The sample estimating equations are the sample equivalents of population expectation equations.

Each EE estimator specifies a set of estimating equations for the effect parameters of interest and a set of estimating equations for the auxiliary parameters in the outcome model (OM) or the treatment model (TM). The next few sections provide tremendous detail about the estimating equations that define the RA, IPW, AIPW, and IPWRA estimators.

Ignoring the details for a moment, EE estimators solve systems of equations to compute estimates. A standard robust estimator is consistent for the variance of the estimator (VCE). All the details involve the equations specified by choices of estimator and functional forms for the OM or TM.

When used, the OM is a model for the conditional mean of the outcome variable. We let $\mu(\mathbf{x}, t, \beta_t)$ denote a conditional-mean model for the outcome y conditional on covariates \mathbf{x} and treatment level t . Mathematically, $E(y|\mathbf{x}, t) = \mu(\mathbf{x}, t, \beta_t)$, where β_t are the parameters of the conditional-mean model given treatment level t . The table below provides details about the available functional forms.

Outcome model	Functional form for $\mu(\mathbf{x}, t, \beta_t)$
linear	$\mathbf{x}\beta_t$
logit, flogit	$\exp(\mathbf{x}\beta_t)/\{1 + \exp(\mathbf{x}\beta_t)\}$
probit, fprobit	$\Phi(\mathbf{x}\beta_t)$
poisson	$\exp(\mathbf{x}\beta_t)$
hetprobit, fhetprobit	$\Phi\{\dot{\mathbf{x}}\beta_t/\exp(\ddot{\mathbf{x}}\beta_t)\}$

In the cases of `hetprobit` and `fhetprobit`, we use $\dot{\mathbf{x}}$ and $\dot{\beta}_t$ to denote the variables and parameters in the index function, and we use $\ddot{\mathbf{x}}$ and $\ddot{\beta}_t$ to denote the variables and parameters in the variance equation. We define $\mathbf{x}' = (\dot{\mathbf{x}}', \ddot{\mathbf{x}}')$ and $\beta'_t = (\dot{\beta}'_t, \ddot{\beta}'_t)$.

We write the vector of parameters for the outcome model over all treatment levels as $\beta' = (\beta'_0, \beta'_1, \dots, \beta'_q)$.

Next we provide details about the estimating equations implied by each functional form choice.

When used, the TM is a model for the conditional probability of treatment. We let $p(\mathbf{z}, t, \gamma)$ denote the conditional probability model for the probability that a person receives treatment t , conditional on covariates \mathbf{z} . The table below provides details about the functional form options allowed in the case of a binary treatment.

Treatment model	Functional form for $p(\mathbf{z}, t, \gamma)$
logit	$\exp(\mathbf{z}\gamma)/\{1 + \exp(\mathbf{z}\gamma)\}$
probit	$\Phi(\mathbf{z}\gamma)$
hetprobit	$\Phi\{\dot{\mathbf{z}}\gamma/\exp(\ddot{\mathbf{z}}\gamma)\}$

In the case of `hetprobit`, we use $\dot{\mathbf{z}}$ and $\dot{\gamma}$ to denote the variables and parameters in the index function, and we use $\ddot{\mathbf{z}}$ and $\ddot{\gamma}$ to represent the variables and parameters in the variance equation. We define $\mathbf{z}' = (\dot{\mathbf{z}}', \ddot{\mathbf{z}}')$, and $\gamma' = (\dot{\gamma}', \ddot{\gamma}')$.

In the multivalued-treatment case, $p(\mathbf{z}, t, \gamma)$ is specified as a multinomial logit with $p(\mathbf{z}, t, \gamma) = \exp(\mathbf{z}\gamma_t)/\{1 + \sum_{k=1}^q \exp(\mathbf{z}\gamma_k)\}$ and $\gamma' = (\gamma'_1, \gamma'_2, \dots, \gamma'_q)$. (We present formulas for the case with treatment level 0 as the base with $\gamma'_0 = \mathbf{0}'$; see [R] `mlogit` for background.) In `teffects`, the `logit` option in the treatment-model specification means binary logit for the binary-treatment case and multinomial logit for the multivalued-treatment case: this simplifies the use of the command and makes statistical sense.

Below we provide details about the estimating equations implied by each functional form choice. The effect parameters of interest are

1. the POMs denoted by $\alpha' = (\alpha_0, \alpha_1, \dots, \alpha_q)$;
2. the ATEs denoted by $\tau' = (\tau_1, \tau_2, \dots, \tau_q)$; and
3. the ATETs denoted by $\delta' = (\delta_1, \delta_2, \dots, \delta_q)$.

We denote the effect parameters by ϑ and all the parameters in any particular case by θ . More formally, θ is the concatenation of the effect parameters, the OM parameters, and the TM parameters; $\theta' = (\vartheta', \beta', \gamma')$, where ϑ is α , τ , or δ , and β or γ may not be present, depending on the case at hand.

In the subsections below, we discuss estimators for the elements in θ in detail and note how these elements change over the cases defined by effect parameters and estimators. The parameter vector θ denotes all the parameters, no matter which particular case is under consideration.

The EE estimators described in this section are defined by a set of equations,

$$E\{\mathbf{s}(\mathbf{x}, \mathbf{z}, \theta)\} = \mathbf{0}$$

where $\mathbf{s}(\mathbf{x}, \mathbf{z}, \theta)$ is a vector of estimating functions. Note the notation: estimating equations equate the expected value of a vector of estimating functions to zero.

Because each of the estimating functions has mean zero, we can construct estimators that find the estimates $\hat{\theta}$ by solving a system of equations,

$$\frac{1}{N} \sum_i^N \mathbf{s}_i(\mathbf{x}_i, \mathbf{z}_i, \hat{\theta}) = \mathbf{0}$$

where $\mathbf{s}_i(\mathbf{x}_i, \mathbf{z}_i, \hat{\theta})$ are the sample realizations of the estimating functions. In other words, the parameter estimates set the average of the realizations of each estimating function to zero. Almost all the details below involve specifying the sample realizations $\mathbf{s}_i(\mathbf{x}_i, \mathbf{z}_i, \hat{\theta})$.

Estimators that set the expected value of estimating functions to zero are known as estimating-equations (EE) estimators, M estimators, or Z estimators in the statistics literature and as generalized method of moments (GMM) estimators in the econometrics literature. See [van der Vaart \(1998, 41\)](#), [Stefanski and Boos \(2002\)](#), and [Tsiatis \(2006, sec. 3.2\)](#) for statistics; and see [Wooldridge \(2010, chap. 14\)](#), [Cameron and Trivedi \(2005, chap. 6\)](#), and [Newey and McFadden \(1994\)](#) for econometrics.

We refer to them as EE estimators because this name is closest to being independent of any discipline. The estimators are implemented using `gmm` because they are exactly identified generalized method-of-moments (GMM) estimators. When weights are specified by the user, they are applied to the estimating equations just as `gmm` applies user-specified weights.

Each estimator has a set of estimating equations for the effect parameters and either an OM or a TM, or both. The OM parameters or the TM parameters are auxiliary parameters used to estimate the effect parameters of interest.

Each set of parameters has its own set of sample estimating equations:

$1/N \sum_i \mathbf{s}_{e,i}(\mathbf{x}_i, \mathbf{z}_i, \hat{\theta}) = \mathbf{0}$ are the sample estimating equations for the effect parameters.

These equations determine the effect parameter estimates $\hat{\vartheta}$ as functions of the data and the other estimated parameters.

$1/N \sum_i \mathbf{s}_{om,i}(\mathbf{x}_i, w_i, \hat{\beta}) = \mathbf{0}$ are the sample estimating equations for OM parameters that use the weights w_i , which are functions of the TM parameters.

$1/N \sum_i \mathbf{s}_{tm,i}(\mathbf{z}_i, \hat{\gamma}) = \mathbf{0}$ are the sample estimating equations for TM parameters.

The whole set of sample estimating functions is $\mathbf{s}_i(\mathbf{x}_i, \mathbf{z}_i, \hat{\theta})$ with

$$\mathbf{s}_i(\mathbf{x}_i, \mathbf{z}_i, \hat{\theta})' = (\mathbf{s}_{e,i}(\mathbf{x}_i, \mathbf{z}_i, \hat{\theta})', \mathbf{s}_{om,i}(\mathbf{x}_i, w_i(t), \hat{\beta})', \mathbf{s}_{tm,i}(\mathbf{z}_i, \hat{\gamma})')$$

although not all the estimators have each of three components.

VCE for EE estimators

The Huber/White/robust sandwich estimator is consistent for the variance–covariance of the estimator (VCE). See [van der Vaart \(1998, 41\)](#), [Stefanski and Boos \(2002\)](#), and [Tsiatis \(2006, sec. 3.2\)](#) for statistics; and see [Wooldridge \(2010, chap. 14\)](#), [Cameron and Trivedi \(2005, chap. 6\)](#), and [Newey and McFadden \(1994\)](#) for econometrics.

The formula is

$$\hat{\mathbf{V}} = (1/N) \bar{\mathbf{G}} \bar{\mathbf{S}} \bar{\mathbf{G}}'$$

where

$$\bar{\mathbf{G}} = \left\{ (1/N) \sum_i \frac{\partial s_i(\mathbf{x}_i, \mathbf{z}_i, \hat{\boldsymbol{\theta}})}{\partial \hat{\boldsymbol{\theta}}} \right\}^{-1}$$

and

$$\bar{\mathbf{S}} = (1/N) \sum_i s_i(\mathbf{x}_i, \mathbf{z}_i, \hat{\boldsymbol{\theta}}) s_i(\mathbf{x}_i, \mathbf{z}_i, \hat{\boldsymbol{\theta}})'$$

The matrix $\bar{\mathbf{G}}$ is not symmetric because our EE estimators come from stacking moment conditions instead of optimizing a single objective function. The implication is that the robust formula should always be used because, even under correct specification, the nonsymmetric $\bar{\mathbf{G}}$ and the symmetric $\bar{\mathbf{S}}$ converge to different matrices.

TM and OM estimating functions

Although the sample estimating functions for the effect parameters, the $s_{e,i}(\mathbf{x}_i, \mathbf{z}_i, \hat{\boldsymbol{\theta}})$, are estimator specific, the sample estimating functions for the TM parameters, the $s_{tm,i}(\mathbf{z}_i, \hat{\boldsymbol{\gamma}})$, and the sample estimating functions for the OM parameters, the $s_{om,i}(\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}})'$, are used in multiple estimators. We provide details about the TM and the OM sample estimating functions here.

TM estimating functions

The sample estimating functions used to estimate the parameters of the TM $p(\mathbf{z}, t, \boldsymbol{\gamma})$ are the sample score equations from the quasimaximum likelihood (QML) estimator.

In the binary-treatment case, $p(\mathbf{z}, t, \boldsymbol{\gamma})$ may be logit, probit, or heteroskedastic probit. In the multivalued-treatment case, $p(\mathbf{z}, t, \boldsymbol{\gamma})$ is a multinomial logit. We now give formulas for the $s_{tm,i}(\mathbf{z}_i, \hat{\boldsymbol{\gamma}})$ for each case.

logit and probit

In the logit and probit cases,

$$s_{tm,i}(\mathbf{z}_i, \hat{\boldsymbol{\gamma}}) = \begin{bmatrix} \frac{g(\mathbf{z}_i \hat{\boldsymbol{\gamma}}') \{t_i - G(\mathbf{z}_i \hat{\boldsymbol{\gamma}}')\}}{G(\mathbf{z}_i \hat{\boldsymbol{\gamma}}') \{1 - G(\mathbf{z}_i \hat{\boldsymbol{\gamma}}')\}} \end{bmatrix} \mathbf{z}_i$$

where $G(z)$ is the logistic cumulative distribution function for the logit, $G(z)$ is the normal cumulative distribution function for the probit, and $g(\cdot) = \{\partial G(z)\}/(\partial z)$ is the corresponding density function.

hetprobit

In the **hetprobit** case, there are two sets of sample score equations, $s_{\text{tm},1,i}(\mathbf{z}_i, \hat{\gamma})$ and $s_{\text{tm},2,i}(\mathbf{z}_i, \hat{\gamma})$:

$$s_{\text{tm},1,i}(\mathbf{z}_i, \hat{\gamma}) = \left(\frac{\phi\{q(\mathbf{z}_i, \hat{\gamma})\} [t_i - \Phi\{q(\mathbf{z}_i, \hat{\gamma})\}]}{\Phi\{q(\mathbf{z}_i, \hat{\gamma})\} [1 - \Phi\{q(\mathbf{z}_i, \hat{\gamma})\}] \exp(\ddot{\mathbf{z}}_i \hat{\gamma}'')} \right) \dot{\mathbf{z}}'_i$$

and

$$s_{\text{tm},2,i}(\mathbf{z}_i, \hat{\gamma}) = \left(\frac{\phi\{q(\mathbf{z}_i, \hat{\gamma})\} \dot{\mathbf{z}}_i \hat{\gamma}'' [\Phi\{q(\mathbf{z}_i, \hat{\gamma})\} - t_i]}{\Phi\{q(\mathbf{z}_i, \hat{\gamma})\} [1 - \Phi\{q(\mathbf{z}_i, \hat{\gamma})\}] \exp(\ddot{\mathbf{z}}_i \hat{\gamma}'')} \right) \ddot{\mathbf{z}}'_i$$

where $\phi(\cdot)$ is the standard normal density function, and $q(\mathbf{z}_i, \hat{\gamma}) = (\dot{\mathbf{z}}_i \hat{\gamma}' / \exp(\ddot{\mathbf{z}}_i \hat{\gamma}''))$.

mlogit

In the **mlogit** case, $p(\mathbf{z}, t, \gamma) = \exp(\mathbf{z}\gamma_t) / \{1 + \sum_{k=1}^q \exp(\mathbf{z}\gamma_k)\}$. We present formulas for the case with treatment level 0 as the base with $\gamma'_0 = \mathbf{0}'$; see [R] **mlogit** for background.

There are q vectors of sample estimating functions for the **mlogit** case, $s_{\text{tm},k,i}(\mathbf{z}_i, \hat{\gamma})$ for each $k \in \{1, \dots, q\}$, 1 for each vector $\hat{\gamma}_k$, $k \in \{1, \dots, q\}$. These sample estimating functions are

$$s_{\text{tm},k,i}(\mathbf{z}_i, \hat{\gamma}) = \begin{cases} \{1 - p(\mathbf{z}_i, k, \hat{\gamma})\} \mathbf{z}'_i & t_i = k \\ -p(\mathbf{z}_i, k, \hat{\gamma}) \mathbf{z}'_i & \text{otherwise} \end{cases}$$

OM estimating functions

The parameters of the OM $\mu(\mathbf{x}, t, \beta_t)$ are estimated either by weighted QML or by weighted nonlinear least squares. The estimating functions used to estimate the parameters of the OM are either the score equations from the weighted QML estimator or the moment conditions for the weighted nonlinear least-squares estimator.

The estimating functions for the OM parameters in $\mu(\mathbf{x}, t, \beta_t)$ vary over the models for the conditional mean because $\mu(\mathbf{x}, t, \beta_t)$ may be linear, logit, probit, heteroskedastic probit, or poisson.

Let N_t be the number of observations in treatment level t , and let $t_i(t) = 1$ if $t_i = t$, with $t_i(t) = 0$ if $t_i \neq t$.

There are two sets of sample estimating functions for the OM parameters with weights $w_i(t)$:

1. $s_{\text{ml,om},i}\{\mathbf{x}_i, w_i(t), \hat{\beta}_t\}$ are the sample estimating functions for the weighted QML estimator.
2. $s_{\text{nls,om},i}\{\mathbf{x}_i, w_i(t), \hat{\beta}_t\}$ are the sample estimating functions for the weighted nonlinear least-squares estimator.

OM QML

Here are the formulas for the $s_{\text{ml,om},i}\{\mathbf{x}_i, w_i(t), \hat{\beta}_t\}$ for each functional form choice.

linear

In the linear case,

$$\mathbf{s}_{\text{ml,om},i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\} = w_i(t)t_i(t)(y_i - \mathbf{x}_i \hat{\boldsymbol{\beta}}'_t) \mathbf{x}'_i$$

logit, flogit, probit, and fprobit

In the logit, flogit, probit, and fprobit cases,

$$\mathbf{s}_{\text{ml,om},i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\} = w_i(t)t_i(t) \left[\frac{g(\mathbf{x}_i \hat{\boldsymbol{\beta}}'_t) \{y_i - G(\mathbf{x}_i \hat{\boldsymbol{\beta}}'_t)\}}{G(\mathbf{x}_i \hat{\boldsymbol{\beta}}'_t) \{1 - G(\mathbf{x}_i \hat{\boldsymbol{\beta}}'_t)\}} \right] \mathbf{x}_i$$

where $G(z)$ is the logistic cumulative distribution function for the logit and flogit, $G(z)$ is the normal cumulative distribution function for the probit and fprobit, and $g(\cdot) = \{\partial G(z)\}/(\partial z)$ is the corresponding density function.

hetprobit and fhetprobit

In the hetprobit and fhetprobit cases, there are two sets of sample score equations, $\mathbf{s}_{\text{ml,om},1,i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\}$ and $\mathbf{s}_{\text{ml,om},2,i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\}$:

$$\mathbf{s}_{\text{ml,om},1,i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\} = w_i(t)t_i(t) \left(\frac{\phi\{q(\mathbf{x}_i, \hat{\boldsymbol{\beta}}_t)\} [y_i - \Phi\{q(\mathbf{x}_i, \hat{\boldsymbol{\beta}}_t)\}]}{\Phi\{q(\mathbf{x}_i, \hat{\boldsymbol{\beta}}_t)\} [1 - \Phi\{q(\mathbf{x}_i, \hat{\boldsymbol{\beta}}_t)\}] \exp(\ddot{\mathbf{x}}_i \hat{\boldsymbol{\beta}}'_t)} \right) \dot{\mathbf{x}}'_i$$

and

$$\mathbf{s}_{\text{ml,om},2,i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\} = w_i(t)t_i(t) \left(\frac{\phi\{q(\mathbf{x}_i, \hat{\boldsymbol{\beta}}_t)\} \dot{\mathbf{x}}_i \hat{\boldsymbol{\beta}}'_t [\Phi\{q(\mathbf{x}_i, \hat{\boldsymbol{\beta}}_t)\} - y_i]}{\Phi\{q(\mathbf{x}_i, \hat{\boldsymbol{\beta}}_t)\} [1 - \Phi\{q(\mathbf{x}_i, \hat{\boldsymbol{\beta}}_t)\}] \exp(\ddot{\mathbf{x}}_i \hat{\boldsymbol{\beta}}'_t)} \right) \dot{\mathbf{x}}'_i$$

where $\phi(\cdot)$ is the standard normal density function, $\mathbf{s}_{\text{ml,om},i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\}' = [\mathbf{s}_{\text{ml,om},1,i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\}', \mathbf{s}_{\text{ml,om},2,i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\}']$, and $q(\mathbf{x}_i, \hat{\boldsymbol{\beta}}_t) = (\dot{\mathbf{x}}_i \hat{\boldsymbol{\beta}}'_t / \exp(\ddot{\mathbf{x}}_i \hat{\boldsymbol{\beta}}'_t))$.

poisson

In the poisson case,

$$\mathbf{s}_{\text{ml,om},i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\} = w_i(t)t_i(t)\{y_i - \exp(\mathbf{x}_i \hat{\boldsymbol{\beta}}'_t)\} \mathbf{x}'_i$$

OM WNL

Here are the formulas for the $\mathbf{s}_{\text{nls,om},i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\}$ for each functional form choice.

linear

In the linear case,

$$\mathbf{s}_{\text{nls},\text{om},i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\} = w_i(t)t_i(t)(y_i - \mathbf{x}_i\hat{\boldsymbol{\beta}}_t')\mathbf{x}'_i$$

logit, flogit, probit, and fprobit

In the **logit**, **flogit**, **probit**, and **fprobit** cases,

$$\mathbf{s}_{\text{nls},\text{om},i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\} = w_i(t)t_i(t) \left[g(\mathbf{x}_i\hat{\boldsymbol{\beta}}_t') \left\{ y_i - G(\mathbf{x}_i\hat{\boldsymbol{\beta}}_t') \right\} \right] \mathbf{x}'_i$$

where $G(z)$ is the logistic cumulative distribution function for the logit and flogit, $G(z)$ is the normal cumulative distribution function for the probit and fprobit, and $g(\cdot) = \{\partial G(z)\}/(\partial z)$ is the corresponding density function.

hetprobit and fhetprobit

In the **hetprobit** and **fhetprobit** cases, there are two sets of sample score equations, $\mathbf{s}_{\text{nls},\text{om},1,i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\}$ and $\mathbf{s}_{\text{nls},\text{om},2,i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\}$:

$$\mathbf{s}_{\text{nls},\text{om},1,i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\} = w_i(t)t_i(t) \left(\frac{\phi\left\{q\left(\mathbf{x}_i, \hat{\boldsymbol{\beta}}_t\right)\right\}}{\exp(\ddot{\mathbf{x}}_i\hat{\boldsymbol{\beta}}_t')} \left[y_i - \Phi\left\{q\left(\mathbf{x}_i, \hat{\boldsymbol{\beta}}_t\right)\right\} \right] \right) \dot{\mathbf{x}}'_i$$

and

$$\mathbf{s}_{\text{nls},\text{om},2,i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\} = w_i(t)t_i(t) \left(\frac{\phi\left\{q\left(\mathbf{x}_i, \hat{\boldsymbol{\beta}}_t\right)\right\}}{\exp(\ddot{\mathbf{x}}_i\hat{\boldsymbol{\beta}}_t')} \dot{\mathbf{x}}_i\hat{\boldsymbol{\beta}}_t' \left[\Phi\left\{q\left(\mathbf{x}_i, \hat{\boldsymbol{\beta}}_t\right)\right\} - y_i \right] \right) \ddot{\mathbf{x}}'_i$$

where $\phi(\cdot)$ is the standard normal density function, $\mathbf{s}_{\text{nls},\text{om},i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\}' = [\mathbf{s}_{\text{nls},\text{om},1,i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\}', \mathbf{s}_{\text{nls},\text{om},2,i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\}]'$, and $q\left(\mathbf{x}_i, \hat{\boldsymbol{\beta}}_t\right) = \left(\dot{\mathbf{x}}_i\hat{\boldsymbol{\beta}}_t' / \exp(\ddot{\mathbf{x}}_i\hat{\boldsymbol{\beta}}_t') \right)$.

poisson

In the **poisson** case,

$$\mathbf{s}_{\text{nls},\text{om},i}\{\mathbf{x}_i, w_i(t), \hat{\boldsymbol{\beta}}_t\} = w_i(t)t_i(t)\{y_i - \exp(\mathbf{x}_i\hat{\boldsymbol{\beta}}_t')\} \exp(\mathbf{x}_i\hat{\boldsymbol{\beta}}_t')\mathbf{x}'_i$$

Effect estimating functions

We now describe the sample estimating functions for the effect parameters, which vary over estimator and effect parameter.

RA estimators

RA estimators estimate the effect parameters using means of the observation-level predictions of the conditional means of the outcomes. There is no model for the conditional probability of treatment.

