Title

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stcrreg postestimation — Postestimation tools for stcrreg

Postestimation commands

The following postestimation command is of special interest after `stcrreg`:

Command	Description
`stcurve`	plot the cumulative subhazard and cumulative incidence functions

For information on `stcurve`, see [ST] **stcurve**.

The following standard postestimation commands are also available:

Command	Description
`contrast`	contrasts and ANOVA-style joint tests of estimates
`estat ic`	Akaike's and Schwarz's Bayesian information criteria (AIC and BIC)
`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
`margins`	marginal means, predictive margins, marginal effects, and average marginal effects
`marginsplot`	graph the results from margins (profile plots, interaction plots, etc.)
`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
`pwcompare`	pairwise comparisons of estimates
`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 subhazard ratios, linear predictions, standard errors, baseline cumulative incidence and subhazard functions, Kaplan–Meier survivor curves, pseudolikelihood scores, efficient score and Schoenfeld residuals, and DFBETA measures of influence.

Menu for predict

Statistics > Postestimation

Syntax for predict

`predict` [*type*] *newvar* [*if*] [*in*] [, *sv_statistic* `nooffset`]

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

sv_statistic	Description
Main	
`shr`	predicted subhazard ratio, also known as the relative subhazard; the default
`xb`	linear prediction $\mathbf{x}_j\boldsymbol{\beta}$
`stdp`	standard error of the linear prediction; SE$(\mathbf{x}_j\boldsymbol{\beta})$
* `basecif`	baseline cumulative incidence function (CIF)
* `basecshazard`	baseline cumulative subhazard function
* `kmcensor`	Kaplan–Meier survivor curve for the censoring distribution

mv_statistic	Description
Main	
* `scores`	pseudolikelihood scores
* `esr`	efficient score residuals
* `dfbeta`	DFBETA measures of influence
* `schoenfeld`	Schoenfeld residuals

Unstarred statistics are available both in and out of sample; type `predict ... if e(sample) ...` if wanted only for the estimation sample. Starred statistics are calculated only for the estimation sample, even when `if e(sample)` is not specified.

`nooffset` is allowed only with unstarred statistics.

Options for predict

Main

`shr`, the default, calculates the relative subhazard (subhazard ratio), that is, the exponentiated linear prediction, $\exp(\mathbf{x}_j\widehat{\boldsymbol{\beta}})$.

`xb` calculates the linear prediction from the fitted model. That is, you fit the model by estimating a set of parameters, $\beta_1, \beta_2, \ldots, \beta_k$, and the linear prediction is $\widehat{\beta}_1 x_{1j} + \widehat{\beta}_2 x_{2j} + \cdots + \widehat{\beta}_k x_{kj}$, often written in matrix notation as $\mathbf{x}_j\widehat{\boldsymbol{\beta}}$.

The x_{1j}, x_{2j}, ..., x_{kj} used in the calculation are obtained from the data currently in memory and need not correspond to the data on the independent variables used in estimating $\boldsymbol{\beta}$.

`stdp` calculates the standard error of the prediction, that is, the standard error of $\mathbf{x}_j\widehat{\boldsymbol{\beta}}$.

`basecif` calculates the baseline CIF. This is the CIF of the subdistribution for the cause-specific failure process.

`basecshazard` calculates the baseline cumulative subhazard function. This is the cumulative hazard function of the subdistribution for the cause-specific failure process.

`kmcensor` calculates the Kaplan–Meier survivor function for the censoring distribution. These estimates are used to weight within risk pools observations that have experienced a competing event. As such, these values are not predictions or diagnostics in the strict sense, but are provided for those who wish to reproduce the pseudolikelihood calculations performed by `stcrreg`; see [ST] **stcrreg**.

`nooffset` is allowed only with `shr`, `xb`, and `stdp`, and is relevant only if you specified `offset(`*varname*`)` for `stcrreg`. It modifies the calculations made by `predict` so that they ignore the offset variable; the linear prediction is treated as $\mathbf{x}_j\widehat{\boldsymbol{\beta}}$ rather than $\mathbf{x}_j\widehat{\boldsymbol{\beta}} + \text{offset}_j$.

`scores` calculates the pseudolikelihood scores for each regressor in the model. These scores are components of the robust estimate of variance. For multiple-record data, by default only one score per subject is calculated and it is placed on the last record for the subject.

