

stcurve — Plot the survivor or related function after `streg`, `stcox`, and more

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Description

`stcurve` plots the survivor, failure, hazard, or cumulative hazard function after `stcox`, `streg`, `stintreg`, `stintcox`, `mestreg`, `xtstreg`, `lasso cox`, or `elasticnet cox`. `stcurve` also plots the cumulative subhazard or cumulative incidence function (CIF) after `stcrreg`.

Quick start

Plot the survivor function with covariates at their means after `stcox`, `streg`, `stintreg`, `stintcox`, `mestreg`, `xtstreg`, `lasso cox`, or `elasticnet cox`

```
stcurve, survival
```

Same as above, but plot separate survivor functions for covariate `x` set to 1, 2, and 3

```
stcurve, survival at1(x=1) at2(x=2) at3(x=3)
```

Same as above, but specify a numlist for `x` in `at()`

```
stcurve, survival at(x=(1 2 3))
```

Same as above, but specify a different pattern for each line

```
stcurve, survival at(x=(1 2 3)) lpattern(solid dash dot)
```

Same as above, and save the graph as `mygraph.gph`

```
stcurve, survival at(x=(1 2 3)) saving(mygraph)
```

Plot the estimated hazard function after `stcox`, `streg`, `stintreg`, `stintcox`, `mestreg`, `xtstreg`, `lasso cox`, or `elasticnet cox`

```
stcurve, hazard
```

Smooth the estimated hazard contributions using the Gaussian kernel function for the kernel-density estimate after `stcox` or `stintcox`, and set `x` to 1

```
stcurve, hazard kernel(gaussian) at(x=1)
```

Plot the cumulative hazard function after `stcox`, `streg`, `stintreg`, `stintcox`, `mestreg`, `xtstreg`, `lasso cox`, or `elasticnet cox`

```
stcurve, cumhaz
```

Plot the cumulative subhazard function after `stcrreg`

```
stcurve, cumhaz
```

Plot the cumulative incidence function after `stcrreg`

```
stcurve, cif
```

Same as above, but set `x` to 0

```
stcurve, cif at(x=0)
```

Menu

Statistics > Survival analysis > Regression models > Plot survivor or related function

Syntax

```
stcurve [ , options ]
```

options

Description

Main

| | |
|-----------------------------------------------------|--------------------------------------------------------------------------------|
| * survival | plot survivor function |
| * failure | plot failure function |
| * hazard | plot hazard function |
| * cumhaz | plot cumulative hazard function |
| * cif | plot cumulative incidence function |
| atomeans | evaluate function at overall means; the default |
| attmeans | evaluate function at time-specific means; available only after stintcox |
| at(atspec) | values of the specified covariates and means of unspecified covariates |
| [at1(atspec1) [at2(atspec2) [...]]] | |
| atframe(frame) | use covariate values from frame; available only after stintcox |

Options

| | |
|----------------------------------------|-----------------------------------------------------|
| alpha1 | conditional frailty model |
| fixedonly | set all random effects to zero |
| unconditional | unconditional frailty model or random-effects model |
| marginal | synonym for unconditional |
| range(# #) | range of analysis time |
| outfile(filename) [, replace] | save values used to plot the curves |
| width(#) | override “optimal” width; use with hazard |
| kernel(kernel) | kernel function; use with hazard |
| noboundary | no boundary correction; use with hazard |

Plot

| | |
|------------------------|--------------------------------------------------------------------------------------|
| connect_options | affect rendition of plotted survivor, failure, hazard, or cumulative hazard function |
|------------------------|--------------------------------------------------------------------------------------|

Add plots

| | |
|----------------------|----------------------------------------|
| addplot(plot) | add other plots to the generated graph |
|----------------------|----------------------------------------|

Y axis, X axis, Titles, Legend, Overall

| | |
|-----------------------|------------------------------------------------------------------------------|
| twoway_options | any options other than by() documented in [G-3] twoway_options |
|-----------------------|------------------------------------------------------------------------------|

*One of **survival**, **failure**, **hazard**, **cumhaz**, or **cif** must be specified.

survival, **failure**, and **hazard** are not allowed after estimation with **stcrreg**; see [ST] **stcrreg**

cif is allowed only after estimation with **stcrreg**; see [ST] **stcrreg**.

stcurve is not supported after stratified estimation.

For the **stcurve** syntax following **lasso cox** and **elasticnet cox**, see [LASSO] **lasso postestimation**.

Options

Main

survival specifies that the survivor function be plotted. **survival** is not allowed after estimation with **stcrreg**.

failure specifies that the failure function be plotted. **failure** is not allowed after estimation with **stcrreg**.

hazard specifies that the hazard function be plotted. **hazard** is not allowed after estimation with **stcrreg**.

cumhaz specifies that the cumulative hazard function be plotted when used after **stcox**, **streg**, **stintreg**, **stintcox**, **mestreg**, or **xtstreg** and specifies that the cumulative subhazard function be plotted when used after **stcrreg**.

cif specifies that the cumulative incidence function be plotted. This option is available only after estimation with **stcrreg**.

atomeans specifies that the estimates of the survivor or other function be evaluated at the overall means of covariates. This is the default.

attmeans is supported after **stintcox** in a multiple-record-per-subject format. It specifies that the estimates of the survivor or other function be evaluated at the time-specific means of covariates. This option is useful to incorporate time profiles for time-varying covariates present in the dataset. Also see option **atframe()**.