The RA estimators use unweighted QML estimators to estimate the parameters of the conditional mean model. In other words, the RA estimators use the sample estimating functions $s_{\text{ml},\text{om},i}(\mathbf{x}_i, 1, \hat{\beta})$, given above.

For the RA estimators, the vector of sample estimating functions is the concatenation of the sample estimating functions for the effect parameters with the sample estimating functions for the OM parameters. Algebraically,

$$\mathbf{s}_{\text{ra},i}(\mathbf{x}_i, \hat{\theta})' = \mathbf{s}_{\text{ra},e,i}(\mathbf{x}_i, \hat{\theta}, \hat{\beta})', \mathbf{s}_{\text{ml},\text{om},i}(\mathbf{x}_i, 1, \hat{\beta})'$$

The estimating functions $\mathbf{s}_{\text{ra},e,i}(\mathbf{x}_i, \hat{\theta}, \hat{\beta})'$ vary over the effect parameter.

RA for POM

The RA estimators for the POM parameters estimate $\theta' = (\alpha', \beta')$ using two types of estimating equations: 1) those for the POM parameters α , and 2) those for the conditional-mean model parameters β_t in $\mu(\mathbf{x}, t, \beta_t)$.

The sample estimating functions for the $\hat{\beta}_t$ are given in [OM estimating functions](#) above.

The elements of $\mathbf{s}_{\text{ra},e,i}(\mathbf{x}_i, \hat{\alpha}, \hat{\beta})$ for the POM parameters α are given by

$$\mu(\mathbf{x}_i, t, \hat{\beta}_t) - \hat{\alpha}_t \quad (\text{RAPOM})$$

RA for ATE

The RA estimators for the ATE parameters estimate $\theta' = (\tau', \beta')$ using two types of estimating equations: 1) those for the ATE parameters τ , and 2) those for the OM parameters β_t in $\mu(\mathbf{x}, t, \beta_t)$.

The sample estimating functions that determine the $\hat{\beta}_t$ are given in [OM estimating functions](#) with $w_i(t) = 1$.

The elements of $\mathbf{s}_{\text{ra},e,i}(\mathbf{x}_i, \hat{\tau}, \hat{\beta})$ for the ATE parameters τ are given by

$$\mu(\mathbf{x}_i, t, \hat{\beta}_t) - \mu(\mathbf{x}_i, 0, \hat{\beta}_t) - \hat{\tau}_t \quad (\text{RAATE})$$

RA for ATET

The RA estimators for the ATET parameters estimate $\theta' = (\delta', \beta')$ using two types of estimating equations: 1) those for the ATET parameters δ , and 2) those for the OM parameters β_t in $\mu(\mathbf{x}, t, \beta_t)$.

The sample estimating functions that determine the $\hat{\beta}_t$ are given in [OM estimating functions](#) above with $w_i(t) = 1$.

The elements of $\mathbf{s}_{\text{ra},e,i}(\mathbf{x}_i, \hat{\delta}, \hat{\beta})$ for the ATET parameters δ are given by

$$Nt_i(\tilde{t})/N_{\tilde{t}} \left\{ \mu(\mathbf{x}_i, t, \hat{\beta}_t) - \mu(\mathbf{x}_i, 0, \hat{\beta}_t) - \hat{\delta}_t \right\} \quad (\text{RAATET})$$

IPW estimators

IPW estimators estimate the effect parameters using means of the observed outcomes weighted by the inverse probability of treatment. There is no outcome model. The IPW estimators use QML estimators to estimate the parameters of the conditional probability model.

The vector of estimating functions is the concatenation of the estimating functions for the effect parameters with the estimating functions for the conditional-probability parameters. The sample estimating functions used by the IPW estimators are

$$\mathbf{s}_{\text{ipw},i}(\mathbf{x}_i, \hat{\boldsymbol{\theta}})' = \mathbf{s}_{\text{ipw},e,i}(\mathbf{x}_i, \hat{\boldsymbol{\theta}}, \hat{\boldsymbol{\gamma}})', \mathbf{s}_{\text{tm},i}(\mathbf{z}_i, 1, \hat{\boldsymbol{\gamma}})'$$

The estimating functions $\mathbf{s}_{\text{ipw},e,i}(\mathbf{z}_i, \hat{\boldsymbol{\theta}}, \hat{\boldsymbol{\gamma}})'$ vary over the effect parameter.

All the IPW estimators use normalized inverse-probability weights. These weights are not related to the weights $w_i(t)$ that were used in the OM equations. The functional form for the normalized inverse-probability weights varies over the effect parameters POM, ATE, and ATET.

The POM and ATE estimators use normalized inverse-probability weights. The unnormalized weights for individual i and treatment level t are $d_i(t) = t_i(t)/p(\mathbf{z}_i, t, \hat{\boldsymbol{\gamma}})$, and the normalized weights are $\bar{d}_i(t) = N_t d_i(t) / \sum_i^N d_i(t)$.

The ATET estimator uses normalized treatment-adjusted inverse-probability weights. The treatment-adjusted inverse-probability weights adjust the inverse-probability weights for the probability of getting the conditional treatment \tilde{t} . The unnormalized weights are $f_i = p(\mathbf{z}_i, \tilde{t}, \hat{\boldsymbol{\gamma}})/p(\mathbf{z}_i, t_i, \hat{\boldsymbol{\gamma}})$, and the normalized weights are $\bar{f}_i = N f_i / \sum_i^N f_i$.

The IPW effect estimators are weighted cell averages. The sample estimating functions used in POM estimators are the sample estimating functions from weighted OLS regression on treatment-cell indicators. The POM estimators use a full set of $q + 1$ of treatment indicator variables \mathbf{a}_i . (The i th observation on the k th variable in \mathbf{a}_i is 1 if i received treatment $k - 1$ and 0 otherwise, for $k \in \{1, 2, \dots, q + 1\}$.)

The sample estimating functions used in the ATE and the ATET estimators are the sample estimating functions from weighted OLS regression on treatment-cell indicators, excluding the indicator for the control level and including a constant term. The variables $\tilde{\mathbf{a}}_i$ used in the ATE and ATET sample estimating functions include q of treatment indicator variables and a variable that is always 1. (The first q variables in $\tilde{\mathbf{a}}_i$ are treatment indicators: the i th observation on the k th variable in $\tilde{\mathbf{a}}_i$ is 1 if i received treatment k and 0 otherwise, for $k \in \{1, 2, \dots, q\}$. The $(q + 1)$ th variable is always 1.) This definition of $\tilde{\mathbf{a}}_i$ sets the last treatment level to be the control; renaming the treatments handles the more general case allowed for by **teffects**.

Having defined \mathbf{a}_i and $\tilde{\mathbf{a}}_i$, we can give the sample estimating functions that the IPW estimators use for the effects parameters.

IPW for POM

We begin with the IPW estimators for the potential-outcome means. In this case, $\boldsymbol{\theta}' = (\boldsymbol{\alpha}', \boldsymbol{\gamma}')$.

The sample estimating functions for the $\hat{\boldsymbol{\gamma}}$ are given in [TM estimating functions](#) above.

The sample estimating functions for $\hat{\boldsymbol{\alpha}}$ are given by

$$\mathbf{s}_{\text{ipw},e,i,t}(\mathbf{z}_i, \hat{\boldsymbol{\alpha}}, \hat{\boldsymbol{\gamma}})' = \bar{d}_i(t)(y_i - \mathbf{a}_i \hat{\boldsymbol{\alpha}}) \mathbf{a}_i' \quad (\text{IPWPOM})$$

IPW for ATE

The full parameter vector for the IPW estimators for the ATE is $\theta' = (\tau', \gamma')$.

The sample estimating functions for the $\hat{\gamma}$ are given in [TM estimating functions](#) above.

The sample estimating functions for $\hat{\tau}$ are given by

$$\mathbf{s}_{\text{ipw},e,i,t}(\mathbf{z}_i, \hat{\tau}, \hat{\gamma})' = \bar{d}_i(t)(y_i - \tilde{\mathbf{a}}_i \hat{\tau}) \tilde{\mathbf{a}}_i' \quad (\text{IPWATE})$$

IPW for ATET

The full parameter vector for the IPW estimators for the ATET is $\theta' = (\delta', \gamma')$.

The sample estimating functions for the $\hat{\gamma}$ are given in [TM estimating functions](#) above.

The sample estimating functions for $\hat{\delta}$ are given by

$$\mathbf{s}_{\text{ipw},e,i,t}(\mathbf{z}_i, \hat{\delta}, \hat{\gamma})' = \bar{f}_i(t)(y_i - \tilde{\mathbf{a}}_i \hat{\delta}) \tilde{\mathbf{a}}_i' \quad (\text{IPWATET})$$

AIPW estimators

This section documents the sample estimating functions used by the augmented inverse-probability-weighted (AIPW) estimators implemented in `teffects`. These AIPW estimators are efficient-influence-function estimators as discussed in [\[TE\] teffects intro](#) and [\[TE\] teffects intro advanced](#). The `teffects` implementation was primarily inspired by Cattaneo, Drukker, and Holland (2013), which was based on Cattaneo (2010). Tan (2010) was influential by identifying the implemented weighted nonlinear least-squares estimator as having relatively good properties when both the conditional mean function and the conditional probability function are misspecified.

The AIPW estimating functions for the treatment parameters include terms from a conditional probability model and from a conditional mean model for the outcome.

The sample-estimation-equations vector has three parts for the AIPW estimators:

$$\mathbf{s}_{\text{aipw},i}(\mathbf{x}_i, \mathbf{z}_i, \hat{\theta})' = [\mathbf{s}_{\text{aipw},e,i}(\mathbf{x}_i, \mathbf{z}_i, \hat{\theta})', \mathbf{s}_{\text{aipw},tm,i}(\mathbf{z}_i, \hat{\gamma})', \mathbf{s}_{\text{aipw},om,i}\{\mathbf{x}_i, w_i(t), \hat{\beta}\}']$$

The sample estimating functions for the parameters of the TM are the $\mathbf{s}_{\text{tm},i}(\mathbf{z}_i, \hat{\gamma})$ given in [TM estimating functions](#) above.

`teffects aipw` implements three AIPW estimators: the standard AIPW estimator, the NLS AIPW estimator, and the WNLS AIPW estimator.

The three AIPW estimators differ in how they estimate the parameters of the OM.

By default, `teffects aipw` uses the standard AIPW estimator that estimates the parameters of the OM by the unweighted ML estimator, whose sample estimating functions, $\mathbf{s}_{\text{ml},om,i}(\mathbf{x}_i, 1, \hat{\beta})$, are given in [OM estimating functions](#) above.

When the `nls` option is specified, `teffects aipw` uses the NLS AIPW estimator that estimates the parameters of the OM by the unweighted NLS estimator, whose sample estimating functions, $\mathbf{s}_{\text{nls},om,i}(\mathbf{x}_i, 1, \hat{\beta})$, are given in [OM estimating functions](#) above.

When the `wnls` option is specified, `teffects aipw` uses the WNLS AIPW estimator that estimates the parameters of the OM by the WNLS estimator, whose sample estimating functions, $s_{\text{nl},\text{om},i}\{\mathbf{x}_i, \tilde{w}_i(t), \hat{\beta}\}$, are given in [OM estimating functions](#) above. The weights for person i in treatment level t are

$$\tilde{w}_i(t) = \frac{t_i(t)}{p(\mathbf{z}_i, t, \hat{\gamma})} \left\{ \frac{t_i(t)}{p(\mathbf{z}_i, t, \hat{\gamma})} - 1 \right\} \quad (\text{WNLSW})$$

Now we discuss the sample estimating functions for the effect parameters, the $s_{e,i}(\mathbf{x}_i, \mathbf{z}_i, \hat{\theta})$.

AIPW for POM

We begin with the AIPW estimators for the potential-outcome means. In this case, $\theta' = (\alpha', \gamma', \beta')$, and the elements of $s_{\text{aipw},e,i}(\mathbf{x}_i, \mathbf{z}_i, \hat{\theta})$ are given by

$$\frac{t_i(t)}{p(\mathbf{z}_i, t, \hat{\gamma})} y_i - \mu(\mathbf{x}_i, \hat{\beta}_t) \left\{ \frac{t_i(t)}{p(\mathbf{z}_i, t, \hat{\gamma})} - 1 \right\} - \alpha_t$$

AIPW for ATE

The AIPW estimators for the ATE estimate $\theta' = (\tau', \gamma', \beta')$, and the elements of $s_{\text{aipw},e,i}(\mathbf{x}_i, \mathbf{z}_i, \hat{\theta})$ are given by

$$\begin{aligned} & \frac{t_i(t)}{p(\mathbf{z}_i, t, \hat{\gamma})} y_i - \mu(\mathbf{x}_i, \hat{\beta}_t) \left\{ \frac{t_i(t)}{p(\mathbf{z}_i, t, \hat{\gamma})} - 1 \right\} - \tau_0 \text{ if } t = 0 \\ & \frac{t_i(t)}{p(\mathbf{z}_i, t, \hat{\gamma})} y_i - \mu(\mathbf{x}_i, \hat{\beta}_t) \left\{ \frac{t_i(t)}{p(\mathbf{z}_i, t, \hat{\gamma})} - 1 \right\} - \tau_t - \tau_0 \text{ if } t > 0 \end{aligned}$$

IPWRA estimators

The IPWRA estimators combine inverse-probability weighting (IPW) with regression-adjustment (RA) methods. The sample estimating functions for IPWRA include sample estimating functions from both RA and IPW. The vector of sample estimating functions is

$$s_{\text{ipwra},i}(\mathbf{x}_i, \hat{\theta}') = s_{\text{ra},e,i}(\mathbf{x}_i, \hat{\vartheta}, \hat{\beta})', s_{\text{ml},\text{om},i}\{\mathbf{x}_i, w_i(j), \hat{\beta}\}', s_{\text{tm},i}(\mathbf{z}_i, \hat{\gamma})'$$

where $\hat{\theta}' = (\hat{\vartheta}', \hat{\beta}', \hat{\gamma}')$, $\hat{\vartheta} = \hat{\alpha}$ for POM, $\hat{\vartheta} = \hat{\tau}_t$ for ATE, and $\hat{\vartheta} = \hat{\delta}_t$ for ATET. The sample estimating functions, $s_{\text{ra},e,i}(\mathbf{x}_i, \hat{\vartheta}, \hat{\beta})$, for POM, ATE, and ATET are given in equations (RAPOM), (RAATE), and (RAATET). For the OM sample estimating functions, $s_{\text{ml},\text{om},i}(\cdot)$, we replace the RA unity weights, $w_i(t) = 1$, with $d_i(j)$ for POM or ATE and \bar{f}_i for ATET, the normalized inverse-probability weights described in [IPW estimators](#) above. The specific form of the OM sample estimating functions are given in [OM estimating functions](#) above. The TM sample estimating functions are given in [TM estimating functions](#) above.

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Also see

- [TE] **teffects postestimation** — Postestimation tools for teffects
- [TE] **teffects** — Treatment-effects estimation for observational data
- [TE] **teffects ipwra** — Inverse-probability-weighted regression adjustment
- [U] **20 Estimation and postestimation commands**

teffects ipw — Inverse-probability weighting

Description	Quick start	Menu	Syntax
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References	Also see		

Description

teffects ipw estimates the average treatment effect (ATE), the average treatment effect on the treated (ATET), and the potential-outcome means (POMs) from observational data by inverse-probability weighting (IPW). IPW estimators use estimated probability weights to correct for missing data on the potential outcomes. **teffects ipw** accepts a continuous, binary, count, fractional, or nonnegative outcome and allows a multivalued treatment.

See [TE] **teffects intro** or [TE] **teffects intro advanced** for more information about estimating treatment effects from observational data.

Quick start

ATE of binary `treat2` on `y` by IPW using a logistic model of `treat2` on `x` and `w`
`teffects ipw (y) (treat2 x w)`

As above, but estimate ATET

`teffects ipw (y) (treat2 x w), atet`

As above, but estimate potential-outcome means

`teffects ipw (y) (treat2 x w), pomeans`

ATE of `treat2` on `y` using heteroskedastic probit for `treat2` as a function of `x` and `w`
`teffects ipw (y) (treat2 x w, hetprobit(x w))`

ATE for treatment levels 2 and 3 of three-valued treatment `treat3`

`teffects ipw (y) (treat3 x w)`

As above, and specify that `treat3 = 3` is the control level

`teffects ipw (y) (treat3 x w), control(3)`

Same as above, specified using the label “MyControl” corresponding to `treat3 = 3`

`teffects ipw (y) (treat3 x w), control(MyControl)`

Menu

Statistics > Treatment effects > Continuous outcomes > Inverse-probability weighting (IPW)

Statistics > Treatment effects > Binary outcomes > Inverse-probability weighting (IPW)

Statistics > Treatment effects > Count outcomes > Inverse-probability weighting (IPW)

Statistics > Treatment effects > Fractional outcomes > Inverse-probability weighting (IPW)

Statistics > Treatment effects > Nonnegative outcomes > Inverse-probability weighting (IPW)

Syntax

```
teffects ipw (ovar) (tvar tmvarlist [ , tmodel noconstant] ) [if] [in] [weight]  
[ , stat options ]
```

ovar is a binary, count, continuous, fractional, or nonnegative outcome of interest.

tvar must contain integer values representing the treatment levels.

tmvarlist specifies the variables that predict treatment assignment in the treatment model.

<i>tmodel</i>	Description
---------------	-------------

Model

<i>logit</i>	logistic treatment model; the default
<i>probit</i>	probit treatment model
<i>hetprobit</i> (<i>varlist</i>)	heteroskedastic probit treatment model

tmodel specifies the model for the treatment variable.

For multivalued treatments, only *logit* is available and multinomial logit is used.

<i>stat</i>	Description
-------------	-------------

Stat

<i>ate</i>	estimate average treatment effect in population; the default
<i>atet</i>	estimate average treatment effect on the treated
<i>pomeans</i>	estimate potential-outcome means

<i>options</i>	Description
----------------	-------------

SE/Robust

<i>vce</i> (<i>vcetype</i>)	<i>vcetype</i> may be <i>robust</i> , <i>cluster</i> <i>clustvar</i> , <i>bootstrap</i> , or <i>jackknife</i>
-------------------------------	---

Reporting

<i>level</i> (#)	set confidence level; default is <i>level</i> (95)
<i>aequations</i>	display auxiliary-equation results
<i>display_options</i>	control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling

Maximization

<i>maximize_options</i>	control the maximization process; seldom used
-------------------------	---

Advanced

<i>pstolerance</i> (#)	set tolerance for overlap assumption
<i>osample</i> (<i>newvar</i>)	<i>newvar</i> identifies observations that violate the overlap assumption
<i>control</i> (# <i>label</i>)	specify the level of <i>tvar</i> that is the control
<i>tlevel</i> (# <i>label</i>)	specify the level of <i>tvar</i> that is the treatment
<i>coeflegend</i>	display legend instead of statistics

tmvarlist may contain factor variables; see [U] 11.4.3 Factor variables.

bootstrap, **by**, **jackknife**, and **statsby** are allowed; see [U] 11.1.10 Prefix commands.

Weights are not allowed with the **bootstrap** prefix; see [R] bootstrap.

fweights, **iweights**, and **pweights** are allowed; see [U] 11.1.6 weight.

coeflegend does not appear in the dialog box.

See [U] 20 Estimation and postestimation commands for more capabilities of estimation commands.

Options

Model

noconstant; see [R] Estimation options.

Stat

stat is one of three statistics: **ate**, **atet**, or **pomeans**. **ate** is the default.

ate specifies that the average treatment effect be estimated.

atet specifies that the average treatment effect on the treated be estimated.

pomeans specifies that the potential-outcome means for each treatment level be estimated.

SE/Robust

vce(vcetype) specifies the type of standard error reported, which includes types that are robust to some kinds of misspecification (**robust**), that allow for intragroup correlation (**cluster clustvar**), and that use bootstrap or jackknife methods (**bootstrap**, **jackknife**); see [R] vce_option.

Reporting

level(#); see [R] Estimation options.

aequations specifies that the results for the outcome-model or the treatment-model parameters be displayed. By default, the results for these auxiliary parameters are not displayed.

display_options: **noci**, **nopvalues**, **noomitted**, **vsquish**, **noemptycells**, **baselevels**, **allbaselevels**, **nofvlabel**, **fvwrap(#)**, **fvrapon(style)**, **cformat(%fmt)**, **pformat(%fmt)**, **sformat(%fmt)**, and **nolstretch**; see [R] Estimation options.

Maximization

maximize_options: **iterate(#)**, **[no]log**, and **from(init_specs)**; see [R] Maximize. These options are seldom used.

init_specs is one of

matname [**,** **skip copy**]

[**,** **# ...**], **copy**

Advanced

pstolerance(#) specifies the tolerance used to check the overlap assumption. The default value is **pstolerance(1e-5)**. **teffects** will exit with an error if an observation has an estimated propensity score smaller than that specified by **pstolerance()**.

osample(newvar) specifies that indicator variable *newvar* be created to identify observations that violate the overlap assumption.

`tlevel(#|label)` specifies the level of `tvar` that is the control. The default is the first treatment level. You may specify the numeric level # (a nonnegative integer) or the label associated with the numeric level. `control()` may not be specified with statistic `pmeans`. `control()` and `tlevel()` may not specify the same treatment level.

`tlevel(#|label)` specifies the level of `tvar` that is the treatment for the statistic `atet`. The default is the second treatment level. You may specify the numeric level # (a nonnegative integer) or the label associated with the numeric level. `tlevel()` may only be specified with statistic `atet`. `tlevel()` and `control()` may not specify the same treatment level.

The following option is available with `teffects ipw` but is not shown in the dialog box:
`coeflegend`; see [R] **Estimation options**.

Remarks and examples

Remarks are presented under the following headings:

[Overview](#)
[Video example](#)

Overview

IPW estimators use estimated probability weights to correct for the missing-data problem arising from the fact that each subject is observed in only one of the potential outcomes. IPW estimators use a two-step approach to estimating treatment effects:

1. They estimate the parameters of the treatment model and compute the estimated inverse-probability weights.
2. They use the estimated inverse-probability weights to compute weighted averages of the outcomes for each treatment level. The contrasts of these weighted averages provide the estimates of the ATES. Using this weighting scheme corrects for the missing potential outcomes.

These steps produce consistent estimates of the effect parameters because the treatment is assumed to be independent of the potential outcomes after conditioning on the covariates. The overlap assumption ensures that predicted inverse-probability weights do not get too large. In fact, `teffects ipw` uses an estimation technique that implements both steps at once so that we do not need to correct the standard errors in the second step to reflect the uncertainty associated with the predicted treatment probabilities.

We will illustrate the use of `teffects ipw` by using data from a study of the effect of a mother's smoking status during pregnancy (`mbsmoke`) on infant birthweight (`bweight`) as reported by Cattaneo (2010). This dataset also contains information about each mother's age (`mage`), education level (`medu`), marital status (`mmarried`), whether the first prenatal exam occurred in the first trimester (`prenatal1`), and whether this baby was the mother's first birth (`fbaby`).