Adding the `partial` option will produce partial scores, one for each record within subject; see `partial` below. Partial pseudolikelihood scores are the additive contributions to a subject's overall pseudolikelihood score. In single-record data, the partial pseudolikelihood scores are the pseudolikelihood scores.

One score variable is created for each regressor in the model; the first new variable corresponds to the first regressor, the second to the second, and so on.

`esr` calculates the efficient score residuals for each regressor in the model. Efficient score residuals are diagnostic measures equivalent to pseudolikelihood scores, with the exception that efficient score residuals treat the censoring distribution (that used for weighting) as known rather than estimated. For multiple-record data, by default only one score per subject is calculated and it is placed on the last record for the subject.

Adding the `partial` option will produce partial efficient score residuals, one for each record within subject; see `partial` below. Partial efficient score residuals are the additive contributions to a subject's overall efficient score residual. In single-record data, the partial efficient scores are the efficient scores.

One efficient variable is created for each regressor in the model; the first new variable corresponds to the first regressor, the second to the second, and so on.

`dfbeta` calculates the DFBETA measures of influence for each regressor of in the model. The DFBETA value for a subject estimates the change in the regressor's coefficient due to deletion of that subject.

For multiple-record data, by default only one value per subject is calculated and it is placed on the last record for the subject.

Adding the `partial` option will produce partial DFBETAs, one for each record within subject; see `partial` below. Partial DFBETAs are interpreted as effects due to deletion of individual records rather than deletion of individual subjects. In single-record data, the partial DFBETAs are the DFBETAs.

One DFBETA variable is created for each regressor in the model; the first new variable corresponds to the first regressor, the second to the second, and so on.

`schoenfeld` calculates the Schoenfeld-like residuals. Schoenfeld-like residuals are diagnostic measures analogous to Schoenfeld residuals in Cox regression. They compare a failed observation's covariate values to the (weighted) average covariate values for all of those at risk at the time of failure. Schoenfeld-like residuals are calculated only for those observations that end in failure; missing values are produced otherwise.

One Schoenfeld residual variable is created for each regressor in the model; the first new variable corresponds to the first regressor, the second to the second, and so on.

Note: The easiest way to use the preceding four options is, for example,

```
. predict double stub*, scores
```

where *stub* is a short name of your choosing. Stata then creates variables *stub*1, *stub*2, etc. You may also specify each variable name explicitly, in which case there must be as many (and no more) variables specified as there are regressors in the model.

`partial` is relevant only for multiple-record data and is valid with `scores`, `esr`, and `dfbeta`. Specifying `partial` will produce "partial" versions of these statistics, where one value is calculated for each record instead of one for each subject. The subjects are determined by the `id()` option to `stset`.

Specify `partial` if you wish to perform diagnostics on individual records rather than on individual subjects. For example, a partial DFBETA would be interpreted as the effect on a coefficient due to deletion of one record, rather than the effect due to deletion of all records for a given subject.

margins

Description for margins

`margins` estimates margins of response for subhazard ratios and linear predictions.

Menu for margins

Statistics > Postestimation

Syntax for margins

`margins` [*marginlist*] [`,` *options*]

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

statistic	Description
`shr`	predicted subhazard ratio, also known as the relative subhazard; the default
`xb`	linear prediction $\mathbf{x}_j\boldsymbol{\beta}$
`stdp`	not allowed with `margins`
`basecif`	not allowed with `margins`
`basecshazard`	not allowed with `margins`
`kmcensor`	not allowed with `margins`
`scores`	not allowed with `margins`
`esr`	not allowed with `margins`
`dfbeta`	not allowed with `margins`
`schoenfeld`	not allowed with `margins`

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

For the full syntax, see [R] **margins**.

Remarks and examples

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Remarks are presented under the following headings:

Baseline functions
Null models
Measures of influence

Baseline functions

▷ Example 1: Cervical cancer study

In example 1 of [ST] **stcrreg**, we fit a proportional subhazards model on data from a cervical cancer study.

```
. use http://www.stata-press.com/data/r14/hypoxia
(Hypoxia study)
. stset dftime, failure(failtype == 1)
  (output omitted)
. stcrreg ifp tumsize pelnode, compete(failtype == 2)
  (output omitted)
```

```
Competing-risks regression                    No. of obs       =        109
                                              No. of subjects  =        109
Failure event  : failtype == 1                No. failed       =         33
Competing event: failtype == 2                No. competing    =         17
                                              No. censored     =         59

                                              Wald chi2(3)     =      33.21
Log pseudolikelihood =  -138.5308             Prob > chi2      =     0.0000
```