▷ Example 1: Estimating the ATE

We begin by using `teffects ipw` to estimate the average treatment effect of smoking on birthweight. We will use a probit model to predict treatment status, using `prenatal1`, `mmarried`, `mage`, the square of `mage`, and `fbaby` as explanatory variables:

```
. use https://www.stata-press.com/data/r16/cattaneo2
(Excerpt from Cattaneo (2010) Journal of Econometrics 155: 138–154)

. 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

Table: Robust Coefficients
```

bweight	Coef.	Robust 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
P0mean					
mbsmoke nonsmoker	3403.463	9.571369	355.59	0.000	3384.703 3422.222

The average birthweight if all mothers were to smoke would be 231 grams less than the average of 3,403 grams that would occur if none of the mothers had smoked.



Sometimes, we are mainly concerned about those subjects that did in fact receive treatment, and we want to know how much the outcome changes as a result of treatment for that subpopulation. The ATET provides us with the answer. Moreover, the ATET can be estimated using weaker assumptions than are required to estimate the ATE; see [TE] **teffects intro advanced**.

▷ Example 2: Estimating the ATET

```
. teffects ipw (bweight) (mbsmoke mmarried c.mage##c.mage fbaby medu, probit),
> atet
Iteration 0:   EE criterion =  4.636e-21
Iteration 1:   EE criterion =  6.467e-27

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

Table: Robust Coefficients
```

bweight	Coef.	Robust Std. Err.	z	P> z	[95% Conf. Interval]
ATET					
mbsmoke (smoker vs nonsmoker)	-225.1773	23.66458	-9.52	0.000	-271.559 -178.7955
P0mean					
mbsmoke nonsmoker	3362.837	14.20149	236.79	0.000	3335.003 3390.671

The average birthweight is 225 grams less when all the mothers who smoke do so than the average of 3,363 grams that would have occurred if none of these mothers had smoked.



We often express statistics as percentages to alleviate scaling issues and aid interpretation. In the present context, we may wish to express an ATE as a percentage of the untreated POM to gain a more intuitive measure of the effect of treatment.

▷ Example 3: Reporting the ATE as a percentage

Here we use the same model as in example 1, but we report the ATE as a percentage of the mean birthweight that would occur if no mothers smoke. First, we use `teffects ipw` to fit the model. We use the `coeflegend` option so that `teffects ipw` reports the names of the parameters. Then we use `nlcom` to obtain the statistic we want along with its delta-method-based standard error. We type

```
. teffects ipw (bweight) (mbsmoke mmarried c.mage##c.mage fbaby medu, probit),
> coeflegend
```

```
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	Coef. Legend
ATE mbsmoke (smoker vs nonsmoker)	-230.6886 _b[ATE:r1vs0.mbsmoke]
P0mean mbsmoke nonsmoker	3403.463 _b[P0mean:0.mbsmoke]

```
. nlcom _b[ATE:r1vs0.mbsmoke] / _b[P0mean:0.mbsmoke]
      _nl_1: _b[ATE:r1vs0.mbsmoke] / _b[P0mean:0.mbsmoke]
```

bweight	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
_nl_1	-.0677806	.0075169	-9.02	0.000	-.0825133 - .0530478

The average birthweight falls by an estimated 6.8% when every mother smokes relative to the case when no mothers smoke. We also obtain a 95% confidence interval of a 5.3% to 8.3% reduction.



Video example

Treatment effects: Inverse-probability weighting

Stored results

teffects ipw stores the following in `e()`:

Scalars

<code>e(N)</code>	number of observations
<code>e(nj)</code>	number of observations for treatment level j
<code>e(N_clust)</code>	number of clusters
<code>e(k_eq)</code>	number of equations in <code>e(b)</code>
<code>e(k_levels)</code>	number of levels in treatment variable
<code>e(treated)</code>	level of treatment variable defined as treated
<code>e(control)</code>	level of treatment variable defined as control
<code>e(converged)</code>	1 if converged, 0 otherwise

Macros

<code>e(cmd)</code>	teffects
<code>e(cmdline)</code>	command as typed
<code>e(depyvar)</code>	name of outcome variable
<code>e(tvar)</code>	name of treatment variable
<code>e(subcmd)</code>	<code>ipw</code>
<code>e(tmodel)</code>	<code>logit</code> , <code>probit</code> , or <code>hetprobit</code>
<code>e(stat)</code>	statistic estimated, <code>ate</code> , <code>atet</code> , or <code>pomeans</code>
<code>e(wtype)</code>	weight type
<code>e(wexp)</code>	weight expression
<code>e(title)</code>	title in estimation output
<code>e(clustvar)</code>	name of cluster variable
<code>e(levels)</code>	levels of treatment variable
<code>e(vce)</code>	<code>vcetype</code> specified in <code>vce()</code>
<code>e(vcetype)</code>	title used to label Std. Err.
<code>e(properties)</code>	<code>b V</code>
<code>e(estat_cmd)</code>	program used to implement <code>estat</code>
<code>e(predict)</code>	program used to implement <code>predict</code>
<code>e(marginsnotok)</code>	predictions disallowed by <code>margins</code>
<code>e(asbalanced)</code>	factor variables <code>fvset</code> as <code>asbalanced</code>
<code>e(asobserved)</code>	factor variables <code>fvset</code> as <code>asobserved</code>

Matrices

<code>e(b)</code>	coefficient vector
<code>e(V)</code>	variance–covariance matrix of the estimators

Functions

<code>e(sample)</code>	marks estimation sample
------------------------	-------------------------

Methods and formulas

teffects ipw implements a smooth treatment-effects estimator. All smooth treatment-effects estimators are documented in [Methods and formulas of \[TE\] teffects aipw](#).

References

- Cattaneo, M. D. 2010. Efficient semiparametric estimation of multi-valued treatment effects under ignorability. *Journal of Econometrics* 155: 138–154.
- Cerulli, G. 2014. `treatrew`: A user-written command for estimating average treatment effects by reweighting on the propensity score. *Stata Journal* 14: 541–561.
- Drukker, D. M. 2014. Using gmm to solve two-step estimation problems. *The Stata Blog: Not Elsewhere Classified*. <http://blog.stata.com/2014/12/08/using-gmm-to-solve-two-step-estimation-problems/>.
- Huber, C. 2015. Introduction to treatment effects in Stata: Part 1. *The Stata Blog: Not Elsewhere Classified*. <http://blog.stata.com/2015/07/07/introduction-to-treatment-effects-in-stata-part-1/>.

Also see

- [TE] **teffects postestimation** — Postestimation tools for teffects
- [TE] **teffects** — Treatment-effects estimation for observational data
- [U] **20 Estimation and postestimation commands**

teffects ipwra — Inverse-probability-weighted regression adjustment

Description	Quick start	Menu	Syntax
Options	Remarks and examples	Stored results	Methods and formulas
References	Also see		

Description

teffects ipwra estimates the average treatment effect (ATE), the average treatment effect on the treated (ATET), and the potential-outcome means (POMs) from observational data by inverse-probability-weighted regression adjustment (IPWRA). IPWRA estimators use weighted regression coefficients to compute averages of treatment-level predicted outcomes, where the weights are the estimated inverse probabilities of treatment. The contrasts of these averages estimate the treatment effects. IPWRA estimators have the double-robust property. **teffects ipwra** accepts a continuous, binary, count, fractional, or nonnegative outcome and allows a multivalued treatment.

See [TE] **teffects intro** or [TE] **teffects intro advanced** for more information about estimating treatment effects from observational data.

Quick start

ATE of binary treatment `treat2` estimated by IPWRA using a linear model for outcome `y1` on `x1` and `x2` and a logistic model for `treat2` on `x1` and `w`

```
teffects ipwra (y1 x1 x2) (treat2 x1 w)
```

As above, but estimate the ATET

```
teffects ipwra (y1 x1 x2) (treat2 x1 w), atet
```

Probit model for binary outcome `y3`

```
teffects ipwra (y3 x1 x2, probit) (treat2 x1 w)
```

As above, but use a heteroskedastic probit model for `y3` and a probit model for `treat2`

```
teffects ipwra (y3 x1 x2, hetprobit(x1 x2)) (treat2 x1 w, probit)
```

As above, but use a fractional heteroskedastic probit model for `y4` and a probit model for `treat2`

```
teffects ipwra (y4 x1 x2, fhetprobit(x1 x2)) (treat2 x1 w, probit)
```

ATE for each level of a three-valued treatment `treat3`

```
teffects ipwra (y1 x1 x2) (treat3 x1 w)
```

As above, and specify that `treat3 = 3` is the control level using the value label “MyControl” for 3

```
teffects ipwra (y1 x1 x2) (treat3 x1 w), control(MyControl)
```

Menu

Statistics > Treatment effects > Continuous outcomes > Regression adjustment with IPW

Statistics > Treatment effects > Binary outcomes > Regression adjustment with IPW

Statistics > Treatment effects > Count outcomes > Regression adjustment with IPW

Statistics > Treatment effects > Fractional outcomes > Regression adjustment with IPW

Statistics > Treatment effects > Nonnegative outcomes > Regression adjustment with IPW

Syntax

```
teffects ipwra (ovar omvarlist [ , omodel noconstant ] )
    (tvar tmvarlist [ , tmodel noconstant ]) [if] [in] [weight]
    [ , stat options ]
```

ovar is a binary, count, continuous, fractional, or nonnegative outcome of interest.

omvarlist specifies the covariates in the outcome model.

tvar must contain integer values representing the treatment levels.

tmvarlist specifies the covariates in the treatment-assignment model.

<i>omodel</i>	Description
Model	
<code>linear</code>	linear outcome model; the default
<code>logit</code>	logistic outcome model
<code>probit</code>	probit outcome model
<code>hetprobit</code> (<i>varlist</i>)	heteroskedastic probit outcome model
<code>poisson</code>	exponential outcome model
<code>flogit</code>	fractional logistic outcome model
<code>fprobit</code>	fractional probit outcome model
<code>fhetprobit</code> (<i>varlist</i>)	fractional heteroskedastic probit outcome model

omodel specifies the model for the outcome variable.

<i>tmodel</i>	Description
Model	
<code>logit</code>	logistic treatment model; the default
<code>probit</code>	probit treatment model
<code>hetprobit</code> (<i>varlist</i>)	heteroskedastic probit treatment model

tmodel specifies the model for the treatment variable.

For multivalued treatments, only `logit` is available and multinomial logit is used.

<i>stat</i>	Description
Stat	
<code>ate</code>	estimate average treatment effect in population; the default
<code>atet</code>	estimate average treatment effect on the treated
<code>pomeans</code>	estimate potential-outcome means

options	Description
SE/Robust	
<code>vce(vcetype)</code>	<code>vcetype</code> may be <code>robust</code> , <code>cluster clustvar</code> , <code>bootstrap</code> , or <code>jackknife</code>
Reporting	
<code>level(#)</code>	set confidence level; default is <code>level(95)</code>
<code>aequations</code>	display auxiliary-equation results
<code>display_options</code>	control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling
Maximization	
<code>maximize_options</code>	control the maximization process; seldom used
Advanced	
<code>pstolerance(#)</code>	set tolerance for overlap assumption
<code>osample(newvar)</code>	<code>newvar</code> identifies observations that violate the overlap assumption
<code>control(# label)</code>	specify the level of <code>tvar</code> that is the control
<code>tlevel(# label)</code>	specify the level of <code>tvar</code> that is the treatment
<code>coeflegend</code>	display legend instead of statistics

omvarlist and *tmvarlist* may contain factor variables; see [U] 11.4.3 Factor variables.

`bootstrap`, `by`, `jackknife`, and `statsby` are allowed; see [U] 11.1.10 Prefix commands.

Weights are not allowed with the `bootstrap` prefix; see [R] bootstrap.

`fweights`, `iweights`, and `pweights` are allowed; see [U] 11.1.6 weight.

`coeflegend` does not appear in the dialog box.

See [U] 20 Estimation and postestimation commands for more capabilities of estimation commands.

Options

Model

`noconstant`; see [R] Estimation options.

Stat

`stat` is one of three statistics: `ate`, `atet`, or `pomeans`. `ate` is the default.

`ate` specifies that the average treatment effect be estimated.

`atet` specifies that the average treatment effect on the treated be estimated.

`pomeans` specifies that the potential-outcome means for each treatment level be estimated.

SE/Robust

`vce(vcetype)` specifies the type of standard error reported, which includes types that are robust to some kinds of misspecification (`robust`), that allow for intragroup correlation (`cluster clustvar`), and that use bootstrap or jackknife methods (`bootstrap`, `jackknife`); see [R] vce_option.

Reporting

`level(#)`; see [R] **Estimation options**.

`aequations` specifies that the results for the outcome-model or the treatment-model parameters be displayed. By default, the results for these auxiliary parameters are not displayed.

`display_options`: `noci`, `nopvalues`, `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `nofvlabel`, `fwrap(#)`, `fwrapon(style)`, `cformat(%fmt)`, `pformat(%fmt)`, `sformat(%fmt)`, and `nolstretch`; see [R] **Estimation options**.

Maximization

`maximize_options`: `iterate(#)`, `[no]log`, and `from(init_specs)`; see [R] **Maximize**. These options are seldom used.

`init_specs` is one of

```
matname [, skip copy]
# [, # ...], copy
```

Advanced

`pstolerance(#)` specifies the tolerance used to check the overlap assumption. The default value is `pstolerance(1e-5)`. `teffects` will exit with an error if an observation has an estimated propensity score smaller than that specified by `pstolerance()`.

`osample(newvar)` specifies that indicator variable `newvar` be created to identify observations that violate the overlap assumption.

`control(#|label)` specifies the level of `tvar` that is the control. The default is the first treatment level. You may specify the numeric level `#` (a nonnegative integer) or the label associated with the numeric level. `control()` may not be specified with statistic `pomeans`. `control()` and `tlevel()` may not specify the same treatment level.

`tlevel(#|label)` specifies the level of `tvar` that is the treatment for the statistic `atet`. The default is the second treatment level. You may specify the numeric level `#` (a nonnegative integer) or the label associated with the numeric level. `tlevel()` may only be specified with statistic `atet`. `tlevel()` and `control()` may not specify the same treatment level.

The following option is available with `teffects ipwra` but is not shown in the dialog box:
`coeflegend`; see [R] **Estimation options**.

Remarks and examples

Remarks are presented under the following headings:

[Overview](#)
[Video example](#)

Overview

IPWRA estimators use probability weights to obtain outcome-regression parameters that account for the missing-data problem arising from the fact that each subject is observed in only one of the potential outcomes. The adjusted outcome-regression parameters are used to compute averages of treatment-level predicted outcomes. The contrasts of these averages provide estimates of the treatment effects.

IPWRA estimators use a model to predict treatment status, and they use another model to predict outcomes. Because IPWRA estimators have the double-robust property, only one of the two models must be correctly specified for the IPWRA estimator to be consistent.

IPWRA estimators use a three-step approach to estimating treatment effects:

1. They estimate the parameters of the treatment model and compute inverse-probability weights.
2. Using the estimated inverse-probability weights, they fit weighted regression models of the outcome for each treatment level and obtain the treatment-specific predicted outcomes for each subject.
3. They compute the means of the treatment-specific predicted outcomes. The contrasts of these averages provide the estimates of the ATEs. By restricting the computations of the means to the subset of treated subjects, we can obtain the ATETs.

These steps produce consistent estimates of the effect parameters because the treatment is assumed to be independent of the potential outcomes after conditioning on the covariates. The overlap assumption ensures that predicted inverse-probability weights do not get too large. The standard errors reported by **teffects ipwra** correct for the three-step process. See [TE] **teffects intro** or [TE] **teffects intro advanced** for more information about this estimator.

We will illustrate the use of **teffects ipwra** by using data from a study of the effect of a mother's smoking status during pregnancy (**mbsmoke**) on infant birthweight (**bweight**) as reported by Cattaneo (2010). This dataset also contains information about each mother's age (**mage**), education level (**medu**), marital status (**mmarried**), whether the first prenatal exam occurred in the first trimester (**prenatal1**), and whether this baby was the mother's first birth (**fbaby**).

▷ Example 1: Estimating the ATE

We begin by using **teffects ipwra** to estimate the average treatment effect of smoking on birthweight. We will use a probit model to predict treatment status as a function of **mmarried**, **mage**, and **fbaby**; to maximize the predictive power of this model, we use factor-variable notation to incorporate quadratic effects of the mother's age, the only continuous covariate in our model. We will use linear regression (the default) to model birthweight, using **prenatal1**, **mmarried**, **mage**, and **fbaby** as explanatory variables. We type

<pre>. use https://www.stata-press.com/data/r16/cattaneo2 (Excerpt from Cattaneo (2010) Journal of Econometrics 155: 138-154) . teffects ipwra (bweight prenatal1 mmarrried mage fbaby) > (mbsmoke mmarrried c.mage##c.mage fbaby medu, probit) Iteration 0: EE criterion = 9.885e-21 Iteration 1: EE criterion = 7.847e-26 Treatment-effects estimation Number of obs = 4,642 Estimator : IPW regression adjustment Outcome model : linear Treatment model: probit</pre>						
<hr/>						
bweight	Robust Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
ATE mbsmoke (smoker vs nonsmoker)	-229.9671	26.62668	-8.64	0.000	-282.1544	-177.7798
P0mean mbsmoke nonsmoker	3403.336	9.57126	355.58	0.000	3384.576	3422.095

The average birthweight if all mothers were to smoke would be 230 grams less than the average of 3,403 grams that would occur if none of the mothers had smoked.



By default, `teffects ipwra` displays the ATE and untreated POM. We can specify the `pomeans` option to display both the treated and untreated POMs, and we can use the `aequations` option to display the regression model coefficients used to predict the POMs as well as the coefficients from the model used to predict treatment.

► Example 2: Displaying the POMs and equations

```
. use https://www.stata-press.com/data/r16/cattaneo2
(Excerpt from Cattaneo (2010) Journal of Econometrics 155: 138–154)
. teffects ipwra (bweight prenatal1 mmarried mage fbaby)
> (mbsmoke mmarried c.mage##c.mage fbaby medu, probit), pomeans aequations
Iteration 0: EE criterion = 9.885e-21
Iteration 1: EE criterion = 6.922e-26
Treatment-effects estimation                               Number of obs      =     4,642
Estimator        : IPW regression adjustment
Outcome model   : linear
Treatment model: probit
```

bweight	Robust					
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
POmeans						
mbsmoke						
nonsmoker	3403.336	9.57126	355.58	0.000	3384.576	3422.095
smoker	3173.369	24.86997	127.60	0.000	3124.624	3222.113
OME0						
prenatal1	67.98549	28.78428	2.36	0.018	11.56933	124.4017
mmarried	155.5893	26.46903	5.88	0.000	103.711	207.4677
mage	2.893051	2.134788	1.36	0.175	-1.291056	7.077158
fbaby	-71.9215	20.39317	-3.53	0.000	-111.8914	-31.95162
_cons	3194.808	55.04911	58.04	0.000	3086.913	3302.702
OME1						
prenatal1	34.76923	43.18534	0.81	0.421	-49.87248	119.4109
mmarried	124.0941	40.29775	3.08	0.002	45.11193	203.0762
mage	-5.068833	5.954425	-0.85	0.395	-16.73929	6.601626
fbaby	39.89692	56.82072	0.70	0.483	-71.46966	151.2635
_cons	3175.551	153.8312	20.64	0.000	2874.047	3477.054
TME1						
mmarried	-.6484821	.0554173	-11.70	0.000	-.757098	-.5398663
mage	.1744327	.0363718	4.80	0.000	.1031452	.2457202
c.mage# c.mage	-.0032559	.0006678	-4.88	0.000	-.0045647	-.0019471
fbaby	-.2175962	.0495604	-4.39	0.000	-.3147328	-.1204595
medu	-.0863631	.0100148	-8.62	0.000	-.1059917	-.0667345
_cons	-1.558255	.4639691	-3.36	0.001	-2.467618	-.6488926



As is well known, the standard probit model assumes that the error terms in the latent-utility framework are homoskedastic; the model is not robust to departures from this assumption. An alternative is to use the heteroskedastic probit model, which explicitly models the error variance as a function of a set of variables.

► Example 3: Heteroskedastic probit treatment model

Here we use the variables as before, but we use a heteroskedastic probit model to predict treatment status, modeling the heteroskedasticity as a quadratic function of the mother's age:

Treatment-effects estimation							Number of obs = 4,642
		Robust					
bweight		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
ATE	mbsmoke (smoker vs nonsmoker)	-229.6322	26.33452	-8.72	0.000	-281.2469	-178.0175
P0mean	mbsmoke nonsmoker	3403.74	9.545798	356.57	0.000	3385.03	3422.449
OME0	prenatal1 mmarried fbaby mage _cons	64.95125 154.2297 -71.61131 3.010148 3195.355	28.62159 26.45867 20.33774 2.133812 55.05451	2.27 5.83 -3.52 1.41 58.04	0.023 0.000 0.000 0.158 0.000	8.853958 102.3717 -111.4725 -1.172047 3087.45	121.0485 206.0878 -31.75006 7.192343 3303.26
OME1	prenatal1 mmarried fbaby mage _cons	38.55274 126.3377 45.43547 -6.069913 3195.795	43.57024 40.7398 56.4483 5.95251 152.3979	0.88 3.10 0.80 -1.02 20.97	0.376 0.002 0.421 0.308 0.000	-46.84336 46.48921 -65.20116 -17.73662 2897.101	123.9488 206.1863 156.0721 5.596792 3494.49
TME1	mmarried mage c.mage# c.mage fbaby medu _cons	-.0295523 .0157893 -.0002837 -.0093306 -.0036773 -.1822201	.0238951 .0105486 .0001901 .0080003 .0030317 .1180587	-.1.24 1.50 -1.49 -1.17 -1.21 -1.54	0.216 0.134 0.136 0.244 0.225 0.123	-.0763857 -.0048857 -.0006563 -.025011 -.0096193 -.4136109	.0172812 .0364643 .0000888 .0063497 .0022647 .0491707
TME1_lnsigma	mage c.mage# c.mage	-.2211492 .0037613	.0631504 .0012437	-3.50 3.02	0.000 0.002	-.3449217 .0013236	-.0973767 .006199

The estimated ATE and base-level POM are essentially the same as those produced by the model that used a homoskedastic probit.



Video example

Treatment effects: Inverse-probability-weighted regression adjustment

Stored results

teffects ipwra stores the following in `e()`:

Scalars

<code>e(N)</code>	number of observations
<code>e(nj)</code>	number of observations for treatment level j
<code>e(N_clust)</code>	number of clusters
<code>e(k_eq)</code>	number of equations in <code>e(b)</code>
<code>e(k_levels)</code>	number of levels in treatment variable
<code>e(treated)</code>	level of treatment variable defined as treated
<code>e(control)</code>	level of treatment variable defined as control
<code>e(converged)</code>	1 if converged, 0 otherwise

Macros

<code>e(cmd)</code>	teffects
<code>e(cmdline)</code>	command as typed
<code>e(depvar)</code>	name of outcome variable
<code>e(tvar)</code>	name of treatment variable
<code>e(subcmd)</code>	ipwra
<code>e(tmodel)</code>	logit , probit , or hetprobit
<code>e(omodel)</code>	linear , logit , probit , hetprobit , Poisson , flogit , fprobit , or hetfprobit
<code>e(stat)</code>	statistic estimated, ate , atet , or pomeans
<code>e(wtype)</code>	weight type
<code>e(wexp)</code>	weight expression
<code>e(title)</code>	title in estimation output
<code>e(clustvar)</code>	name of cluster variable
<code>e(levels)</code>	levels of treatment variable
<code>e(vce)</code>	<i>vcetype</i> specified in <code>vce()</code>
<code>e(vcetype)</code>	title used to label Std. Err.
<code>e(properties)</code>	b V
<code>e(estat_cmd)</code>	program used to implement <code>estat</code>
<code>e(predict)</code>	program used to implement <code>predict</code>
<code>e(marginsnotok)</code>	predictions disallowed by <code>margins</code>
<code>e(asbalanced)</code>	factor variables <code>fvset</code> as <code>asbalanced</code>
<code>e(asobserved)</code>	factor variables <code>fvset</code> as <code>asobserved</code>

Matrices

<code>e(b)</code>	coefficient vector
<code>e(V)</code>	variance–covariance matrix of the estimators

Functions

<code>e(sample)</code>	marks estimation sample
------------------------	-------------------------

Methods and formulas

teffects ipwra implements a smooth treatment-effects estimator. All smooth treatment-effects estimators are documented in *Methods and formulas* of [TE] **teffects aipw**.

References

- Cattaneo, M. D. 2010. Efficient semiparametric estimation of multi-valued treatment effects under ignorability. *Journal of Econometrics* 155: 138–154.
- Huber, C. 2015. Introduction to treatment effects in Stata: Part 1. *The Stata Blog: Not Elsewhere Classified*. <http://blog.stata.com/2015/07/07/introduction-to-treatment-effects-in-stata-part-1/>.

Also see

- [TE] **teffects postestimation** — Postestimation tools for teffects
- [TE] **teffects** — Treatment-effects estimation for observational data
- [TE] **teffects aipw** — Augmented inverse-probability weighting
- [U] **20 Estimation and postestimation commands**

Description

This entry discusses the use of `teffects` when the treatment is multivalued. This entry presumes you are already familiar with the potential-outcome framework and the use of the `teffects` commands with binary treatments. See [TE] `teffects intro` or [TE] `teffects intro advanced` for more information.

Remarks and examples

Remarks are presented under the following headings:

Introduction

Parameters and notation

Illustrating multivalued treatments

Examples

Introduction

When the treatment is binary, each subject could either receive the treatment or not receive the treatment. In contrast, multivalued treatments refer to cases in which each subject could receive one of several different treatments or else not receive treatment at all. For example, in testing the efficacy of a drug, a patient could receive a 10 milligram (mg) dose, a 20 mg dose, a 30 mg dose, or no dose at all. We first want to be able to compare a patient receiving the 10 mg dose with a patient receiving no dose, a patient receiving the 20 mg dose with a patient receiving no dose, and a patient receiving the 30 mg dose with a patient receiving no dose. Once we can make those comparisons, we can then, for example, compare the efficacy of a 30 mg dose with that of a 20 mg dose or a 10 mg dose.

To highlight an example in economics, we consider an unemployed person who could participate in a comprehensive skills training program, attend a one-day workshop that helps job seekers write their resumés, or choose not to participate in either. We want to know how effective each of those programs is relative to not participating; once we know that, we can then compare the effectiveness of the comprehensive program with that of the one-day program.

Multivalued treatments increase the number of parameters that must be estimated and complicate the notation. Fortunately, however, using the `teffects` commands is not much more difficult with multivalued treatments than with binary treatments.

You can use `teffects ra`, `teffects ipw`, `teffects ipwra`, and `teffects aipw` to estimate multivalued treatment effects. However, the theory developed in [Abadie and Imbens \(2006, 2012\)](#) has not been extended to handle multivalued treatments, so you cannot use `teffects nnmatch` or `teffects psmatch` in these cases.

[Cattaneo \(2010\)](#), [Imbens \(2000\)](#), and [Wooldridge \(2010, sec. 21.6.3\)](#) discuss aspects of treatment-effect estimation with multivalued treatments.

Parameters and notation

We denote the potential outcome that subject i would obtain if given treatment-level t as y_{ti} , where y_{ti} is the realization of the random variable y_t . Throughout this entry, i subscripts denote realizations of the corresponding unsubscripted random variables. We again let y_0 denote the potential outcome of a subject who did not receive any treatment. To handle the case of multivalued treatments, we extend the definition of the unobservable, individual-level treatment effects to be $y_t - y_0$ for $t \in \{1, \dots, q\}$.

As in the binary-valued case, we again focus on three parameters of interest: the average treatment effect (ATE), the potential-outcome mean (POM), and the average treatment effect on the treated (ATET).

ATE The ATE is the average effect of giving each individual treatment t instead of treatment 0:

$$\text{ATE}_t = E(y_t - y_0)$$

POM The POM for each treatment level is an average of each potential outcome:

$$\text{POM}_t = E(y_t)$$

ATET The ATET is the average effect among those subjects that receive treatment level \tilde{t} of giving each subject treatment \tilde{t} instead of treatment 0:

$$\text{ATET}_{\tilde{t}, \tilde{t}} = E \{(y_{\tilde{t}} - y_0) | t = \tilde{t}\}$$

The extra notation required to define the ATET in this case indicates the difficulties surrounding this parameter.

Defining the ATET in the multivalued treatment case requires three different treatment levels: \tilde{t} defines the treatment level of the treated potential outcome; 0 is the treatment level of the control potential outcome; and $t = \tilde{t}$ restricts the expectation to include only those individuals who actually receive treatment level \tilde{t} .

Illustrating multivalued treatments

To illustrate the concept of a potential outcome and the parameters we would like to estimate, we consider the following table:

y	t	y_0	y_1	y_2
-0.50	0	-0.50	1.06	1.93
2.42	1	2.13	2.42	2.43
3.15	2	1.26	2.57	3.15
-0.39	0	-0.39	-0.18	0.52
2.22	2	-0.24	-0.01	2.22

We observe the outcome y as well as the treatment indicator t . There are three levels of treatment: 0, 1, or 2. Ideally, we would observe y_0 , y_1 , and y_2 , but in fact all we have is y . In the first row, the subject received treatment level 0, so $y = y_0$ for that subject. In the last row, the subject received treatment 2, so $y = y_2$. We reiterate that we do not actually observe y_0 , y_1 , or y_2 .

If we did have data on y_0 , y_1 , and y_2 , then we could define subject-level treatment variables $te_1 = y_1 - y_0$ and $te_2 = y_2 - y_0$. Here we would be following the convention of taking treatment level 0 to be the control level. The following table adds these two variables:

y	t	y_0	y_1	y_2	te_1	te_2
-0.50	0	-0.50	1.06	1.93	1.56	2.43
2.42	1	2.13	2.42	2.43	0.29	0.30
3.15	2	1.26	2.57	3.15	1.31	1.89
-0.39	0	-0.39	-0.18	0.52	0.21	0.91
2.22	2	-0.24	-0.01	2.22	0.23	2.46

Once we have te_1 and te_2 , obtaining the ATEs is straightforward. The ATE of going from treatment 0 to treatment 1 is simply the mean of the five entries in the column labeled te_1 , which here works out to 0.72. Going from treatment level 0 to treatment level 1 causes the outcome to increase an average of 0.72. Similarly, the ATE of going from treatment 0 to treatment 2 is the mean of the entries in the column labeled te_2 , which is 1.60. Exposing all subjects to treatment level 2 would cause the outcome to rise by an average of 1.60 relative to the outcome obtained by exposing them to treatment level 0.

The ATET is the average difference in the potential outcomes among those that get a particular treatment level. To compute this, we must specify two treatment levels: the actual treatment level the subjects we are interested in received as well as the treatment level we want to compare them with. For example, suppose we are interested in the ATET of going from treatment 0 to treatment 1 for those who received treatment 0. This ATET is the average of te_1 for those subjects for which $t = 0$. Here that ATET is just $(1.56 + 0.21)/2 \approx 0.89$. If we exposed the subjects who received treatment 0 to treatment 1 instead, the outcome would increase an average of 0.89.

The ATET of going from treatment 0 to treatment 2 for those subjects who received treatment 2 is the mean of te_2 for those subjects for which $t = 2$, which is $(1.89 + 2.46)/2 \approx 2.18$. Receiving treatment 2 increased the outcome of those who received treatment 2 by an average of 2.18 relative to receiving the control.

Examples

In the remainder of this entry, we provide several examples demonstrating how to estimate multivalued treatments using **teffects**.

Example 1: Potential outcomes with four treatment levels

`bdsianesi5.dta` contains an extract of data from Blundell, Dearden, and Sianesi (2005). In this dataset on individuals in the United Kingdom, `wages` records hourly wages in pounds; `ed` records the highest educational degree obtained; `paed` records the highest educational level obtained by each individual's father; `math7` records a score obtained on a standardized math test when the individual was seven; `read7` records a score obtained on a standardized reading test when the individual was seven; and `london` and `eastern` are indicators for whether an individual lives in the expensive area of London or the east. We want to know how the level of education obtained affects a person's wage.

We begin by using `mean` to report the estimated means of wages over the four education levels. The value labels on `mean` are coded as `none` for no degree, `0` for an O-level degree, `A` for an A-level degree, or `H` for a higher-education degree.

```
. use https://www.stata-press.com/data/r16/bdsianesi5
(Excerpt from Blundell, Dearden, & Sianesi (2005) JRSSA 168: 473)
```

```
. mean wage, over(ed)
```

Mean estimation	Number of obs	=	1,693
-----------------	---------------	---	-------

	Mean	Std. Err.	[95% Conf. Interval]	
c.wage@ed				
none	6.057816	.154332	5.755114	6.360518
O	7.501648	.1807359	7.147158	7.856137
A	8.220637	.1540359	7.918516	8.522758
H	10.87703	.2257888	10.43417	11.31988

The output reveals that the estimated mean wage increases as the education level goes from no degree to an O-level degree, to an A-level degree, and to a higher-education degree, as we would expect. Once we control for other characteristics of each individual, do we still observe a positive effect of education on wage?

We use **teffects ra** (see [TE] **teffects ra**) to estimate the ATEs of the different education levels by regression adjustment (RA), controlling for each person's location, math score, and father's education level:

wage	Coef.	Robust Std. Err.	z	P> z	[95% Conf. Interval]
Treatment-effects estimation					
Estimator	: regression adjustment				
Outcome model	: Poisson				
Treatment model:	none				
ATE					
ed					
(O vs none)	1.181543	.3520371	3.36	0.001	.4915626 1.871523
(A vs none)	1.743079	.3282152	5.31	0.000	1.099789 2.386369
(H vs none)	3.972829	.3840024	10.35	0.000	3.220199 4.72546
P0mean					
ed					
none	6.525873	.2931933	22.26	0.000	5.951224 7.100521

Because wages are necessarily positive, we used the **poisson** option inside the outcome-model specification. The estimated POM of the control level of no degree is 6.53 pounds per hour. The estimated ATE of going from no degree to an O-level degree is 1.18 pounds per hour; the estimated ATE of going from no degree to an A-level degree is 1.74 pounds per hour; and the estimated ATE of going from no degree to a higher-education degree is 3.97 pounds per hour. All of these effects are highly significant.

For comparison purposes, we also use **teffects aipw** (see [TE] **teffects aipw**). We use the same outcome model as before. We use a multinomial logit model to predict education level, using math and reading scores and both the father's and the mother's educational attainment levels as predictors:

```
. teffects aipw (wage london eastern paed math7, poisson)
> (ed math7 read7 maed paed)
```

Iteration 0: EE criterion = 1.877e-18

Iteration 1: EE criterion = 1.029e-30

Treatment-effects estimation Number of obs = 1,693
Estimator : augmented IPW
Outcome model : Poisson by ML
Treatment model: (multinomial) logit

wage	Robust				
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ATE					
ed					
(O vs none)	1.748197	.3911167	4.47	0.000	.9816221 2.514771
(A vs none)	2.363228	.3741584	6.32	0.000	1.629891 3.096565
(H vs none)	4.359777	.4133059	10.55	0.000	3.549712 5.169842
P0mean					
ed					
none	5.946184	.3391531	17.53	0.000	5.281456 6.610912

The results indicate slightly higher treatment effects relative to those indicated by `teffects ra`. That is largely because the AIPW estimator predicts a lower no-higher-education POM than the RA estimator.



▷ Example 2: Expressing ATEs as percentages

As in the binary-treatment case, expressing the ATEs as percentages of the POM for the control level often aids interpretation. Here we first use the replay facility of `teffects aipw` along with the `coeflegend` option to see how the parameters are named.

```
. teffects, coeflegend
Treatment-effects estimation Number of obs = 1,693
Estimator : augmented IPW
Outcome model : Poisson by ML
Treatment model: (multinomial) logit
```

wage	Coef. Legend
ATE	
ed	
(O vs none)	1.748197 _b[ATE:r1vs0.ed]
(A vs none)	2.363228 _b[ATE:r2vs0.ed]
(H vs none)	4.359777 _b[ATE:r3vs0.ed]
P0mean	
ed	
none	5.946184 _b[P0mean:0.ed]

Now that we know the names, we can use `nlcom` to obtain the ATEs relative to the base-level POM:

```
. nlcom (_b[ATE:r1vs0.ed] / _b[P0mean:0.ed])
>      (_b[ATE:r2vs0.ed] / _b[P0mean:0.ed])
>      (_b[ATE:r3vs0.ed] / _b[P0mean:0.ed])

_nl_1: _b[ATE:r1vs0.ed] / _b[P0mean:0.ed]
_nl_2: _b[ATE:r2vs0.ed] / _b[P0mean:0.ed]
_nl_3: _b[ATE:r3vs0.ed] / _b[P0mean:0.ed]
```

wage	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
_nl_1	.2940031	.0808156	3.64	0.000	.1356075 .4523988
_nl_2	.3974361	.0840545	4.73	0.000	.2326923 .5621799
_nl_3	.7332059	.1068848	6.86	0.000	.5237156 .9426962

Wages are 29% higher when everyone receives an O-level degree than if no one receives a degree.
 Wages are 40% higher when everyone receives an A-level degree than if no one receives a degree.
 Wages are 73% higher when everyone receives an H-level degree than if no one receives a degree.

Although impressive, these changes are not presented in the way that is most commonly discussed. (There is a large amount of literature on the treatment effect of getting a higher-education degree.) In particular, we might rather want to know the percentage changes in wages relative to a person with an A-level degree. Next we estimate the ATEs treating an A-level degree as the control level; to do that, we use the `control()` option. We also specify `coeflegend` again because we are more interested in how the parameters are named rather than in their standard errors at this point:

```
. teffects aipw (wage london eastern paed math7, poisson)
> (ed math7 read7 maed paed), control(A) coeflegend

Iteration 0:  EE criterion =  1.870e-18
Iteration 1:  EE criterion =  2.882e-30

Treatment-effects estimation                               Number of obs      =      1,693
Estimator        : augmented IPW
Outcome model   : Poisson by ML
Treatment model: (multinomial) logit
```

wage	Coef. Legend
ATE	
ed	
(none vs A)	-2.363228 _b[ATE:r0vs2.ed]
(O vs A)	-.6150312 _b[ATE:r1vs2.ed]
(H vs A)	1.996549 _b[ATE:r3vs2.ed]
P0mean	
ed	
A	8.309412 _b[P0mean:2.ed]

Now we use `nlcom` to obtain the ATE of obtaining a higher-education degree as a percentage of the expected A-level wage:

```
. nlcom _b[ATE:r3vs2.ed] / _b[P0mean:2.ed], noheader
```

wage	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
_nl_1	.2402756	.0355404	6.76	0.000	.1706177 .3099335

The average wage increases by 24% when everyone receives an H-level degree relative to when everyone receives an A-level degree.



▷ Example 3: Obtaining ATETs

In the previous example, we showed that on average, a higher-education degree increases a person's wage by 24% relative to someone with only an A-level degree. Sometimes, though, we would rather know how much the higher-education degree increases wages among the people who actually have a higher-education degree. To answer that question, we want to examine the ATET rather than the ATE.

Here we use the IPWRA estimator to obtain our answer. We specify the `control(A)` option so that an A-level education is treated as the basis for comparisons. We specify the `atet` option to obtain ATETs rather than ATEs, and we specify the `tlevel(H)` option to indicate that we want the ATETs to be calculated for the subset of people who actually receive higher-education degrees.

Treatment-effects estimation						
		Number of obs = 1,693				
		Estimator : IPW regression adjustment				
		Outcome model : Poisson				
		Treatment model: (multinomial) logit				
wage		Robust				
		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ATET	ed					
(none vs A)	ed	-2.87423	.361093	-7.96	0.000	-3.58196 -2.166501
(O vs A)	ed	-.8246604	.3609131	-2.28	0.022	-1.532037 -.1172837
(H vs A)	ed	1.866757	.3277701	5.70	0.000	1.224339 2.509174
P0mean	A	9.010271	.2503971	35.98	0.000	8.519501 9.50104

The point estimates are similar to the ATEs we obtained above, suggesting that the means of the covariates among those with a higher-education degree are similar to the means for the entire population.

In output not shown to save space, we replayed the previous results with the `coeflegend` option to determine how the parameters are named. Armed with that information, we call `nlcom`:

```
. nlcom _b[ATET:r3vs2.ed] / _b[P0mean:2.ed], noheader
```

wage	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
_nl_1	.207181	.0407528	5.08	0.000	.127307 .287055

Our estimate of the percentage increase is now noticeably smaller once we restrict ourselves to only those people who actually received a higher-education degree. However, because of the width of the confidence intervals, there is no evidence to suggest that the difference between the estimates is statistically significant.



► Example 4: ATEs comparing adjacent treatments

In the [first example](#), we obtained the three ATEs, and they were all expressed relative to the base level of no degree. Now we show how we can express the gains to an O-level degree relative to no degree, the gains to an A-level degree relative to an O-level degree, and the gains to a higher-education degree relative to an A-level degree.

First, we use an AIPW estimator to obtain all the POMs for our example dataset:

```
. teffects aipw (wage london eastern paed math7, poisson)
> (ed math7 read7 maed paed), pom
Iteration 0: EE criterion = 1.877e-18
Iteration 1: EE criterion = 1.542e-30
Treatment-effects estimation
Number of obs      =      1,693
Estimator       : augmented IPW
Outcome model   : Poisson by ML
Treatment model: (multinomial) logit
```

wage	Robust				
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
P0means					
ed					
none	5.946184	.3391531	17.53	0.000	5.281456 6.610912
O	7.694381	.1915192	40.18	0.000	7.31901 8.069752
A	8.309412	.1563348	53.15	0.000	8.003001 8.615823
H	10.30596	.2285837	45.09	0.000	9.857945 10.75398

ATEs are contrasts of POMs, and here we show how to use `contrast` to obtain the estimated ATEs:

```
. contrast r.ed, nowald
Warning: cannot perform check for estimable functions.
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	Contrast	Std. Err.	[95% Conf. Interval]
P0means			
ed			
(O vs none)	1.748197	.3911167	.9816221 2.514771
(A vs none)	2.363228	.3741584	1.629891 3.096565
(H vs none)	4.359777	.4133059	3.549712 5.169842

These estimated ATEs match those we obtained in [example 2](#).

Now that we know how to use `contrast` to obtain the ATEs based on the POMs, we can take advantage of `contrast`'s ability to obtain “reverse adjacent” contrasts, which compare each level with the previous level. We use the `ar.` operator with `contrast` to accomplish this:

```
. contrast ar.ed, nowald
Warning: cannot perform check for estimable functions.
Contrasts of marginal linear predictions
Margins      : asbalanced
```

	Contrast	Std. Err.	[95% Conf. Interval]	
P0means				
ed				
(0 vs none)	1.748197	.3911167	.9816221	2.514771
(A vs 0)	.6150312	.2432806	.13821	1.091852
(H vs A)	1.996549	.2730712	1.461339	2.531759

These ATEs are for incremental increases. In contrast, the ATEs considered above had a common base. 

□ Technical note

The multivalued treatment AIPW estimators implemented in **teffects aipw** are EIF estimators based on the results of Cattaneo (2010). The results in Cattaneo (2010) are for semiparametric estimators, and we implement parametric versions. Of more practical importance, Cattaneo (2010) contains results for quantile treatment effects that are not implemented in **teffects** but implemented in the community-contributed **popargs** command discussed in Cattaneo, Drukker, and Holland (2013). See Emsley et al. (2008) for another implementation of the AIPW estimator, and see Frölich and Melly (2010) for other commands that estimate quantile treatment effects. 

References

- Abadie, A., and G. W. Imbens. 2006. Large sample properties of matching estimators for average treatment effects. *Econometrica* 74: 235–267.
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Also see

- [TE] **teffects** — Treatment-effects estimation for observational data
- [TE] **teffects intro** — Introduction to treatment effects for observational data
- [TE] **teffects intro advanced** — Advanced introduction to treatment effects for observational data

teffects nnmatch — Nearest-neighbor matching

Description
Options
References

Quick start
Remarks and examples
Also see

Menu
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Syntax
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Description

teffects nnmatch estimates the average treatment effect (ATE) and average treatment effect on the treated (ATET) from observational data by nearest-neighbor matching (NNM). NNM estimators impute the missing potential outcome for each subject by using an average of the outcomes of similar subjects that receive the other treatment level. Similarity between subjects is based on a weighted function of the covariates for each observation. The treatment effect is computed by taking the average of the difference between the observed and imputed potential outcomes for each subject. **teffects nnmatch** accepts a continuous, binary, count, fractional, or nonnegative outcome.

See [TE] **teffects intro** or [TE] **teffects intro advanced** for more information about estimating treatment effects from observational data.

Quick start

ATE of `treat` on `y` estimated by NNM on `x1` and `indicators` for levels of categorical variable `a`

```
teffects nnmatch (y x1 i.a) (treat)
```

As above, but estimate the ATET

```
teffects nnmatch (y x1 i.a) (treat), atet
```

Add continuous covariate `x2` and perform bias correction

```
teffects nnmatch (y x1 x2 i.a) (treat), biasadj(x1 x2)
```

As above, and match exactly on values of `a`

```
teffects nnmatch (y x1 x2 i.a) (treat), biasadj(x1 x2) ematch(i.a)
```

With robust standard errors

```
teffects nnmatch (y x1 x2 i.a) (treat), vce(robust)
```

With four matches per observation

```
teffects nnmatch (y x1 x2 i.a) (treat), nneighbor(4)
```

Menu

Statistics > Treatment effects > Continuous outcomes > Nearest-neighbor matching

Statistics > Treatment effects > Binary outcomes > Nearest-neighbor matching

Statistics > Treatment effects > Count outcomes > Nearest-neighbor matching

Statistics > Treatment effects > Fractional outcomes > Nearest-neighbor matching

Statistics > Treatment effects > Nonnegative outcomes > Nearest-neighbor matching

Syntax

```
teffects nnmatch (ovar omvarlist) (tvar) [if] [in] [weight]
[ , stat options ]
```

ovar is a binary, count, continuous, fractional, or nonnegative outcome of interest.

omvarlist specifies the covariates in the outcome model.

tvar must contain integer values representing the treatment levels. Only two treatment levels are allowed.