_t	SHR	Robust Std. Err.	z	P>|z|	[95% Conf.	Interval]
ifp	1.033206	.0178938	1.89	0.059	.9987231	1.068879
tumsize	1.297332	.1271191	2.66	0.008	1.070646	1.572013
pelnode	.4588123	.1972067	-1.81	0.070	.1975931	1.065365

After fitting the model, we can predict the baseline cumulative subhazard, $\overline{H}_{1,0}(t)$, and the baseline CIF, $\text{CIF}_{1,0}(t)$:

```
. predict bch, basecsh
. predict bcif, basecif
. list dftime failtype ifp tumsize pelnode bch bcif in 1/15
```

	dftime	failtype	ifp	tumsize	pelnode	bch	bcif
1.	6.152	0	8	7	1	.0658792	.063756
2.	8.008	0	8.2	2	1	.0813224	.0781036
3.	.003	1	8.6	10	1	.0260186	.025683
4.	1.073	1	3.3	8	1	.0379107	.0372011
5.	.003	1	18.5	8	0	.0260186	.025683
6.	7.929	0	20	8	1	.0813224	.0781036
7.	8.454	0	21.8	4	1	.0813224	.0781036
8.	7.107	1	31.6	5	1	.0813224	.0781036
9.	8.378	0	16.5	5	1	.0813224	.0781036
10.	8.178	0	31.5	3	1	.0813224	.0781036
11.	3.395	0	18.5	4	1	.0658792	.063756
12.	.003	1	12.8	5	0	.0260186	.025683
13.	1.35	1	18.4	4	1	.051079	.0497964
14.	.003	1	18.5	8	1	.0260186	.025683
15.	.512	2	21	10	0	.0260186	.025683

The baseline functions are for subjects who have zero-valued covariates, which in this example are not representative of the data. If baseline is an extreme departure from the covariate patterns in your data, then we recommend recentering your covariates to avoid numerical overflows when predicting baseline functions; see *Making baseline reasonable* in [ST] **stcox postestimation** for more details.

For our data, baseline is close enough to not cause any numerical problems, but far enough to not be of scientific interest (zero tumor size?). You can transform the baseline functions to those for other covariate patterns according to the relationships

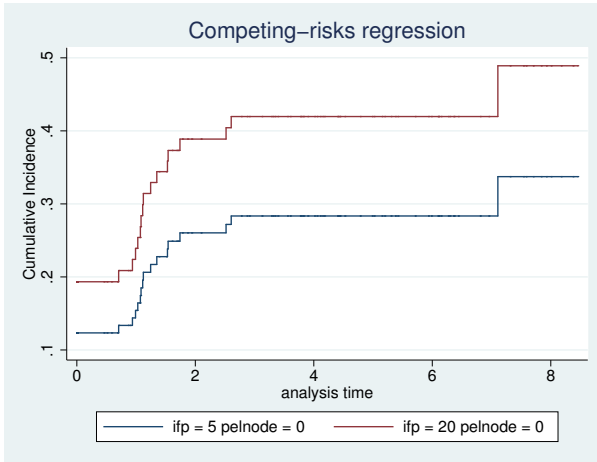
$$\overline{H}_1(t) = \exp(\mathbf{x}\boldsymbol{\beta})\overline{H}_{1,0}(t)$$

and

$$\text{CIF}_1(t) = 1 - \exp\{-\exp(\mathbf{x}\boldsymbol{\beta})\overline{H}_{1,0}(t)\}$$

but it is rare that you will ever have to do that. `stcurve` will predict, transform, and graph these functions for you. When you use `stcurve`, you specify the covariate settings, and any you leave unspecified are set at the mean over the data used in the estimation.

```
. stcurve, cif at1(ifp = 5 pelnode = 0) at2(ifp = 20 pelnode = 0)
```



Because they were left unspecified, the cumulative incidence curves are for mean tumor size. If you wish to graph cumulative subhazards instead of CIFs, use the `stcurve` option `cumhaz` in place of `cif`.

◁

Null models

Predicting baseline functions after fitting a null model (one without covariates) yields nonparametric estimates of the cumulative subhazard and the CIF.