<i>stat</i>	Description
Stat	
ate	estimate average treatment effect in population; the default
atet	estimate average treatment effect on the treated

<i>options</i>	Description
Model	

nneighbor (#)	specify number of matches per observation; default is nneighbor (1)
biasadj (<i>varlist</i>)	correct for large-sample bias using specified variables
ematch (<i>varlist</i>)	match exactly on specified variables
SE/Robust	
vce (<i>vcetype</i>)	<i>vcetype</i> may be vce(robust [, nn (#)]) ; use robust Abadie–Imbens standard errors with # matches vce(iid) ; use independently and identically distributed Abadie–Imbens standard errors
Reporting	
level (#)	set confidence level; default is level (95)
dmvariables	display names of matching variables
display_options	control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling
Advanced	
caliper (#)	specify the maximum distance for which two observations are potential neighbors
dtolerance (#)	set maximum distance between individuals considered equal
osample (<i>newvar</i>)	<i>newvar</i> identifies observations that violate the overlap assumption
control (# <i>label</i>)	specify the level of <i>tvar</i> that is the control
tlevel (# <i>label</i>)	specify the level of <i>tvar</i> that is the treatment
generate (<i>stub</i>)	generate variables containing the observation numbers of the nearest neighbors
metric (<i>metric</i>)	select distance metric for covariates
coeflegend	display legend instead of statistics

metric	Description
<code>mahalanobis</code>	inverse sample covariate covariance; the default
<code>ivariance</code>	inverse diagonal sample covariate covariance
<code>euclidean</code>	identity
<code>matrix matname</code>	user-supplied scaling matrix

`omvarlist` may contain factor variables; see [U] 11.4.3 Factor variables.

`by` and `statsby` are allowed; see [U] 11.1.10 Prefix commands.

`fweights` are allowed; see [U] 11.1.6 weight.

`coeflegend` does not appear in the dialog box.

See [U] 20 Estimation and postestimation commands for more capabilities of estimation commands.

Options

Model

`nneighbor(#)` specifies the number of matches per observation. The default is `nneighbor(1)`. Each observation is matched with at least the specified number of observations from the other treatment level. `nneighbor()` must specify an integer greater than or equal to 1 but no larger than the number of observations in the smallest treatment group.

`biasadj(varlist)` specifies that a linear function of the specified covariates be used to correct for a large-sample bias that exists when matching on more than one continuous covariate. By default, no correction is performed.

Abadie and Imbens (2006, 2011) show that nearest-neighbor matching estimators are not consistent when matching on two or more continuous covariates and propose a bias-corrected estimator that is consistent. The correction term uses a linear function of variables specified in `biasadj()`; see example 3.

`ematch(varlist)` specifies that the variables in `varlist` match exactly. All variables in `varlist` must be numeric and may be specified as factors. `teffects nnmatch` exits with an error if any observations do not have the requested exact match.

Stat

`stat` is one of two statistics: `ate` or `atet`. `ate` is the default.

`ate` specifies that the average treatment effect be estimated.

`atet` specifies that the average treatment effect on the treated be estimated.

SE/Robust

`vce(vcetype)` specifies the standard errors that are reported. By default, `teffects nnmatch` uses robust standard errors estimated using two matches.

`vce(robust [, nn(#)])` specifies that robust standard errors be reported and that the requested number of matches be used optionally.

`vce(iid)` specifies that standard errors for independently and identically distributed data be reported.

The standard derivative-based standard-error estimators cannot be used by `teffects nnmatch`, because these matching estimators are not differentiable. The implemented methods were derived by Abadie and Imbens (2006, 2011, 2012); see Methods and formulas.

As discussed in Abadie and Imbens (2008), bootstrap estimators do not provide reliable standard errors for the estimator implemented by **teffects nnmatch**.

Reporting

level(#); see [R] **Estimation options**.

dmvariables specifies that the matching variables be displayed.

display_options: **noci**, **nopvalues**, **noomitted**, **vsquish**, **noemptycells**, **baselevels**, **allbaselevels**, **nofvlabel**, **fwrap(#)**, **fvwrapon(style)**, **cformat(%fmt)**, **pformat(%fmt)**, **sformat(%fmt)**, and **nolstretch**; see [R] **Estimation options**.

Advanced

caliper(#) specifies the maximum distance at which two observations are a potential match. By default, all observations are potential matches regardless of how dissimilar they are.

The distance is based on *omvarlist*. If an observation does not have at least **nneighbor(#)** matches, **teffects nnmatch** exits with an error message. Use option **osample(newvar)** to identify all observations that are deficient in matches.

dtolerance(#) specifies the tolerance used to determine exact matches. The default value is **dtolerance(sqrt(c(epsdoublle)))**.

Integer-valued variables are usually used for exact matching. The **dtolerance()** option is useful when continuous variables are used for exact matching.

osample(newvar) specifies that indicator variable *newvar* be created to identify observations that violate the overlap assumption. This variable will identify all observations that do not have at least **nneighbor(#)** matches in the opposite treatment group within **caliper(#)** (for **metric()** distance matching) or **dtolerance(#)** (for **ematch(varlist)** exact matches).

The **vce(robust, nn(#))** option also requires at least # matches in the same treatment group within the distance specified by **caliper(#)** or within the exact matches specified by **dtolerance(#)**.

The average treatment effect on the treated, option **atet**, using **vce(iid)** requires only **nneighbor(#)** control group matches for the treated group.

control(#|label) specifies the level of *tvar* that is the control. The default is the first treatment level. You may specify the numeric level # (a nonnegative integer) or the label associated with the numeric level. **control()** and **tlevel()** may not specify the same treatment level.

tlevel(#|label) specifies the level of *tvar* that is the treatment for the statistic **atet**. The default is the second treatment level. You may specify the numeric level # (a nonnegative integer) or the label associated with the numeric level. **tlevel()** may only be specified with statistic **atet**. **tlevel()** and **control()** may not specify the same treatment level.

generate(stub) specifies that the observation numbers of the nearest neighbors be stored in the new variables *stub1*, *stub2*, This option is required if you wish to perform postestimation based on the matching results. The number of variables generated may be more than **nneighbor(#)** because of tied distances. These variables may not already exist.

metric(metric) specifies the distance matrix used as the weight matrix in a quadratic form that transforms the multiple distances into a single distance measure; see **Nearest-neighbor matching estimator** in *Methods and formulas* for details.

The following option is available with **teffects nnmatch** but is not shown in the dialog box: **coeflegend**; see [R] **Estimation options**.

Remarks and examples

The NNM method of treatment-effect estimation imputes the missing potential outcome for each individual by using an average of the outcomes of similar subjects that receive the other treatment level. Similarity between subjects is based on a weighted function of the covariates for each observation. The average treatment effect (ATE) is computed by taking the average of the difference between the observed and potential outcomes for each subject.

`teffects nnmatch` determines the “nearest” by using a weighted function of the covariates for each observation. By default, the Mahalanobis distance is used, in which the weights are based on the inverse of the covariates’ variance–covariance matrix. `teffects nnmatch` also allows you to request exact matching for categorical covariates. For example, you may want to force all matches to be of the same gender or race.

NNM is nonparametric in that no explicit functional form for either the outcome model or the treatment model is specified. This flexibility comes at a price; the estimator needs more data to get to the true value than an estimator that imposes a functional form. More formally, the NNM estimator converges to the true value at a rate slower than the parametric rate, which is the square root of the sample size, when matching on more than one continuous covariate. `teffects nnmatch` uses bias correction to fix this problem. `teffects psmatch` implements an alternative to bias correction; the method matches on a single continuous covariate, the estimated treatment probabilities. See [TE] `teffects intro` or [TE] `teffects intro advanced` for more information about this estimator.

We will illustrate the use of `teffects nnmatch` by using data from a study of the effect of a mother’s smoking status during pregnancy (`mbsmoke`) on infant birthweight (`bweight`) as reported by Cattaneo (2010). This dataset also contains information about each mother’s age (`mage`), education level (`medu`), marital status (`mmarried`), whether the first prenatal exam occurred in the first trimester (`prenatal1`), whether this baby was the mother’s first birth (`fbaby`), and the father’s age (`fage`).

▷ Example 1: Estimating the ATE

We begin by using `teffects nnmatch` to estimate the average treatment effect of `mbsmoke` on `bweight`. Subjects are matched using the Mahalanobis distance defined by covariates `mage`, `prenatal1`, `mmarried`, and `fbaby`.

<pre>. use https://www.stata-press.com/data/r16/cattaneo3 (Excerpt from Cattaneo (2010) Journal of Econometrics 155: 138–154) . teffects nnmatch (bweight mage prenatal1 mmarried fbaby) (mbsmoke)</pre>						
Treatment-effects estimation		Number of obs	=	4,642		
Estimator	: nearest-neighbor matching	Matches: requested	=	1		
Outcome model	: matching	min	=	1		
Distance metric:	Mahalanobis	max	=	139		
		AI Robust Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ATE	mbsmoke (smoker vs nonsmoker)	-240.3306	28.43006	-8.45	0.000	-296.0525 -184.6087

The average birthweight if all mothers were to smoke would be 240 grams less than the average that would occur if none of the mothers had smoked.



When the model includes indicator and categorical variables, you may want to restrict matches to only those subjects who are in the same category. The `ematch()` option of `teffects nnmatch` allows you to specify such variables that must match exactly.

▷ Example 2: Exact matching

Here we use the `ematch()` option to require exact matches on the binary variables `prenatal1`, `mmarried`, and `fbaby`. We also use Euclidean distance, rather than the default Mahalanobis distance, to match on the continuous variable `mage`.

Treatment-effects estimation						
Estimator		Number of obs = 4,642				
Outcome model		Matches: requested = 1				
Distance metric: Euclidean		min = 1				
		max = 139				
<hr/>						
		AI Robust				
		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ATE						
mbsmoke (smoker vs nonsmoker)		-240.3306	28.43006	-8.45	0.000	-296.0525 -184.6087



Abadie and Imbens (2006, 2011) have shown that nearest-neighbor matching estimators are not consistent when matching on two or more continuous covariates. A bias-corrected estimator that uses a linear function of variables can be specified with `biasadj()`.

▷ Example 3: Bias adjustment

Here we match on two continuous variables, `mage` and `fage`, and we use the bias-adjusted estimator:

Treatment-effects estimation						
Estimator		Number of obs = 4,642				
Outcome model		Matches: requested = 1				
Distance metric: Mahalanobis		min = 1				
		max = 25				
<hr/>						
		AI Robust				
		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ATE						
mbsmoke (smoker vs nonsmoker)		-223.8389	26.19973	-8.54	0.000	-275.1894 -172.4883

These results are similar to those reported in [example 1](#).



► Example 4: NNM can reduce to RA

NNM reduces to RA when matching exactly and all the covariates are discrete. We begin our illustration of this point by estimating the ATE by NNM using exact matching on `mmarried` and the mother's age-categories `magecat`.

Treatment-effects estimation						
Estimator		Number of obs = 4,642				
Outcome model		Matches: requested = 1				
Distance metric:		min = 11				
Distance metric:		max = 1310				
bweight	ATE	AI Robust				
		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ATE	mbsmoke (smoker vs nonsmoker)	-241.5264	24.39661	-9.90	0.000	-289.3429 -193.71

The RA estimator that includes the interactions among the discrete covariates produces the same point estimate.

Treatment-effects estimation						
Estimator		Number of obs = 4,642				
Outcome model		Matches: requested = 1				
Treatment model:		min = 11				
Treatment model:		max = 1310				
bweight	ATE	Robust				
		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ATE	mbsmoke (smoker vs nonsmoker)	-241.5264	24.26233	-9.95	0.000	-289.0797 -193.9732
P0mean	mbsmoke nonsmoker	3403.651	9.492683	358.56	0.000	3385.046 3422.256

The two estimates of the ATE are the same. The standard errors differ in finite samples because the RA and NNM estimators use different robust estimators of the variance of the estimator.

With exact matching on discrete covariates, the NNM estimator reduces to an average of differences in cell means. With fully interacted discrete covariates, the RA estimator reduces to the same average of difference in cell means.



Video example

Treatment effects in Stata: Nearest-neighbor matching

Stored results

`teffects nnmatch` stores the following in `e()`:

Scalars

<code>e(N)</code>	number of observations
<code>e(nj)</code>	number of observations for treatment level j
<code>e(k_levels)</code>	number of levels in treatment variable
<code>e(treated)</code>	level of treatment variable defined as treated
<code>e(control)</code>	level of treatment variable defined as control
<code>e(k_nneighor)</code>	requested number of matches
<code>e(k_nnmin)</code>	minimum number of matches
<code>e(k_nnmax)</code>	maximum number of matches
<code>e(k_robust)</code>	matches for robust VCE

Macros

<code>e(cmd)</code>	<code>teffects</code>
<code>e(cmdline)</code>	command as typed
<code>e(devar)</code>	name of outcome variable
<code>e(tvar)</code>	name of treatment variable
<code>e(emvarlist)</code>	exact match variables
<code>e(bavarlist)</code>	variables used in bias adjustment
<code>e(mvarlist)</code>	match variables
<code>e(subcmd)</code>	<code>nnmatch</code>
<code>e(metric)</code>	<code>mahalanobis</code> , <code>ivariance</code> , <code>euclidean</code> , or matrix <code>matname</code>
<code>e(stat)</code>	statistic estimated, <code>ate</code> or <code>atet</code>
<code>e(wtype)</code>	weight type
<code>e(wexp)</code>	weight expression
<code>e(title)</code>	title in estimation output
<code>e(tlevels)</code>	levels of treatment variable
<code>e(vce)</code>	<code>vcetype</code> specified in <code>vce()</code>
<code>e(vcetype)</code>	title used to label Std. Err.
<code>e(datasignature)</code>	the checksum
<code>e(datasignaturevars)</code>	variables used in calculation of checksum
<code>e(properties)</code>	<code>b V</code>
<code>e(estat_cmd)</code>	program used to implement <code>estat</code>
<code>e(predict)</code>	program used to implement <code>predict</code>
<code>e(marginsnotok)</code>	predictions disallowed by <code>margins</code>
<code>e(asbalanced)</code>	factor variables <code>fvset</code> as <code>asbalanced</code>
<code>e(asobserved)</code>	factor variables <code>fvset</code> as <code>asobserved</code>

Matrices

<code>e(b)</code>	coefficient vector
<code>e(V)</code>	variance–covariance matrix of the estimators

Functions

<code>e(sample)</code>	marks estimation sample
------------------------	-------------------------

Methods and formulas

The methods and formulas presented here provide the technical details underlying the estimators implemented in `teffects nnmatch` and `teffects psmatch`. See [Methods and formulas of \[TE\] teffects aipw](#) for the methods and formulas used by `teffects aipw`, `teffects ipw`, `teffects ipwra`, and `teffects ra`.

Methods and formulas are presented under the following headings:

- Nearest-neighbor matching estimator
- Bias-corrected matching estimator
- Propensity-score matching estimator
- PSM, ATE, and ATET variance adjustment

Nearest-neighbor matching estimator

`teffects nnmatch` implements the nearest-neighbor matching (NNM) estimator for the average treatment effect (ATE) and the average treatment effect on the treated (ATET). This estimator was derived by [Abadie and Imbens \(2006, 2011\)](#) and was previously implemented in Stata as discussed in [Abadie et al. \(2004\)](#).

`teffects psmatch` implements nearest-neighbor matching on an estimated propensity score. A propensity score is a conditional probability of treatment. The standard errors implemented in `teffects psmatch` were derived by [Abadie and Imbens \(2012\)](#).

`teffects nnmatch` and `teffects psmatch` permit two treatment levels: the treatment group with $t = 1$ and a control group with $t = 0$.

Matching estimators are based on the potential-outcome model, in which each individual has a well-defined outcome for each treatment level; see [\[TE\] teffects intro](#). In the binary-treatment potential-outcome model, y_1 is the potential outcome obtained by an individual if given treatment-level 1 and y_0 is the potential outcome obtained by each individual i if given treatment-level 0. The problem posed by the potential-outcome model is that only y_{1i} or y_{0i} is observed, never both. y_{0i} and y_{1i} are realizations of the random variables y_0 and y_1 . Throughout this document, i subscripts denote realizations of the corresponding, unsubscripted random variables.

Formally, the ATE is

$$\tau_1 = E(y_1 - y_0)$$

and the ATET is

$$\delta_1 = E(y_1 - y_0 | t = 1)$$

These expressions imply that we must have some solution to the missing-data problem that arises because we only observe either y_{1i} or y_{0i} , not both.

For each individual, NNM uses an average of the individuals that are most similar, but get the other treatment level, to predict the unobserved potential outcome. NNM uses the covariates $\{x_1, x_2, \dots, x_p\}$ to find the most similar individuals that get the other treatment level.

More formally, consider the vector of covariates $\mathbf{x}_i = \{x_{i,1}, x_{i,2}, \dots, x_{i,p}\}$ and frequency weight w_i for observation i . The distance between \mathbf{x}_i and \mathbf{x}_j is parameterized by the vector norm

$$\|\mathbf{x}_i - \mathbf{x}_j\|_S = \{(\mathbf{x}_i - \mathbf{x}_j)' \mathbf{S}^{-1} (\mathbf{x}_i - \mathbf{x}_j)\}^{1/2}$$

where \mathbf{S} is a given symmetric, positive-definite matrix.

Using this distance definition, we find that the set of nearest-neighbor indices for observation i is

$$\Omega_m^{\mathbf{x}}(i) = \{j_1, j_2, \dots, j_{m_i} \mid t_{j_k} = 1 - t_i, \|\mathbf{x}_i - \mathbf{x}_{j_k}\|_S < \|\mathbf{x}_i - \mathbf{x}_l\|_S, t_l = 1 - t_i, l \neq j_k\}$$

Here m_i is the smallest number such that the number of elements in each set, $m_i = |\Omega_m^{\mathbf{x}}(i)| = \sum_{j \in \Omega_m^{\mathbf{x}}(i)} w_j$, is at least m , the desired number of matches. You set the size of m using the `nneighbor(#)` option. The number of matches for the i th observation may not equal m because of ties or if there are not enough observations with a distance from observation i within the caliper limit, c , $\|\mathbf{x}_i - \mathbf{x}_j\|_S \leq c$. You may set the caliper limit by using the `caliper(#)` option. For ease of notation, we will use the abbreviation $\Omega(i) = \Omega_m^{\mathbf{x}}(i)$.

With the `metric(string)` option, you have three choices for the scaling matrix \mathbf{S} : Mahalanobis, inverse variance, or Euclidean.

$$\mathbf{S} = \begin{cases} \frac{(\mathbf{X} - \bar{\mathbf{x}}' \mathbf{1}_n)' \mathbf{W} (\mathbf{X} - \bar{\mathbf{x}}' \mathbf{1}_n)}{\sum_i^n w_i - 1} & \text{if } \text{metric} = \text{mahalanobis} \\ \text{diag} \left\{ \frac{(\mathbf{X} - \bar{\mathbf{x}}' \mathbf{1}_n)' \mathbf{W} (\mathbf{X} - \bar{\mathbf{x}}' \mathbf{1}_n)}{\sum_i^n w_i - 1} \right\} & \text{if } \text{metric} = \text{ivariance} \\ \mathbf{I}_p & \text{if } \text{metric} = \text{euclidean} \end{cases}$$

where $\mathbf{1}_n$ is an $n \times 1$ vector of ones, \mathbf{I}_p is the identity matrix of order p , $\bar{\mathbf{x}} = (\sum_i^n w_i \mathbf{x}_i) / (\sum_i^n w_i)$, and \mathbf{W} is an $n \times n$ diagonal matrix containing frequency weights.

The NNM method predicting the potential outcome for the i th observation as a function of the observed y_i is

$$\hat{y}_{ti} = \begin{cases} y_i & \text{if } t_i = t \\ \frac{\sum_{j \in \Omega(i)} w_j y_j}{\sum_{j \in \Omega(i)} w_j} & \text{otherwise} \end{cases}$$

for $t \in \{0, 1\}$.

We are now set to provide formulas for estimates $\hat{\tau}_1$, the ATE, and $\hat{\delta}_1$, the ATET,

$$\begin{aligned} \hat{\tau}_1 &= \frac{\sum_{i=1}^n w_i (\hat{y}_{1i} - \hat{y}_{0i})}{\sum_{i=1}^n w_i} = \frac{\sum_{i=1}^n w_i (2t_i - 1)\{1 + K_m(i)\}y_i}{\sum_{i=1}^n w_i} \\ \hat{\delta}_1 &= \frac{\sum_{i=1}^n t_i w_i (\hat{y}_{1i} - \hat{y}_{0i})}{\sum_{i=1}^n t_i w_i} = \frac{\sum_{i=1}^n \{t_i - (1 - t_i)K_m(i)\}y_i}{\sum_{i=1}^n t_i w_i} \end{aligned}$$

where

$$K_m(i) = \sum_{j=1}^n I\{i \in \Omega(j)\} \frac{w_j}{\sum_{k \in \Omega(j)} w_k}$$

The estimated variance of $\hat{\tau}_1$ and $\hat{\delta}_1$ are computed as

$$\begin{aligned} \hat{\sigma}_{\tau}^2 &= \frac{\sum_{i=1}^n w_i \left[(\hat{y}_{1i} - \hat{y}_{0i} - \hat{\tau}_1)^2 + \hat{\xi}_i^2 \{K_m^2(i) + 2K_m(i) - K'_m(i)\} \right]}{(\sum_{i=1}^n w_i)^2} \\ \hat{\sigma}_{\delta}^2 &= \frac{\sum_{i=1}^n t_i w_i \left[(\hat{y}_{1i} - \hat{y}_{0i} - \hat{\delta}_1)^2 + \hat{\xi}_i^2 \{K_m^2(i) - K'_m(i)\} \right]}{(\sum_{i=1}^n t_i w_i)^2} \end{aligned}$$

where

$$K'_m(i) = \sum_{j=1}^n I\{i \in \Omega(j)\} \frac{w_j}{\left(\sum_{k \in \Omega(j)} w_k \right)^2}$$

and $\xi_i^2 = \text{var}(y_{ti} | \mathbf{x}_i)$ is the conditional outcome variance. If we can assume that ξ_i^2 does not vary with the covariates or treatment (homoskedastic), then we can compute an ATE estimate of ξ_{τ}^2 as

$$\widehat{\xi}_\tau^2 = \frac{1}{2 \sum_i^n w_i} \sum_{i=1}^n w_i \left[\frac{\sum_{j \in \Omega(i)} w_j \{y_i - y_j(1 - t_i) - \widehat{\delta}_1\}^2}{\sum_{j \in \Omega(i)} w_j} \right]$$

and an ATET estimate of ξ_δ^2 as

$$\widehat{\xi}_\delta^2 = \frac{1}{2 \sum_i^n t_i w_i} \sum_{i=1}^n t_i w_i \left[\frac{\sum_{j \in \Omega(i)} t_j w_j \{y_i - y_j(1 - t_i) - \widehat{\delta}_1\}^2}{\sum_{j \in \Omega(i)} t_j w_j} \right]$$

If the conditional outcome variance is dependent on the covariates or treatment, we require an estimate for ξ_i^2 at each observation. In this case, we require a second matching procedure, where we match on observations within the same treatment group.

Define the within-treatment matching set

$$\Psi_h^x(i) = \{j_1, j_2, \dots, j_{h_i} \mid t_{j_k} = t_i, \|x_i - x_{j_k}\|_S < \|x_i - x_l\|_S, t_l = t_i, l \neq j_k\}$$

where h is the desired set size. As before, the number of elements in each set, $h_i = |\Psi_h^x(i)|$, may vary depending on ties and the value of the caliper. You set h using the `vce(robust, nn(#))` option. As before, we will use the abbreviation $\Psi(i) = \Psi_h^x(i)$ where convenient.

We estimate ξ_i^2 by

$$\widehat{\xi}_{t_i}^2(x_i) = \frac{\sum_{j \in \Psi(i)} w_j (y_j - \bar{y}_{\Psi(i)})^2}{\sum_{j \in \Psi(i)} w_j - 1} \quad \text{where} \quad \bar{y}_{\Psi(i)} = \frac{\sum_{j \in \Psi(i)} w_j y_j}{\sum_{j \in \Psi(i)} w_j - 1}$$

Bias-corrected matching estimator

When matching on more than one continuous covariate, the matching estimator described above is biased, even in infinitely large samples; in other words, it is not \sqrt{n} -consistent; see Abadie and Imbens (2006, 2011). Following Abadie and Imbens (2011) and Abadie et al. (2004), `teffects nnmatch` makes an adjustment based on the regression functions $\mu_t(\tilde{x}_i) = E(y_t \mid \tilde{x} = \tilde{x}_i)$, for $t = 0, 1$ and the set of covariates $\tilde{x}_i = (\tilde{x}_{i,1}, \dots, \tilde{x}_{i,q})$. The bias-correction covariates may be the same as the NNM covariates x_i . We denote the least-squares estimates as $\widehat{\mu}_t(\tilde{x}_i) = \widehat{\nu}_t + \widehat{\beta}'_t \tilde{x}_i$, where we regress $\{y_i \mid t_i = t\}$ onto $\{\tilde{x}_i \mid t_i = t\}$ with weights $w_i K_m(i)$, for $t = 0, 1$.

Given the estimated regression functions, the bias-corrected predictions for the potential outcomes are computed as

$$\widehat{y}_{ti} = \begin{cases} y_i & \text{if } t_i = t \\ \frac{\sum_{j \in \Omega_m^x(i)} w_j \{y_j + \widehat{\mu}_t(\tilde{x}_i) - \widehat{\mu}_t(\tilde{x}_j)\}}{\sum_{j \in \Omega_m^x(i)} w_j} & \text{otherwise} \end{cases}$$

The `biasadj(varlist)` option specifies the bias-adjustment covariates \tilde{x}_i .

Propensity-score matching estimator

The propensity-score matching (PSM) estimator uses a treatment model (TM), $p(\mathbf{z}_i, t, \gamma)$, to model the conditional probability that observation i receives treatment t given covariates \mathbf{z}_i . The literature calls $p(\mathbf{z}_i, t, \gamma)$ a propensity score, and PSM matches on the estimated propensity scores.

When matching on the estimated propensity score, the set of nearest-neighbor indices for observation i , $i = 1, \dots, n$, is

$$\Omega_m^p(i) = \{j_1, j_2, \dots, j_{m_i} \mid t_{j_k} = 1 - t_i, |\hat{p}_i(t) - \hat{p}_{j_k}(t)| < |\hat{p}_i(t) - \hat{p}_l(t)|, t_l = 1 - t_i, l \neq j_k\}$$

where $\hat{p}_i(t) = p(\mathbf{z}_i, t, \hat{\gamma})$. As was the case with the NNM estimator, m_i is the smallest number such that the number of elements in each set, $m_i = |\Omega_m^p(i)| = \sum_{j \in \Omega_m^p(i)} w_j$, is at least m , the desired number of matches, set by the `nneighbor(#)` option.

We define the within-treatment matching set analogously,

$$\Psi_h^p(i) = \{j_1, j_2, \dots, j_{h_i} \mid t_{j_k} = t_i, |\hat{p}_i(t) - \hat{p}_{j_k}(t)| < |\hat{p}_i(t) - \hat{p}_l(t)|, t_l = t_i, l \neq j_k\}$$

where h is the desired number of within-treatment matches, and $h_i = |\Psi_h^p(i)|$, for $i = 1, \dots, n$, may vary depending on ties and the value of the caliper. The sets $\Psi_h^p(i)$ are required to compute standard errors for $\hat{\tau}_1$ and $\hat{\delta}_1$.

Once a matching set is computed for each observation, the potential-outcome mean, ATE, and ATET computations are identical to those of NNM. The ATE and ATET standard errors, however, must be adjusted because the TM parameters were estimated; see [Abadie and Imbens \(2012\)](#).

PSM, ATE, and ATET variance adjustment

The variances for $\hat{\tau}_1$ and $\hat{\delta}_1$ must be adjusted because we use $\hat{\gamma}$ instead of γ . The adjusted variances for $\hat{\tau}_1$ and $\hat{\delta}_1$ have the following forms, respectively:

$$\begin{aligned}\hat{\sigma}_{\tau,\text{adj}}^2 &= \hat{\sigma}_\tau^2 + \hat{\mathbf{c}}_\tau' \hat{\mathbf{V}}_\gamma \hat{\mathbf{c}}_\tau \\ \hat{\sigma}_{\delta,\text{adj}}^2 &= \hat{\sigma}_\delta^2 - \hat{\mathbf{c}}_\delta' \hat{\mathbf{V}}_\gamma \hat{\mathbf{c}}_\delta + \frac{\partial \hat{\delta}_1}{\partial \gamma'} \hat{\mathbf{V}}_\gamma \frac{\partial \hat{\delta}_1}{\partial \gamma}\end{aligned}$$

In both equations, the matrix $\hat{\mathbf{V}}_\gamma$ is the TM coefficient variance–covariance matrix.

The adjustment term for ATE can be expressed as

$$\hat{\mathbf{c}}_\tau = \frac{1}{\sum_{i=1}^n w_i} \sum_{i=1}^n w_i f(\mathbf{z}'_i \hat{\gamma}) \left(\frac{\widehat{\text{cov}}(\mathbf{z}_i, \hat{y}_{i1})}{\hat{p}_i(1)} + \frac{\widehat{\text{cov}}(\mathbf{z}_i, \hat{y}_{i0})}{\hat{p}_i(0)} \right)$$

where

$$f(\mathbf{z}'_i \hat{\gamma}) = \frac{d p(\mathbf{z}_i, 1, \hat{\gamma})}{d(\mathbf{z}'_i \hat{\gamma})}$$

is the derivative of $p(\mathbf{z}_i, 1, \hat{\gamma})$ with respect to $\mathbf{z}'_i \hat{\gamma}$, and

$$\widehat{\text{cov}}(\mathbf{z}_i, \hat{y}_{ti}) = \begin{cases} \frac{\sum_{j \in \Psi_h(i)} w_j (\mathbf{z}_j - \bar{\mathbf{z}}_{\Psi_i})(y_j - \bar{y}_{\Psi_i})}{\sum_{j \in \Psi_h(i)} w_j - 1} & \text{if } t_i = t \\ \frac{\sum_{j \in \Omega_h(i)} w_j (\mathbf{z}_j - \bar{\mathbf{z}}_{\Omega_i})(y_j - \bar{y}_{\Omega_i})}{\sum_{j \in \Omega_h(i)} w_j - 1} & \text{otherwise} \end{cases}$$

is a $p \times 1$ vector with

$$\bar{\mathbf{z}}_{\Psi i} = \frac{\sum_{j \in \Psi_h(i)} w_j \mathbf{z}_j}{\sum_{j \in \Psi_h(i)} w_j} \quad \bar{\mathbf{z}}_{\Omega i} = \frac{\sum_{j \in \Omega_h(i)} w_j \mathbf{z}_j}{\sum_{j \in \Omega_h(i)} w_j} \quad \text{and} \quad \bar{y}_{\Omega i} = \frac{\sum_{j \in \Omega_h(i)} w_j y_j}{\sum_{j \in \Omega_h(i)} w_j}$$

Here we have used the notation $\Psi_h(i) = \Psi_h^p(i)$ and $\Omega_h(i) = \Omega_h^p(i)$ to stress that the within-treatment and opposite-treatment clusters used in computing $\hat{\sigma}_{\tau, \text{adj}}^2$ and $\hat{\delta}_{\tau, \text{adj}}^2$ are based on h instead of the cluster $\Omega_m^p(i)$ based on m used to compute $\hat{\tau}_1$ and $\hat{\delta}_1$, although you may desire to have $h = m$.

The adjustment term \mathbf{c}_δ for the ATET estimate has two components, $\mathbf{c}_\delta = \mathbf{c}_{\delta,1} + \mathbf{c}_{\delta,2}$, defined as

$$\begin{aligned} \mathbf{c}_{\delta,1} &= \frac{1}{\sum_{i=1}^n t_i w_i} \sum_{i=1}^n w_i \mathbf{z}_i f(\mathbf{z}'_i \hat{\gamma}) \left(\tilde{y}_{1i} - \tilde{y}_{0i} - \hat{\delta}_1 \right) \\ \mathbf{c}_{\delta,2} &= \frac{1}{\sum_{i=1}^n t_i w_i} \sum_{i=1}^n w_i f(\mathbf{z}'_i \hat{\gamma}) \left\{ \widehat{\text{cov}}(\mathbf{z}_i, \hat{y}_{1i}) + \frac{\hat{p}_i(1)}{\hat{p}_i(0)} \widehat{\text{cov}}(\mathbf{z}_i, \hat{y}_{0i}) \right\} \end{aligned}$$

where

$$\tilde{y}_{ti} = \begin{cases} \frac{\sum_{j \in \Psi_h(-i)} w_j y_j}{\sum_{j \in \Psi_h(-i)} w_j} & \text{if } t = t_i \\ \frac{\sum_{j \in \Omega_h} w_j y_j}{\sum_{j \in \Omega_h} w_j} & \text{otherwise} \end{cases}$$

and the within-treatment matching sets $\Psi_h(-i) = \Psi_h^p(-i)$ are similar to $\Psi_h^p(i)$ but exclude observation i :

$$\Psi_h^p(-i) = \{j_1, j_2, \dots, j_{h_i} \mid j_k \neq i, t_{j_k} = t_i, |\hat{p}_i - \hat{p}_{j_k}| < |\hat{p}_i - \hat{p}_l|, t_l = t_i, l \notin \{i, j_k\}\}$$

Finally, we cover the computation of $\widehat{\frac{\partial \delta_1}{\partial \gamma'}}$ in the third term on the right-hand side of $\widehat{\sigma}_{\delta, \text{adj}}^2$. Here we require yet another clustering, but we match on the opposite treatment by using the covariates $\mathbf{z}_i = (z_{i,1}, \dots, z_{i,p})'$. We will denote these cluster sets as $\Omega_m^{\mathbf{z}}(i)$, for $i = 1, \dots, n$.

The estimator of the $p \times 1$ vector $(\partial \delta_1) / (\partial \gamma')$ is computed as

$$\widehat{\frac{\partial \delta_1}{\partial \gamma'}} = \frac{1}{\sum_i^n t_i w_i} \sum_{i=1}^n \mathbf{z}_i f(\mathbf{z}'_i \hat{\gamma}) \left\{ (2t_i - 1)(y_i - \bar{y}_{\Omega_m^{\mathbf{z}}(i)}) - \hat{\delta}_1 \right\}$$

where

$$\bar{y}_{\Omega_m^{\mathbf{z}}(i)} = \frac{\sum_{j \in \Omega_m^{\mathbf{z}}(i)} w_j y_j}{\sum_{j \in \Omega_m^{\mathbf{z}}(i)} w_j}$$

References

- Abadie, A., D. M. Drukker, J. L. Herr, and G. W. Imbens. 2004. Implementing matching estimators for average treatment effects in Stata. *Stata Journal* 4: 290–311.
- Abadie, A., and G. W. Imbens. 2006. Large sample properties of matching estimators for average treatment effects. *Econometrica* 74: 235–267.
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- . 2011. Bias-corrected matching estimators for average treatment effects. *Journal of Business & Economic Statistics* 29: 1–11.
- . 2012. Matching on the estimated propensity score. Harvard University and National Bureau of Economic Research. <http://www.nber.org/papers/w15301>.
- Cattaneo, M. D. 2010. Efficient semiparametric estimation of multi-valued treatment effects under ignorability. *Journal of Econometrics* 155: 138–154.
- Drukker, D. M. 2016. Exact matching on discrete covariates is the same as regression adjustment. *The Stata Blog: Not Elsewhere Classified*. <http://blog.stata.com/2016/08/16/exact-matching-on-discrete-covariates-is-the-same-as-regression-adjustment/>.
- Huber, C. 2015. Introduction to treatment effects in Stata: Part 2. *The Stata Blog: Not Elsewhere Classified*. <http://blog.stata.com/2015/08/24/introduction-to-treatment-effects-in-stata-part-2/>.

Also see

- [TE] **teffects postestimation** — Postestimation tools for teffects
- [TE] **teffects** — Treatment-effects estimation for observational data
- [TE] **teffects psmatch** — Propensity-score matching
- [U] **20 Estimation and postestimation commands**

teffects overlap — Overlap plots

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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*]

<i>treat_options</i>	Description
Main	
<u>ptlevel</u> (<i>treat_level</i>)	calculate predicted probabilities for treatment level <i>treat_level</i> ; by default, <code>ptlevel()</code> corresponds to the first treatment level
<u>tlevels</u> (<i>treatments</i>)	specify conditioning treatment levels; default is all treatment levels
<u>nolabel</u>	use treatment level values and not value labels in legend and axis titles
kden_options	
Main	
<u>kernel</u> (<i>kernel</i>)	specify kernel function; default is <code>kernel(triangle)</code>
<i>n</i> (#)	estimate densities using # points; default is <code>e(N)</code> , the number of observations in the estimation sample
<u>bwidth</u> (#)	half-width of kernel
<u>at</u> (<i>var_x</i>)	estimate densities using the values specified by <i>var_x</i>
Kernel plots	
<u>line#opts</u> (<i>cline_options</i>)	affect rendition of density for conditioning treatment #
Add plots	
<u>addplot</u> (<i>plot</i>)	add other plots to the generated graph
Y axis, X axis, Titles, Legend, Overall	
<i>twoway_options</i>	any options other than <code>by()</code> documented in [G-3] <i>twoway_options</i>

<i>kernel</i>	Description
<u>triangle</u>	triangle kernel function; the default
<u>epanechnikov</u>	Epanechnikov kernel function
<u>epan2</u>	alternative Epanechnikov kernel function
<u>biweight</u>	biweight kernel function
<u>cosine</u>	cosine trace kernel function
<u>gaussian</u>	Gaussian kernel function
<u>parzen</u>	Parzen kernel function
<u>rectangle</u>	rectangle kernel function

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

`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.

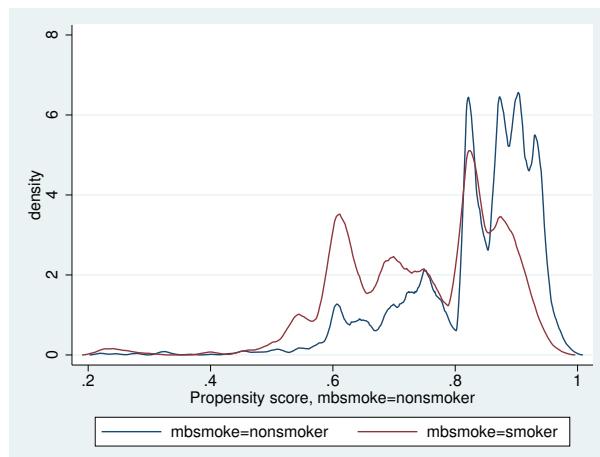
▷ Example 1: Assumption not violated

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  
(Excerpt from Cattaneo (2010) Journal of Econometrics 155: 138–154)  
. 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  
Estimator      : inverse-probability weights  
Outcome model  : weighted mean  
Treatment model: probit
```

bweight	Coef.	Robust 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
P0mean mbsmoke nonsmoker	3403.463	9.571369	355.59	0.000	3384.703 3422.222

```
. teffects overlap
```



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. \triangleleft

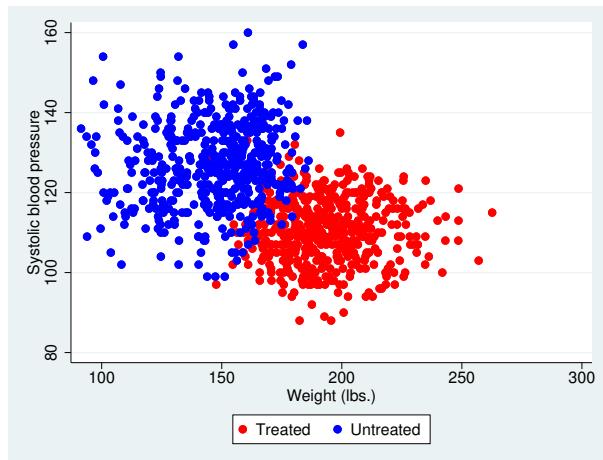
▷ Example 2: Assumption violated

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.

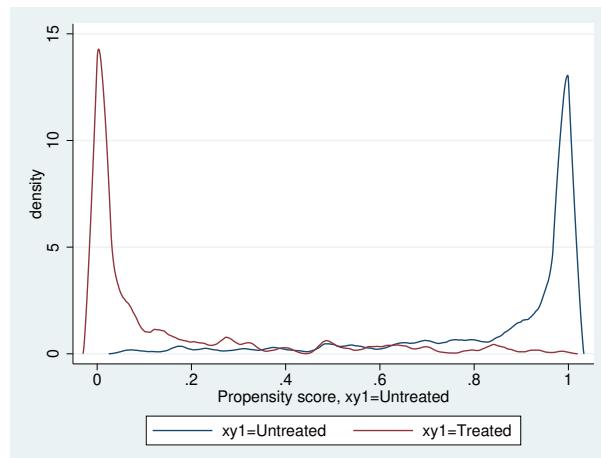
Below we estimate the parameters needed to calculate the predicted probabilities. The `pstolerance(1e-8)` option is specified to ensure that estimation is performed as long as the predicted probabilities are at least as large as $1e-8$.

```
. 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
```

systolic		Robust				
		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ATE						
xy1						
(Treated						
vs						
Untreated)	-16.23679	2.191703	-7.41	0.000	-20.53245	-11.94114
P0mean						
xy1						
Untreated	127.9094	.7004533	182.61	0.000	126.5365	129.2822

Now we can obtain the overlap plot.

```
. teffects overlap
```



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

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

Macros

<code>r(kernel)</code>	name of kernel
------------------------	----------------

References

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- Silverman, B. W. 1986. *Density Estimation for Statistics and Data Analysis*. London: Chapman & Hall.

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] **teffects** — Treatment-effects estimation for observational data
- [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

Postestimation commands

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

Command	Description
teffects overlap	overlap plots
tebalance	check balance of covariates

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
hausman	Hausman’s specification test
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

predict

Description for predict

`predict` creates a new variable containing predictions such as treatment effects, potential outcomes, conditional means, propensity scores, linear predictions, nearest-neighbor distances, and log square root of latent variances.

Menu for predict

Statistics > Postestimation

Syntaxes for predict

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) ]
```

<i>statistic</i>	Description
Main	
<code>te</code>	treatment effect; the default
<code>cmean</code>	conditional mean at treatment level
<code>ps</code>	propensity score
<code>xb</code>	linear prediction
<code>psxb</code>	linear prediction for propensity score
<code>lnsigma</code>	log square root of conditional latent variance (for outcome model <code>hetprobit()</code> at treatment level)
<code>pslnsigma</code>	log square root of latent variance (for treatment model <code>hetprobit()</code>)
<code>scores</code>	parameter-level or equation-level scores for propensity score

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, `cmean`, `ps`, `xb`, and `lnsigma` assume `tlevel()` specifies the first treatment level.

You specify one or *t* new variables with `cmean`, `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

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

<i>statistic</i>	Description
<hr/>	
Main	
<u>ps</u>	propensity score; the default
<u>xb</u>	linear prediction for the propensity score
<u>lnsigma</u>	log square root of latent variance (for treatment model <code>hetprobit()</code>)
<u>scores</u>	parameter-level or equation-level scores

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

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

You specify one or t new variables with `ps`, where t is the number of treatment levels.

You specify one or $t-1$ new variables with `xb` and `lnsigma`.