▷ Example 2: HIV and SI as competing events

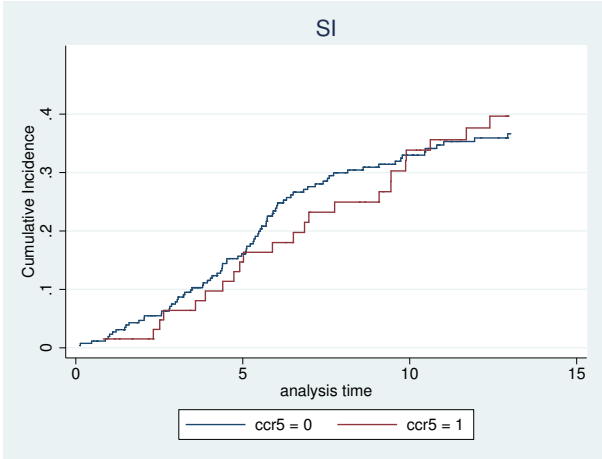
In example 4 of [ST] **stcrreg**, we analyzed the incidence of appearance of the SI HIV phenotype, where a diagnosis of AIDS is a competing event. We modeled SI incidence in reference to a genetic mutation indicated by the covariate `ccr5`. We compared two approaches: one that used `stcrreg` and

assumed that the subhazard of SI was proportional with respect to ccr5 versus one that used stcox and assumed that the cause-specific hazards for both SI and AIDS were each proportional with respect to ccr5. For both approaches, we produced cumulative incidence curves for SI comparing those who did not have the mutation (ccr5==0) to those who did (ccr5==1).

To see which approach better fits these data, we now produce cumulative incidence curves that make no model assumption about the effect of ccr5. We do this by fitting null models on the two subsets of the data defined by ccr5 and predicting the baseline CIF for each. Because the models have no covariates, the estimated baseline CIFs are nonparametric estimators.

```
. use http://www.stata-press.com/data/r14/hiv_si, clear
(HIV and SI as competing risks)
. stset time, failure(status == 2)                // SI is the event of interest
  (output omitted)
. stcrreg if !ccr5, compete(status == 1) noshow   // AIDS is the competing event
Competing-risks regression                        No. of obs       =        259
                                                  No. of subjects  =        259
Failure event  : status == 2                      No. failed       =         84
Competing event: status == 1                      No. competing    =        101
                                                  No. censored     =         74
                                                  Wald chi2(0)     =       0.00
Log pseudolikelihood = -435.80148                 Prob > chi2      =          .
------------------------------------------------------------------------------
             |               Robust
          _t |        SHR   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
. predict cif_si_0, basecif
(65 missing values generated)
. label var cif_si_0 "ccr5 = 0"
. stcrreg if ccr5, compete(status == 1) noshow
Competing-risks regression                        No. of obs       =         65
                                                  No. of subjects  =         65
Failure event  : status == 2                      No. failed       =         23
Competing event: status == 1                      No. competing    =         12
                                                  No. censored     =         30
                                                  Wald chi2(0)     =       0.00
Log pseudolikelihood = -88.306665                 Prob > chi2      =          .
------------------------------------------------------------------------------
             |               Robust
          _t |        SHR   Std. Err.      z    P>|z|     [95% Conf. Interval]
-------------+----------------------------------------------------------------
. predict cif_si_1, basecif
(259 missing values generated)
. label var cif_si_1 "ccr5 = 1"
```

```
. twoway line cif_si* _t if _t<13, connect(J J) sort yscale(range(0 0.5))
> title(SI) ytitle(Cumulative Incidence) xtitle(analysis time)
```



After comparing with the graphs produced in [ST] **stcrreg**, we find that the nonparametric analysis favors the `stcox` approach over the `stcrreg` approach.

◁

❑ Technical note

Predicting the baseline CIF after fitting a null model with `stcrreg` produces a nonparametric CIF estimator that is asymptotically equivalent, but not exactly equal, to an alternate estimator that is often used; see Coviello and Boggess (2004) for the details of that estimator. The estimator used by `predict` after `stcrreg` is a competing-risks extension of the Nelson–Aalen estimator (Nelson 1972; Aalen 1978); see *Methods and formulas*. The other is a competing-risks extension of the Kaplan–Meier (1958) estimator.

In large samples with many failures, the difference is negligible.