Syntax for predict after nnmatch and psmatch

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

<i>statistic</i>	Description
<hr/>	
Main	
<u>te</u>	treatment effect; the default
<u>po</u>	potential outcome
<u>distance</u>	nearest-neighbor distance
<u>ps</u>	propensity score (psmatch only)
<u>lnsigma</u>	log square root of latent variance (for treatment model <code>hetprobit()</code>)

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) ]
```

statistic	Description
<hr/>	
Main	
te	treatment effect; the default
cmean	conditional mean at treatment level
xb	linear prediction
lnsigma	log square root of conditional latent variance (for outcome model hetprobit()) at treatment level
scores	parameter-level or equation-level scores

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

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

You specify one or t new variables with `cmean`, `xb`, and `lnsigma`, where t is the number of treatment levels.

You specify one or $t-1$ new variables with `te`.

Options for predict

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.

tlevel(treat_level) restricts potential-outcome estimation to either the treated group or the control group. This option may only be specified with options `po` and `ps`.

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.

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 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.

	. use https://www.stata-press.com/data/r16/cattaneo2 (Excerpt from Cattaneo (2010) Journal of Econometrics 155: 138–154)						
	. 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						
		<hr/>					
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
P0mean							
mbsmoke nonsmoker		3403.463	9.571369	355.59	0.000	3384.703	3422.222

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%	.544155	.2258079		
10%	.5973879	.2258079	Obs	864
25%	.63777	.2409025	Sum of Wgt.	864
50%	.7601717		Mean	.7456264
		Largest	Std. Dev.	.1276102
75%	.8453946	.9533503		
90%	.8943686	.9596144	Variance	.0162844
95%	.9096801	.961022	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	3,778
25%	.0950869	.0106305	Sum of Wgt.	3,778
50%	.1372589		Mean	.1698913
		Largest	Std. Dev.	.1059434
75%	.2211142	.7547572		
90%	.3242757	.774192	Variance	.011224
95%	.3883457	.7803053	Skewness	1.514456
99%	.501537	.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**

teffects psmatch — Propensity-score matching

Description	Quick start	Menu	Syntax
Options	Remarks and examples	Stored results	Methods and formulas
References	Also see		

Description

teffects psmatch estimates the average treatment effect (ATE) and average treatment effect on the treated (ATET) from observational data by propensity-score matching (PSM). PSM estimators impute the missing potential outcome for each subject by using an average of the outcomes of similar subjects that receive the other treatment level. Similarity between subjects is based on estimated treatment probabilities, known as propensity scores. The treatment effect is computed by taking the average of the difference between the observed and potential outcomes for each subject. **teffects psmatch** accepts a continuous, binary, count, fractional, or nonnegative outcome.

See [TE] **teffects intro** or [TE] **teffects intro advanced** for more information about estimating treatment effects from observational data.

Quick start

ATE of `treat` on `y` estimated by PSM using a logistic model for `treat` on `x` and `indicators` for levels of categorical variable `a`

```
teffects psmatch (y) (treat x i.a)
```

As above, but estimate the ATET

```
teffects psmatch (y) (treat x i.a), atet
```

ATE of `treat` using a heteroskedastic probit model for treatment

```
teffects psmatch (y) (treat x i.a, hetprobit(x i.a))
```

With 4 matches per observation

```
teffects psmatch (y) (treat x i.a), nneighbor(4)
```

Menu

Statistics > Treatment effects > Continuous outcomes > Propensity-score matching

Statistics > Treatment effects > Binary outcomes > Propensity-score matching

Statistics > Treatment effects > Count outcomes > Propensity-score matching

Statistics > Treatment effects > Fractional outcomes > Propensity-score matching

Statistics > Treatment effects > Nonnegative outcomes > Propensity-score matching

Syntax

```
teffects psmatch (ovar) (tvar tmvarlist [ , tmodel ]) [if] [in] [weight]  
[ , stat options ]
```

ovar is a binary, count, continuous, fractional, or nonnegative outcome of interest.

tvar must contain integer values representing the treatment levels.

tmvarlist specifies the variables that predict treatment assignment in the treatment model. Only two treatment levels are allowed.

<i>tmodel</i>	Description
---------------	-------------

Model

<i>logit</i>	logistic treatment model; the default
<i>probit</i>	probit treatment model
<i>hetprobit</i> (<i>varlist</i>)	heteroskedastic probit treatment model

tmodel specifies the model for the treatment variable.

<i>stat</i>	Description
-------------	-------------

Stat

<i>ate</i>	estimate average treatment effect in population; the default
<i>atet</i>	estimate average treatment effect on the treated

<i>options</i>	Description
Model	
<code>nneighbor(#)</code>	specify number of matches per observation; default is <code>nneighbor(1)</code>
SE/Robust	
<code>vce(vcetype)</code>	<p><code>vcetype</code> may be</p> <ul style="list-style-type: none"> <code>vce(robust [, nn(#)])</code>; use robust Abadie–Imbens standard errors with # matches <code>vce(iid)</code>; use independent and identically distributed Abadie–Imbens standard errors
Reporting	
<code>level(#)</code>	set confidence level; default is <code>level(95)</code>
<code>display_options</code>	control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling
Advanced	
<code>caliper(#)</code>	specify the maximum distance for which two observations are potential neighbors
<code>pstolerance(#)</code>	set tolerance for overlap assumption
<code>osample(newvar)</code>	<code>newvar</code> identifies observations that violate the overlap assumption
<code>control(# label)</code>	specify the level of <code>tvar</code> that is the control
<code>tlevel(# label)</code>	specify the level of <code>tvar</code> that is the treatment
<code>generate(stub)</code>	generate variables containing the observation numbers of the nearest neighbors
<code>coeflegend</code>	display legend instead of statistics

tmvarlist may contain factor variables; see [U] 11.4.3 Factor variables.

`by` and `statsby` are allowed; see [U] 11.1.10 Prefix commands.

`fweights` are allowed; see [U] 11.1.6 weight.

`coeflegend` does not appear in the dialog box.

See [U] 20 Estimation and postestimation commands for more capabilities of estimation commands.

Options

Model

`nneighbor(#)` specifies the number of matches per observation. The default is `nneighbor(1)`. Each individual is matched with at least the specified number of individuals from the other treatment level. `nneighbor()` must specify an integer greater than or equal to 1 but no larger than the number of observations in the smallest group.

Stat

`stat` is one of two statistics: `ate` or `atet`. `ate` is the default.

`ate` specifies that the average treatment effect be estimated.

`atet` specifies that the average treatment effect on the treated be estimated.

SE/Robust

`vce(vcetype)` specifies the standard errors that are reported. By default, `teffects psmatch` uses two matches in estimating the robust standard errors.

`vce(robust [, nn(#)])` specifies that robust standard errors be reported and that the requested number of matches be used optionally.

`vce(iid)` specifies that standard errors for independent and identically distributed data be reported.

The standard derivative-based standard-error estimators cannot be used by `teffects psmatch`, because these matching estimators are not differentiable. The implemented methods were derived by Abadie and Imbens (2006, 2011, 2012); see [Methods and formulas](#).

As discussed in Abadie and Imbens (2008), bootstrap estimators do not provide reliable standard errors for the estimator implemented by `teffects psmatch`.

Reporting

`level(#);` see [\[R\] Estimation options](#).

`display_options`: `noci`, `nopvalues`, `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `nofvlabel`, `fvwrap(#)`, `fvwrapon(style)`, `cformat(%fmt)`, `pformat(%fmt)`, `sformat(%fmt)`, and `nolstretch`; see [\[R\] Estimation options](#).

Advanced

`caliper(#)` specifies the maximum distance at which two observations are a potential match. By default, all observations are potential matches regardless of how dissimilar they are.

In `teffects psmatch`, the distance is measured by the estimated propensity score. If an observation has no matches, `teffects psmatch` exits with an error.

`pstolerance(#)` specifies the tolerance used to check the overlap assumption. The default value is `pstolerance(1e-5)`. `teffects` will exit with an error if an observation has an estimated propensity score smaller than that specified by `pstolerance()`.

`osample(newvar)` specifies that indicator variable `newvar` be created to identify observations that violate the overlap assumption. Two checks are made to verify the assumption. The first ensures that the propensity scores are greater than `pstolerance(#)` and less than $1 - \text{pstolerance}(\#)$. The second ensures that each observation has at least `nneighbor(#)` matches in the opposite treatment group within the distance specified by `caliper(#)`.

The `vce(robust, nn(#))` option also requires at least # matches in the same treatment group within the distance specified by `caliper(#)`.

The average treatment effect on the treated, option `atet`, using `vce(iid)` requires only `nneighbor(#)` control group matches for the treated group.

`control(#|label)` specifies the level of `tvar` that is the control. The default is the first treatment level. You may specify the numeric level # (a nonnegative integer) or the label associated with the numeric level. `control()` and `tlevel()` may not specify the same treatment level.

`tlevel(#|label)` specifies the level of `tvar` that is the treatment for the statistic `atet`. The default is the second treatment level. You may specify the numeric level # (a nonnegative integer) or the label associated with the numeric level. `tlevel()` may only be specified with statistic `atet`. `tlevel()` and `control()` may not specify the same treatment level.

`generate(stub)` specifies that the observation numbers of the nearest neighbors be stored in the new variables `stub1`, `stub2`, This option is required if you wish to perform postestimation based

on the matching results. The number of variables generated may be more than `nneighbor(#)` because of tied distances. These variables may not already exist.

The following option is available with `teffects psmatch` but is not shown in the dialog box: `coeflegend`; see [R] **Estimation options**.

Remarks and examples

Propensity-score matching uses an average of the outcomes of similar subjects who get the other treatment level to impute the missing potential outcome for each subject. The ATE is computed by taking the average of the difference between the observed and potential outcomes for each subject. `teffects psmatch` determines how near subjects are to each other by using estimated treatment probabilities, known as propensity scores. This type of matching is known as propensity-score matching (PSM).

PSM does not need bias correction, because PSM matches on a single continuous covariate. In contrast, the nearest-neighbor matching estimator implemented in `teffects nnmatch` uses a bias-correction term when matching on more than one continuous covariate. In effect, the PSM estimator parameterizes the bias-correction term in the treatment probability model. See [TE] **teffects intro** or [TE] **teffects intro advanced** for more information about this estimator.

We will illustrate the use of `teffects psmatch` by using data from a study of the effect of a mother's smoking status during pregnancy (`mbsmoke`) on infant birthweight (`bweight`) as reported by Cattaneo (2010). This dataset also contains information about each mother's age (`mage`), education level (`medu`), marital status (`mmarried`), whether the first prenatal exam occurred in the first trimester (`prenatal1`), whether this baby was the mother's first birth (`fbaby`), and the father's age (`fage`).

▷ Example 1: Estimating the ATE

We begin by using `teffects psmatch` to estimate the ATE of `mbsmoke` on `bweight`. We use a logistic model (the default) to predict each subject's propensity score, using covariates `mage`, `medu`, `mmarried`, and `fbaby`. Because the performance of PSM hinges upon how well we can predict the propensity scores, we will use factor-variable notation to include both linear and quadratic terms for `mage`, the only continuous variable in our model:

```
. use https://www.stata-press.com/data/r16/cattaneo2
(Excerpt from Cattaneo (2010) Journal of Econometrics 155: 138-154)
. teffects psmatch (bweight) (mbsmoke mmarried c.mage##c.mage fbaby medu)
Treatment-effects estimation                               Number of obs      =    4,642
Estimator        : propensity-score matching             Matches: requested =          1
Outcome model   : matching                                min =          1
Treatment model: logit                                 max =         74
```

		AI Robust				
		Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ATE						
	mbsmoke (smoker vs nonsmoker)	-210.9683	32.021	-6.59	0.000	-273.7284 -148.2083

The average birthweight if all mothers were to smoke would be 211 grams less than the average that would occur if none of the mothers had smoked.



By default, **teffects psmatch** estimates the ATE by matching each subject to a single subject with the opposite treatment whose propensity score is closest. Sometimes, however, we may want to ensure that matching occurs only when the propensity scores of a subject and a match differ by less than a specified amount. To do that, we use the `caliper()` option. If a match within the distance specified in the `caliper()` option cannot be found, **teffects psmatch** exits.

▷ Example 2: Specifying the caliper

Here we reconsider the previous example, first specifying that we only want to consider a pair of observations a match if the absolute difference in the propensity scores is less than 0.03:

```
. teffects psmatch (bweight) (mbsmoke mmarried c.mage##c.mage fbaby medu),
> caliper(0.03)
no propensity-score matches for observation 4504 within caliper 0.03; use option
osample() to identify all observations with deficient matches
r(459);
```

The error arose because there is not a smoking mother whose propensity score is within 0.03 of the propensity score of the nonsmoking mother in observation 4504. If we instead raise the caliper to 0.10, we have matches for all subjects and therefore obtain the same results as in [example 1](#):

```
. teffects psmatch (bweight) (mbsmoke mmarried c.mage##c.mage fbaby medu),
> caliper(0.1)

Treatment-effects estimation
Estimator      : propensity-score matching
Outcome model : matching
Treatment model: logit
Number of obs      =      4,642
Matches: requested =          1
                           min =          1
                           max =       74

```

	AI Robust				
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ATE					
mbsmoke (smoker vs nonsmoker)	-210.9683	32.021	-6.59	0.000	-273.7284 -148.2083



□ Technical note

[Example 2](#) highlights that estimating the ATE requires finding matches for both the treated and control subjects. In contrast, estimating the ATET only requires finding matches for the treated subjects. Because subject 4504 is a control subject, we can estimate the ATET using `caliper(0.03)`. We must also specify `vce(iid)` because the default robust standard errors for the estimated ATET require viable matches for both treated subjects and control subjects. (This requirement comes from the nonparametric method derived by [Abadie and Imbens \[2012\]](#).)

Treatment-effects estimation						
Estimator	Number of obs = 4,642					
Outcome model	Matches: requested = 1					
Treatment model:	min = 1 max = 74					
<hr/>						
bweight	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
ATET						
mbsmoke (smoker vs nonsmoker)	-236.7848	26.11698	-9.07	0.000	-287.9731	-185.5964



In the previous examples, each subject was matched to at least one other subject, which is the default behavior for `teffects psmatch`. However, we can request that `teffects psmatch` match each subject to multiple subjects with the opposite treatment level by specifying the `nneighbor()` option. Matching on more distant neighbors can reduce the variance of the estimator at a cost of an increase in bias.

▷ Example 3

Now we request that `teffects psmatch` match a mother to four mothers in the opposite treatment group:

Treatment-effects estimation						
Estimator	Number of obs = 4,642					
Outcome model	Matches: requested = 4					
Treatment model:	min = 4 max = 74					
<hr/>						
bweight	AI Robust					
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
ATE						
mbsmoke (smoker vs nonsmoker)	-224.006	29.88627	-7.50	0.000	-282.582	-165.43

These results are similar to those reported in [example 1](#).



Video example

[Treatment effects in Stata: Propensity-score matching](#)

Stored results

`teffects psmatch` stores the following in `e()`:

Scalars

<code>e(N)</code>	number of observations
<code>e(nj)</code>	number of observations for treatment level j
<code>e(k_levels)</code>	number of levels in treatment variable
<code>e(caliper)</code>	maximum distance between matches
<code>e(treated)</code>	level of treatment variable defined as treated
<code>e(control)</code>	level of treatment variable defined as control
<code>e(k_nneighbor)</code>	requested number of matches
<code>e(k_nnmin)</code>	minimum number of matches
<code>e(k_nnmax)</code>	maximum number of matches
<code>e(k_robust)</code>	matches for robust VCE

Macros

<code>e(cmd)</code>	<code>teffects</code>
<code>e(cmdline)</code>	command as typed
<code>e(depvar)</code>	name of outcome variable
<code>e(tvar)</code>	name of treatment variable
<code>e(subcmd)</code>	<code>psmatch</code>
<code>e(tmodel)</code>	<code>logit</code> , <code>probit</code> , or <code>hetprobit</code>
<code>e(stat)</code>	statistic estimated, <code>ate</code> or <code>atet</code>
<code>e(wtype)</code>	weight type
<code>e(wexp)</code>	weight expression
<code>e(title)</code>	title in estimation output
<code>e(tlevels)</code>	levels of treatment variable
<code>e(psvarlist)</code>	variables in propensity-score model
<code>e(hvarlist)</code>	variables for variance, only if <code>hetprobit</code>
<code>e(vce)</code>	<i>vcetype</i> specified in <code>vce()</code>
<code>e(vcetype)</code>	title used to label Std. Err.
<code>e(datasignature)</code>	the checksum
<code>e(datasignaturevars)</code>	variables used in calculation of checksum
<code>e(properties)</code>	<code>b</code>
<code>e(estat_cmd)</code>	program used to implement <code>estat</code>
<code>e(predict)</code>	program used to implement <code>predict</code>
<code>e(marginsnotok)</code>	predictions disallowed by <code>margins</code>
<code>e(asbalanced)</code>	factor variables <code>fvset</code> as <code>asbalanced</code>
<code>e(asobserved)</code>	factor variables <code>fvset</code> as <code>asobserved</code>

Matrices

<code>e(b)</code>	coefficient vector
<code>e(V)</code>	variance–covariance matrix of the estimators
<code>e(bps)</code>	coefficient vector from propensity-score model
<code>e(Vps)</code>	variance–covariance matrix of the estimators from propensity-score model

Functions

<code>e(sample)</code>	marks estimation sample
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Methods and formulas

The methods and formulas used by `teffects psmatch` are documented in the [Methods and formulas](#) of [TE] [teffects nnmatch](#).

References

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Also see

- [TE] **teffects postestimation** — Postestimation tools for teffects
- [TE] **teffects** — Treatment-effects estimation for observational data
- [TE] **teffects nnmatch** — Nearest-neighbor matching
- [U] **20 Estimation and postestimation commands**

teffects ra — Regression adjustment

Description	Quick start	Menu	Syntax
Options	Remarks and examples	Stored results	Methods and formulas
References	Also see		

Description

teffects ra estimates the average treatment effect (ATE), the average treatment effect on the treated (ATET), and the potential-outcome means (POMS) from observational data by regression adjustment (RA). RA estimators use contrasts of averages of treatment-specific predicted outcomes to estimate treatment effects. **teffects ra** accepts a continuous, binary, count, fractional, or nonnegative outcome and allows a multivalued treatment.

See [TE] **teffects intro** or [TE] **teffects intro advanced** for more information about estimating treatment effects from observational data.

Quick start

ATE from a linear model of *y1* on *x1* and *x2* with binary treatment *treat2*

```
teffects ra (y1 x1 x2) (treat2)
```

As above, but estimate the ATET

```
teffects ra (y1 x1 x2) (treat2), atet
```

As above, but estimate the potential-outcome means

```
teffects ra (y1 x1 x2) (treat2), pomeans
```

ATE of *treat2* using a heteroskedastic probit model for binary outcome *y2*

```
teffects ra (y2 x1 x2, hetprobit(x1 x2)) (treat2)
```

ATE of *treat2* using a Poisson model for count outcome *y3*

```
teffects ra (y3 x1 x2, poisson) (treat2)
```

ATE for each level of three-valued treatment *treat3*

```
teffects ra (y1 x1 x2) (treat3)
```

As above, and specify that *treat3* = 3 is the control level

```
teffects ra (y1 x1 x2) (treat3), control(3)
```

Same as above, specified using the label "MyControl" corresponding to *treat3* = 3

```
teffects ra (y1 x1 x2) (treat3), control("MyControl")
```

Menu

Statistics > Treatment effects > Continuous outcomes > Regression adjustment

Statistics > Treatment effects > Binary outcomes > Regression adjustment

Statistics > Treatment effects > Count outcomes > Regression adjustment

Statistics > Treatment effects > Fractional outcomes > Regression adjustment

Statistics > Treatment effects > Nonnegative outcomes > Regression adjustment

Syntax

```
teffects ra (ovar omvarlist [ , omodel noconstant] ) (tvar) [ if ] [ in ] [ weight ]
[ , stat options ]
```

ovar is a binary, count, continuous, fractional, or nonnegative outcome of interest.

omvarlist specifies the covariates in the outcome model.

tvar must contain integer values representing the treatment levels.

<i>omodel</i>	Description
Model	
linear	linear outcome model; the default
logit	logistic outcome model
probit	probit outcome model
hetprobit(<i>varlist</i>)	heteroskedastic probit outcome model
poisson	exponential outcome model
flogit	fractional logistic outcome model
fprobit	fractional probit outcome model
fhetprobit(<i>varlist</i>)	fractional heteroskedastic probit outcome model

omodel specifies the model for the outcome variable.

<i>stat</i>	Description
Stat	
ate	estimate average treatment effect in population; the default
atet	estimate average treatment effect on the treated
pomeans	estimate potential-outcome means

options	Description
SE/Robust	
vce(<i>vcetype</i>)	<i>vcetype</i> may be <code>robust</code> , <code>cluster</code> <i>clustvar</i> , <code>bootstrap</code> , or <code>jackknife</code>
Reporting	
<code>level(#)</code>	set confidence level; default is <code>level(95)</code>
<code>aequations</code>	display auxiliary-equation results
<code>display_options</code>	control columns and column formats, row spacing, line width, display of omitted variables and base and empty cells, and factor-variable labeling
Maximization	
<code>maximize_options</code>	control the maximization process; seldom used
Advanced	
<code>control(# label)</code>	specify the level of <i>tvar</i> that is the control
<code>tlevel(# label)</code>	specify the level of <i>tvar</i> that is the treatment
<code>coeflegend</code>	display legend instead of statistics

omvarlist may contain factor variables; see [U] 11.4.3 Factor variables.

`bootstrap`, `by`, `jackknife`, and `statsby` are allowed; see [U] 11.1.10 Prefix commands.

Weights are not allowed with the `bootstrap` prefix; see [R] bootstrap.

`fweights`, `iweights`, and `pweights` are allowed; see [U] 11.1.6 weight.

`coeflegend` does not appear in the dialog box.

See [U] 20 Estimation and postestimation commands for more capabilities of estimation commands.

Options

Model

`noconstant`; see [R] Estimation options.

Stat

stat is one of three statistics: `ate`, `atet`, or `pomeans`. `ate` is the default.

`ate` specifies that the average treatment effect be estimated.

`atet` specifies that the average treatment effect on the treated be estimated.

`pomeans` specifies that the potential-outcome means for each treatment level be estimated.

SE/Robust

`vce(vcetype)` specifies the type of standard error reported, which includes types that are robust to some kinds of misspecification (`robust`), that allow for intragroup correlation (`cluster` *clustvar*), and that use bootstrap or jackknife methods (`bootstrap`, `jackknife`); see [R] vce_option.

Reporting

`level(#)`; see [R] Estimation options.

`aequations` specifies that the results for the outcome-model or the treatment-model parameters be displayed. By default, the results for these auxiliary parameters are not displayed.

`display_options`: `noci`, `nopvalues`, `noomitted`, `vsquish`, `noemptycells`, `baselevels`, `allbaselevels`, `nofvlabel`, `fvwrap(#)`, `fvwrapon(style)`, `cformat(%fmt)`, `pformat(%fmt)`, `sformat(%fmt)`, and `nolstretch`; see [R] **Estimation options**.

Maximization

`maximize_options`: `iterate(#)`, `[no]log`, and `from(init_specs)`; see [R] **Maximize**. These options are seldom used.

`init_specs` is one of