❑

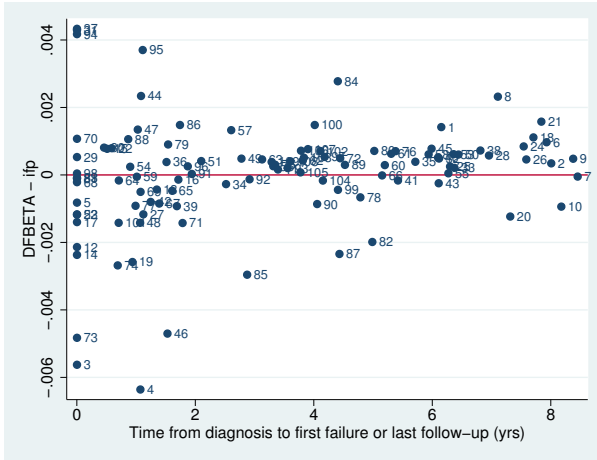
Measures of influence

With `predict` after `stcrreg`, you can obtain pseudolikelihood scores that are used to calculate robust estimates of variance, Schoenfeld residuals that reflect each failure's contribution to the gradient of the log pseudolikelihood, efficient score residuals that represent each subject's (observation's) contribution to the gradient, and DFBETAs that measure the change in coefficients due to deletion of a subject or observation.

▷ Example 3: DFBETAs

Returning to our cervical cancer study, we obtain DFBETAs for each of the three coefficients in the model and graph those for the first with respect to analysis time.

```
. use http://www.stata-press.com/data/r14/hypoxia, clear
(Hypoxia study)
. stset dftime, failure(failtype == 1)
  (output omitted)
. stcrreg ifp tumsize pelnode, compete(failtype == 2)
  (output omitted)
. predict df*, dfbeta
. generate obs = _n
. twoway scatter df1 dftime, yline(0) mlabel(obs)
```



`predict` created the variables `df1`, `df2`, and `df3`, holding DFBETA values for variables `ifp`, `tumsize`, and `pelnode`, respectively. Based on the graph, we see that subject 4 is the most influential on the coefficient for `ifp`, the first covariate in the model.

◁

In the previous example, we had single-record data. If you have data with multiple records per subject, then by default DFBETAs will be calculated at the subject level, with one value representing each subject and measuring the effect of deleting all records for that subject. If you instead want record-level DFBETAs that measure the change due to deleting single records within subjects, add the `partial` option; see [ST] **stcox postestimation** for further details.

Methods and formulas

Continuing the discussion from *Methods and formulas* in [ST] **stcrreg**, the baseline cumulative subhazard function is calculated as

$$\widehat{H}_{1,0}(t) = \sum_{j:t_j \le t} \frac{\delta_j}{\sum_{\ell \in R_j} w_\ell \pi_{\ell j} \exp(z_\ell)}$$

The baseline CIF is $\widehat{\text{CIF}}_{1,0}(t) = 1 - \exp\{-\widehat{H}_{1,0}(t)\}$.

The Kaplan–Meier survivor curve for the censoring distribution is

$$\widehat{S}_c(t) = \prod_{t_{(j)}<t} \left\{ 1 - \frac{\sum_i \gamma_i I(t_i = t_{(j)})}{r(t_{(j)})} \right\}$$

where $t_{(j)}$ indexes the times at which censorings occur.

Both the pseudolikelihood scores, $\widehat{\mathbf{u}}_i$, and the efficient score residuals, $\widehat{\boldsymbol{\eta}}_i$, are as defined previously. DFBETAs are calculated according to Collett (2003):

$$\text{DFBETA}_i = \widehat{\boldsymbol{\eta}}_i' \text{Var}^*(\widehat{\boldsymbol{\beta}})$$

where $\text{Var}^*(\widehat{\boldsymbol{\beta}})$ is the model-based variance estimator, that is, the inverse of the negative Hessian.

Schoenfeld residuals are $\mathbf{r}_i = (\widehat{r}_{1i}, \ldots, \widehat{r}_{mi})$ with

$$\widehat{r}_{ki} = \delta_i \left(x_{ki} - a_{ki} \right)$$

References

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Fyles, A., M. Milosevic, D. Hedley, M. Pintilie, W. Levin, L. Manchul, and R. P. Hill. 2002. Tumor hypoxia has independent predictor impact only in patients with node-negative cervix cancer. *Journal of Clinical Oncology* 20: 680–687.

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Putter, H., M. Fiocco, and R. B. Geskus. 2007. Tutorial in biostatistics: Competing risks and multi-state models. *Statistics in Medicine* 26: 2389–2430.

Also see

[ST] **stcrreg** — Competing-risks regression

[ST] **stcurve** — Plot survivor, hazard, cumulative hazard, or cumulative incidence function

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