```
matname [, skip copy]
# [, # ...], copy
```

Advanced

`control(#|label)` specifies the level of `tvar` that is the control. The default is the first treatment level. You may specify the numeric level `#` (a nonnegative integer) or the label associated with the numeric level. `control()` may not be specified with statistic `pomeans`. `control()` and `tlevel()` may not specify the same treatment level.

`tlevel(#|label)` specifies the level of `tvar` that is the treatment for the statistic `atet`. The default is the second treatment level. You may specify the numeric level `#` (a nonnegative integer) or the label associated with the numeric level. `tlevel()` may only be specified with statistic `atet`. `tlevel()` and `control()` may not specify the same treatment level.

The following option is available with `teffects ra` but is not shown in the dialog box:
`coeflegend`; see [R] **Estimation options**.

Remarks and examples

Remarks are presented under the following headings:

[Overview](#)
[Video example](#)

Overview

Regression adjustment (RA) estimators use the contrasts of the averages of treatment-specific predicted outcomes to estimate treatment effects. RA estimators use a two-step approach to estimating treatment effects:

1. They fit separate regression models of the outcome on a set of covariates for each treatment level.
2. They compute the averages of the predicted outcomes for each subject and treatment level. These averages reflect the POMs. The contrasts of these averages provide estimates of the ATEs. By restricting the computations of the means to the subset of treated subjects, we obtain the ATETs.

RA estimators are consistent as long as the treatment is independent of the potential outcomes after conditioning on the covariates. In fact, `teffects ra` uses an estimation technique that implements both steps at once so that we do not need to correct the standard errors in the second step to reflect the uncertainty surrounding the predicted outcomes.

We will illustrate the use of **teffects ra** by using data from a study of the effect of a mother's smoking status during pregnancy (**mbsmoke**) on infant birthweight (**bweight**) as reported by Cattaneo (2010). This dataset also contains information about each mother's age (**mage**), education level (**medu**), marital status (**mmarried**), whether the first prenatal exam occurred in the first trimester (**prenatal1**), and whether this baby was the mother's first birth (**fbaby**).

▷ Example 1: Estimating the ATE

We begin by using **teffects ra** to estimate the average treatment effect of smoking, controlling for first-trimester exam status, marital status, mother's age, and first-birth status. In Stata, we type

. use https://www.stata-press.com/data/r16/cattaneo2 (Excerpt from Cattaneo (2010) Journal of Econometrics 155: 138–154)					
. teffects ra (bweight prenatal1 mmarried mage fbaby) (mbsmoke)					
Iteration 0: EE criterion = 7.734e-24					
Iteration 1: EE criterion = 1.196e-25					
Treatment-effects estimation	Number of obs = 4,642				
Estimator : regression adjustment					
Outcome model : linear					
Treatment model: none					
bweight	Robust				
	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ATE					
mbsmoke (smoker vs nonsmoker)	-239.6392	23.82402	-10.06	0.000	-286.3334 -192.945
P0mean					
mbsmoke nonsmoker	3403.242	9.525207	357.29	0.000	3384.573 3421.911

The average birthweight if all mothers were to smoke would be 240 grams less than the average of 3,403 grams that would occur if none of the mothers had smoked.

The previous results showed us the average amount by which infants' weights are affected by their mothers' decision to smoke. We may instead be interested in knowing the average amount by which the weight of babies born to smoking mothers was decreased as a result of smoking. The ATET provides us with the answer.

► Example 2: Estimating the ATET

To obtain the ATET rather than the ATE, we use the `atet` option:

Treatment-effects estimation						Number of obs	=	4,642
Estimator : regression adjustment								
Outcome model : linear								
Treatment model: none								
bweight	Coef.	Robust Std. Err.	z	P> z		[95% Conf. Interval]		
ATET								
mbsmoke (smoker vs nonsmoker)	-223.3017	22.7422	-9.82	0.000	-267.8755	-178.7278		
P0mean								
mbsmoke nonsmoker	3360.961	12.75749	263.45	0.000	3335.957	3385.966		

The average birthweight is 223 grams less when all the mothers who smoke do so than the average of 3,361 grams that would have occurred if none of these mothers had smoked.

The ATET differs from the ATE because the distribution of the covariates among mothers who smoke differs from the distribution for nonsmoking mothers. For example, in [TE] **teffects intro**, we remarked that in our sample, mothers who smoked tended to be older than those who did not. The differing distributions of covariates also affect the estimated POMs.

By default, **teffects ra** reports the ATE, which is the difference between the two POMs in the case of a binary treatment variable. Sometimes, we want to know the estimated POMs themselves. We might also want to see the actual regression equations used to estimate the POMs. Obtaining this information is easy, as the next example illustrates.

► Example 3: Estimating the POMs

Here we use the `pomeans` option to display the POMs and the `aequations` option to display the estimated regression coefficients for the treated and untreated subjects.

Treatment-effects estimation							Number of obs	=	4,642
Estimator : regression adjustment									
Outcome model : linear									
Treatment model: none									
bweight	Coef.	Robust Std. Err.	z	P> z	[95% Conf. Interval]				
POmeans									
mbsmoke									
nonsmoker	3403.242	9.525207	357.29	0.000	3384.573	3421.911			
smoker	3163.603	21.86351	144.70	0.000	3120.751	3206.455			
OME0									
prenatal1	64.40859	27.52699	2.34	0.019	10.45669	118.3605			
mmarried	160.9513	26.6162	6.05	0.000	108.7845	213.1181			
mage	2.546828	2.084324	1.22	0.222	-1.538373	6.632028			
fbaby	-71.3286	19.64701	-3.63	0.000	-109.836	-32.82117			
_cons	3202.746	54.01082	59.30	0.000	3096.886	3308.605			
OME1									
prenatal1	25.11133	40.37541	0.62	0.534	-54.02302	104.2457			
mmarried	133.6617	40.86443	3.27	0.001	53.5689	213.7545			
mage	-7.370881	4.21817	-1.75	0.081	-15.63834	.8965804			
fbaby	41.43991	39.70712	1.04	0.297	-36.38461	119.2644			
_cons	3227.169	104.4059	30.91	0.000	3022.537	3431.801			

The nonsmoker POM for infant birthweight is 3,403 grams; that means that if none of the women in our sample smoked during pregnancy, the expected average birthweight would be 3,403 grams. The POM if all mothers did smoke during pregnancy is 3,164 grams, a difference of 240 grams, as we established in [example 1](#). The coefficients for the equation labeled OME0 represent the linear equation used to estimate the nontreated POM, and the coefficients for the equation labeled OME1 represent the linear equation used to estimate the treated POM. The coefficients are identical to those we would obtain using `regress`, but the standard errors differ slightly because `teffects ra does not make the small-sample adjustment that regress does.`

We often express statistics as percentages to alleviate scaling issues and aid interpretation. In the present context, we may wish to express an ATE as a percentage of the untreated POM to gain a more intuitive measure of efficacy.

► Example 4: Reporting the ATE as a percentage

Sometimes, we are interested in reporting the estimated treatment effect as a percentage of the untreated POM. We continue to use the same model as in the previous examples, but we specify the `coeflegend` option so that `teffects ra` reports the names of the parameters. Knowing the correct names to use, we can then use `nlcom` to obtain the percentage change along with its delta-method-based standard error. We type

```
. use https://www.stata-press.com/data/r16/cattaneo2
(Excerpt from Cattaneo (2010) Journal of Econometrics 155: 138–154)
. teffects ra (bweight prenatal1 mmarried mage fbaby) (mbsmoke), coeflegend
Iteration 0:   EE criterion =  7.734e-24
Iteration 1:   EE criterion =  1.196e-25
Treatment-effects estimation                               Number of obs      =      4,642
Estimator        : regression adjustment
Outcome model    : linear
Treatment model: none

```

bweight	Coef. Legend
ATE mbsmoke (smoker vs nonsmoker)	-239.6392 _b[ATE:r1vs0.mbsmoke]
P0mean mbsmoke nonsmoker	3403.242 _b[P0mean:0.mbsmoke]

```
. nlcom _b[ATE:r1vs0.mbsmoke] / _b[P0mean:0.mbsmoke]
_nl_1: _b[ATE:r1vs0.mbsmoke] / _b[P0mean:0.mbsmoke]
```

bweight	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
_nl_1	-.070415	.0069245	-10.17	0.000	-.0839867 -.0568433

The average birthweight falls by an estimated 7.0% when every mother smokes relative to the case when no mothers smoke. We also obtain a 95% confidence interval of a 5.7% to 8.4% reduction. ◇

Birthweights cannot be negative, though it is possible for a linear regression model to make negative predictions. A common way to enforce nonnegative predictions is to use an exponential conditional-mean model, which is commonly fitted using the Poisson quasimaximum-likelihood estimator, as discussed in Cameron and Trivedi (2005, sec. 5.7), Wooldridge (2010, sec. 18.2), and Pawitan (2001, chap. 14). `teffects ra` provides an option to use this model rather than linear regression for the outcomes.

▷ Example 5: Modeling nonnegative outcomes

Now we refit our model of smoking behavior on birthweight, but we specify the `poisson` option in the outcome-model equation so that `teffects ra` uses the Poisson exponential model rather than linear regression:

Treatment-effects estimation							Number of obs	=	4,642	
		Estimator		: regression adjustment						
		Outcome model		: Poisson						
		Treatment model: none								
bweight		Coef.	Robust Std. Err.	z	P> z	[95% Conf. Interval]				
ATE	mbsmoke (smoker vs nonsmoker)	-239.6669	23.83757	-10.05	0.000	-286.3877	-192.9462			
POmean	mbsmoke nonsmoker	3403.178	9.526006	357.25	0.000	3384.508	3421.849			

In this case, using a model that forces outcomes to be nonnegative did not make any substantive difference. In this dataset, nearly 90% of babies weigh at least 2,700 grams, and even the smallest baby weighs 340 grams. When the dependent variable is so large, the predictions from Poisson and linear regression models are remarkably similar.



We now consider models for fractional outcomes. Fractional responses concern outcomes between 0 and 1. These responses may be averaged 0/1 outcomes such as participation rates, or they may be variables that are naturally on a 0 to 1 scale such as pollution levels, patient oxygen saturation, and Gini coefficients (income inequality measures).

▷ Example 6: Modeling fractional outcomes

We will illustrate the use of `teffects ra` with the outcome-model option `fprobit` by using simulated data. The observations are 543 cities at least 200 miles apart. The data contain information about each city's level of industrialization (`industrial`), average annual rainfall in millimeters (`rainfall`), whether or not the city has a metro or train (`train`), and traffic congestion measured by an index (`traffic`).

Our outcome is the level of pollution (`pollution`) measured on a 0 to 1 scale. Values of `pollution` between 0 and 0.3 have no public health implications, but values greater than 0.7 imply that people with breathing or health problems should remain indoors. We study the effect of a tax on gas-guzzler cars (`guzzler`) on air pollution. A tax that is effective in reducing pollution improves public health.

We estimate the ATE of a gas-guzzler tax on pollution, controlling for average yearly rainfall, traffic congestion, the level of industrialization, and whether the city has a train or a metro by using a fractional probit model.

. use https://www.stata-press.com/data/r16/pollution (Simulated Urban Pollution Data)						
. teffects ra (pollution rainfall i.traffic industrial i.train, fprobit) (guzzler)						
Iteration 0: EE criterion = 3.023e-16						
Iteration 1: EE criterion = 9.917e-32						
Treatment-effects estimation	Number of obs = 534					
Estimator : regression adjustment						
Outcome model : fractional probit						
Treatment model: none						
pollution	Robust	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]
ATE guzzler (tax vs no tax)						
		-.0960214	.0113896	-8.43	0.000	-.1183447 -.0736981
P0mean guzzler no tax		.3879346	.0101733	38.13	0.000	.3679952 .407874

The POM if no city were to implement a gas-guzzler tax is an air pollution index of 0.39. If all cities implement a gas-guzzler tax, the air pollution index would decrease by 0.096 relative to a scenario where no city implements the tax.



Video example

Treatment effects: Regression adjustment

Stored results

teffects ra stores the following in `e()`:

Scalars

<code>e(N)</code>	number of observations
<code>e(nj)</code>	number of observations for treatment level j
<code>e(N_clust)</code>	number of clusters
<code>e(k_eq)</code>	number of equations in <code>e(b)</code>
<code>e(k_levels)</code>	number of levels in treatment variable
<code>e(treated)</code>	level of treatment variable defined as treated
<code>e(control)</code>	level of treatment variable defined as control
<code>e(converged)</code>	1 if converged, 0 otherwise

Macros

<code>e(cmd)</code>	<code>teffects</code>
<code>e(cmdline)</code>	command as typed
<code>e(depyvar)</code>	name of outcome variable
<code>e(tvar)</code>	name of treatment variable
<code>e(subcmd)</code>	<code>ra</code>
<code>e(omodel)</code>	<code>linear, logit, probit, hetprobit, poisson, flogit, fprobit, or fhetprobit</code>
<code>e(stat)</code>	statistic estimated, <code>ate</code> , <code>atet</code> , or <code>pomeans</code>
<code>e(wtype)</code>	weight type
<code>e(wexp)</code>	weight expression
<code>e(title)</code>	title in estimation output
<code>e(clustvar)</code>	name of cluster variable
<code>e(tlevels)</code>	levels of treatment variable
<code>e(vce)</code>	<i>vcetype</i> specified in <code>vce()</code>
<code>e(vcetype)</code>	title used to label Std. Err.
<code>e(properties)</code>	<code>b V</code>
<code>e(estat_cmd)</code>	program used to implement <code>estat</code>
<code>e(predict)</code>	program used to implement <code>predict</code>
<code>e(marginsnotok)</code>	predictions disallowed by <code>margins</code>
<code>e(asbalanced)</code>	factor variables <code>fvset</code> as <code>asbalanced</code>
<code>e(asobserved)</code>	factor variables <code>fvset</code> as <code>asobserved</code>

Matrices

<code>e(b)</code>	coefficient vector
<code>e(V)</code>	variance–covariance matrix of the estimators

Functions

<code>e(sample)</code>	marks estimation sample
------------------------	-------------------------

Methods and formulas

teffects ra implements a smooth treatment-effects estimator. All smooth treatment-effects estimators are documented in [TE] **teffects aipw**.

References

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Also see

[TE] **teffects postestimation** — Postestimation tools for teffects

[TE] **teffects** — Treatment-effects estimation for observational data

[ERM] **eregress** — Extended linear regression

[U] **20 Estimation and postestimation commands**

Glossary

AIPW estimator. See [augmented inverse-probability-weighted estimator](#).

analysis time. Analysis time is like time, except that 0 has a special meaning: $t = 0$ is the time of onset of risk, the time when failure first became possible.

Analysis time is usually not what is recorded in a dataset. A dataset of patients might record calendar time. Calendar time must then be mapped to analysis time.

The letter t is reserved for time in analysis-time units. The term *time* is used for time measured in other units.

The *origin* is the *time* corresponding to $t = 0$, which can vary subject to subject. Thus $t = \text{time} - \text{origin}$.

ATE. See [average treatment effect](#).

ATET. See [average treatment effect on the treated](#).

augmented inverse-probability-weighted estimator. An augmented inverse-probability-weighted (AIPW) estimator is an inverse-probability-weighted estimator that includes an augmentation term that corrects the estimator when the treatment model is misspecified. When the treatment is correctly specified, the augmentation term vanishes as the sample size becomes large. An AIPW estimator uses both an outcome model and a treatment model and is a doubly robust estimator.

average treatment effect. The average treatment effect is the average effect of the treatment among all individuals in a population.

average treatment effect on the treated. The average treatment effect on the treated is the average effect of the treatment among those individuals who actually get the treatment.

censored, left-censored, and right-censored. An observation is left-censored when the exact time of failure is not known; it is merely known that the failure occurred before t_l . Suppose that the event of interest is becoming employed. If a subject is already employed when first interviewed, his outcome is left-censored.

An observation is right-censored when the time of failure is not known; it is merely known that the failure occurred after t_r . If a patient survives until the end of a study, the patient's time of death is right-censored.

In common usage, *censored* without a modifier means right-censored.

Also see [truncation, left-truncation, and right-truncation](#).

CI assumption. See [conditional-independence assumption](#).

conditional mean. The conditional mean expresses the average of one variable as a function of some other variables. More formally, the mean of y conditional on \mathbf{x} is the mean of y for given values of \mathbf{x} ; in other words, it is $E(y|\mathbf{x})$.

A conditional mean is also known as a regression or as a conditional expectation.

conditional-independence assumption. The conditional-independence assumption requires that the common variables that affect treatment assignment and treatment-specific outcomes be observable. The dependence between treatment assignment and treatment-specific outcomes can be removed by conditioning on these observable variables.

This assumption is also known as a selection-on-observables assumption because its central tenet is the observability of the common variables that generate the dependence.

counterfactual. A counterfactual is an outcome a subject would have obtained had that subject received a different level of treatment. In the binary-treatment case, the counterfactual outcome for a person who received treatment is the outcome that person would have obtained had the person instead not received treatment; similarly, the counterfactual outcome for a person who did not receive treatment is the outcome that person would have obtained had the person received treatment.

Also see [potential outcome](#).

doubly robust estimator. A doubly robust estimator only needs one of two auxiliary models to be correctly specified to estimate a parameter of interest.

Doubly robust estimators for treatment effects are consistent when either the outcome model or the treatment model is correctly specified.

EE estimator. See [estimating-equation estimator](#).

estimating-equation estimator. An estimating-equation (EE) estimator calculates parameters estimates by solving a system of equations. Each equation in this system is the sample average of a function that has mean zero.

These estimators are also known as M estimators or Z estimators in the statistics literature and as generalized method of moments (GMM) estimators in the econometrics literature.

failure event. Survival analysis is really time-to-failure analysis, and the failure event is the event under analysis. The failure event can be death, heart attack, myopia, or finding employment. Many authors—including Stata—write as if the failure event can occur only once per subject, but when we do, we are being sloppy. Survival analysis encompasses repeated failures, and all of Stata’s survival analysis features can be used with repeated-failure data.

hazard, cumulative hazard, and hazard ratio. The hazard or hazard rate at time t , $h(t)$, is the instantaneous rate of failure at time t conditional on survival until time t . Hazard rates can exceed 1. Say that the hazard rate were 3. If an individual faced a constant hazard of 3 over a unit interval and if the failure event could be repeated, the individual would be expected to experience three failures during the time span.

The cumulative hazard, $H(t)$, is the integral of the hazard function $h(t)$, from 0 (the onset of risk) to t . It is the total number of failures that would be expected to occur up until time t , if the failure event could be repeated. The relationship between the cumulative hazard function, $H(t)$, and the survivor function, $S(t)$, is

$$S(t) = \exp\{-H(t)\}$$

$$H(t) = -\ln\{S(t)\}$$

The hazard ratio is the ratio of the hazard function evaluated at two different values of the covariates: $h(t | \mathbf{x})/h(t | \mathbf{x}_0)$. The hazard ratio is often called the relative hazard, especially when $h(t | \mathbf{x}_0)$ is the baseline hazard function.

i.i.d. sampling assumption. See [independent and identically distributed sampling assumption](#).

independent and identically distributed sampling assumption. The independent and identically distributed (i.i.d.) sampling assumption specifies that each observation is unrelated to (independent of) all the other observations and that each observation is a draw from the same (identical) distribution.

individual-level treatment effect. An individual-level treatment effect is the difference in an individual's outcome that would occur because this individual is given one treatment instead of another. In other words, an individual-level treatment effect is the difference between two potential outcomes for an individual.

For example, the blood pressure an individual would obtain after taking a pill minus the blood pressure an individual would obtain had that person not taken the pill is the individual-level treatment effect of the pill on blood pressure.

inverse-probability-weighted estimators. Inverse-probability-weighted (IPW) estimators use weighted averages of the observed outcome variable to estimate the potential-outcome means. The weights are the reciprocals of the treatment probabilities estimated by a treatment model.

inverse-probability-weighted regression-adjustment estimators.

Inverse-probability-weighted regression-adjustment (IPWRA) estimators use the reciprocals of the estimated treatment probability as weights to estimate missing-data-corrected regression coefficients that are subsequently used to compute the potential-outcome means.

IPW estimators. See *inverse-probability-weighted estimators*.

IPWRA estimators. See *inverse-probability-weighted regression-adjustment estimators*.

left-censored. See *censored, left-censored, and right-censored*.

left-truncation. See *truncation, left-truncation, and right-truncation*.

matching estimator. An estimator that compares differences between the outcomes of similar—that is, matched—individuals. Each individual that receives a treatment is matched to a similar individual that does not get the treatment, and the difference in their outcomes is used to estimate the individual-level treatment effect. Likewise, each individual that does not receive a treatment is matched to a similar individual that does get the treatment, and the difference in their outcomes is used to estimate the individual-level treatment effect.

multiple-record st data. See *st data*.

multivalued treatment effect. A multivalued treatment refers to a treatment that has more than two values. For example, a person could have taken a 20 mg dose of a drug, a 40 mg dose of the drug, or not taken the drug at all.

nearest-neighbor matching. Nearest-neighbor matching uses the distance between observed variables to find similar individuals.

observational data. In observational data, treatment assignment is not controlled by those who collected the data; thus some common variables affect treatment assignment and treatment-specific outcomes.

outcome model. An outcome model is a model used to predict the outcome as a function of covariates and parameters.

overlap assumption. The overlap assumption requires that each individual have a positive probability of each possible treatment level.

POMs. See *potential-outcome means*.

potential outcome. The potential outcome is the outcome an individual would obtain if given a specific treatment.

For example, an individual has one potential blood pressure after taking a pill and another potential blood pressure had that person not taken the pill.

potential-outcome means. The potential-outcome means refers to the means of the potential outcomes for a specific treatment level.

The mean blood pressure if everyone takes a pill and the mean blood pressure if no one takes a pill are two examples.

The average treatment effect is the difference between potential-outcome mean for the treated and the potential-outcome mean for the not treated.

propensity score. The propensity score is the probability that an individual receives a treatment.

propensity-score matching. Propensity-score matching uses the distance between estimated propensity scores to find similar individuals.

regression-adjustment estimators. Regression-adjustment estimators use means of predicted outcomes for each treatment level to estimate each potential-outcome mean.

right-censored. See [censored, left-censored, and right-censored](#).

right-truncation. See [truncation, left-truncation, and right-truncation](#).

selection-on-observables. See [conditional-independence assumption](#).

shape parameter. A shape parameter governs the shape of a probability distribution. One example is the parameter p of the Weibull model.

single-record st data. See [st data](#).

smooth treatment-effects estimator. A smooth treatment-effects estimator is a smooth function of the data so that standard methods approximate the distribution of the estimator. The RA, IPW, AIPW, and IPWRA estimators are all smooth treatment-effects estimators while the nearest-neighbor matching estimator and the propensity-score matching estimator are not.

st data. st stands for survival time. In survival-time data, each observation represents a span of survival, recorded in variables $t0$ and t . For instance, if in an observation $t0$ were 3 and t were 5, the span would be $(t0, t]$, meaning from just after $t0$ up to and including t .

Sometimes variable $t0$ is not recorded; $t0$ is then assumed to be 0. In such a dataset, an observation that had $t = 5$ would record the span $(0, 5]$.

Each observation also includes a variable d , called the failure variable, which contains 0 or nonzero (typically, 1). The failure variable records what happened at the end of the span: 0, the subject was still alive (had not yet failed) or 1, the subject died (failed).

Sometimes variable d is not recorded; d is then assumed to be 1. In such a dataset, all time-span observations would be assumed to end in failure.

Finally, each observation in an st dataset can record the entire history of a subject or each can record a part of the history. In the latter case, groups of observations record the full history. One observation might record the period $(0, 5]$ and the next, $(5, 8]$. In such cases, there is a variable ID that records the subject for which the observation records a time span. Such data are called multiple-record st data. When each observation records the entire history of a subject, the data are called single-record st data. In the single-record case, the ID variable is optional.

See [\[ST\] stset](#).

survival-time data. See [st data](#).

survivor function. Also known as the survivorship function and the survival function, the survivor function, $S(t)$, is 1) the probability of surviving beyond time t , or equivalently, 2) the probability that there is no failure event prior to t , 3) the proportion of the population surviving to time t , or equivalently, 4) the reverse cumulative distribution function of T , the time to the failure event: $S(t) = \Pr(T > t)$. Also see [hazard, cumulative hazard, and hazard ratio](#).

treatment model. A treatment model is a model used to predict treatment-assignment probabilities as a function of covariates and parameters.

truncation, left-truncation, and right-truncation. In survival analysis, truncation occurs when subjects are observed only if their failure times fall within a certain observational period of a study. Censoring, on the other hand, occurs when subjects are observed for the whole duration of a study, but the exact times of their failures are not known; it is known only that their failures occurred within a certain time span.

Left-truncation occurs when subjects come under observation only if their failure times exceed some time t_l . It is only because they did not fail before t_l that we even knew about their existence. Left-truncation differs from left-censoring in that, in the censored case, we know that the subject failed before time t_l , but we just do not know exactly when.

Imagine a study of patient survival after surgery, where patients cannot enter the sample until they have had a post-surgical test. The patients' survival times will be left-truncated. This is a "delayed entry" problem, one common type of left-truncation.

Right-truncation occurs when subjects come under observation only if their failure times do not exceed some time t_r . Right-truncated data typically occur in registries. For example, a cancer registry includes only subjects who developed a cancer by a certain time, and thus survival data from this registry will be right-truncated.

unconfoundedness. See *conditional-independence assumption*.

weighted-regression-adjustment estimator. Weighted-regression-adjustment estimators use means of predicted outcomes for each treatment level to estimate each potential-outcome mean. The weights are used to estimate censoring-adjusted regression coefficients.

Subject and author index

See the [combined subject index](#) and the [combined author index](#) in the *Glossary and Index*.