at(*atspec*) specifies that the estimates of the survivor or other function be evaluated at specific covariate values. By default, **stcurve** evaluates the function by setting each covariate to its overall mean value. This option causes the function to be evaluated at the values of the covariates listed in **at()** and at the overall means of all unlisted covariates. If option **attmeans** is also specified, the unlisted covariates are evaluated at time-specific means. This option can be repeated to produce multiple curves, or you can specify multiple values for a set of covariates in one **at()** option; see *Syntax of at()* in [ST] *adjustfor_option* for details. **at()** may not be combined with **at1()**, **at2()**, and so on.

at1(*atspec1*), **at2**(*atspec2*), ..., **at20**(*atspec20*) are the alternatives to the repeated use of **at()**. They specify that multiple curves (up to 20) be plotted on the same graph. **at1()**, **at2()**, ..., **at20()** work similarly to the **at()** option. **at1()** specifies the values of the covariates for the first curve, **at2()** specifies the values of the covariates for the second curve, and so on. But, unlike **at()**, **at#()** cannot be repeated and may not be combined with **at()**. *atspec1*, *atspec2*, and so on follow the same syntax as *atspec*, except they do not allow *numlists* or multiple values for the same covariate.

atframe(*framename*) is supported after **stintcox** in a multiple-record-per-subject format. It specifies that the estimates of the survivor or other function be evaluated using the values of variables specified in the *framename* frame. The frame must contain a time variable with the same name as the examination time variable specified in **stintcox**'s **time()** option. It must also include at least one covariate as specified with **stintcox** or in its **tvc()** option. **atframe()** may not be combined with **at()**.

Options

alpha1, when used after fitting a frailty model, plots curves that are conditional on a frailty value of one. This is the default for shared-frailty models.

fixedonly specifies that all random effects be set to zero, which is equivalent to using only the fixed portion of the model, when plotting results for random-effects models. This option is allowed only after **xtstreg** or **mestreg**; it is the default after **xtstreg**.

unconditional and **marginal**, when used after fitting a frailty model or a random-effects model, plot curves that are unconditional on the frailty or on the random effects. That is, the curve is “averaged” over the frailty distribution or over the random-effects distributions. This is the default for unshared-frailty models and for random-effects models. This option is not allowed after **stntreg**, **stntcox**, or **xtstreg**.

range(##) specifies the range of the time axis to be plotted. If this option is not specified, **stcurve** plots the desired curve on an interval expanding from the earliest to the latest time in the data.

outfile(filename [, replace]) saves in *filename.dta* the values used to plot the curve(s).

width(#) is for use with **hazard** (and applies only after **stcox**) and is used to specify the bandwidth to be used in the kernel smooth used to plot the estimated hazard function. If left unspecified, a default bandwidth is used, as described in [R] **kdensity**.

kernel(kernel) is for use with **hazard** and is for use only after **stcox** or **stntcox** because, for Cox regression, an estimate of the hazard function is obtained by smoothing the estimated hazard contributions. **kernel()** specifies the kernel function for use in calculating the weighted kernel-density estimate required to produce a smoothed hazard-function estimator. The default is **kernel(epanechnikov)**, yet *kernel* may be any of the kernels supported by **kdensity**; see [R] **kdensity**.

noboundary is for use with **hazard** and applies only to the plotting of smoothed hazard functions after **stcox** or **stntcox**. It specifies that no boundary-bias adjustments are to be made when calculating the smoothed hazard-function estimator. By default, the smoothed hazards are adjusted near the boundaries; see [ST] **sts graph**. If the **epan2**, **biweight**, or **rectangular** kernel is used after estimation using **stcox**, the bias correction near the boundary is performed using boundary kernels. For other kernels, the plotted range of the smoothed hazard function is restricted to be inside of one bandwidth from each endpoint. For these other kernels, specifying **noboundary** merely removes this range restriction. After estimation using **stntcox**, the boundary adjustments correspond to simply restricting the plotted range of the function for all kernels.

Plot

connect_options affect the rendition of the plotted survivor, failure, hazard, or cumulative hazard function; see [G-3] **connect_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

Remarks are presented under the following headings:

stcurve after stcox
stcurve after streg
stcurve after sterreg
stcurve after stintreg and stintcox
Using at() with stcurve

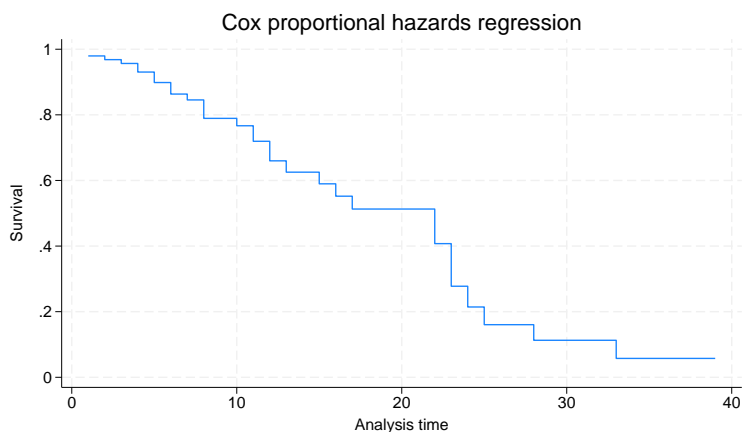
For examples of `stcurve` after `xtstreg` and `mestreg`, see [\[XT\] xtstreg postestimation](#) and [\[ME\] mestreg postestimation](#), respectively.

stcurve after stcox

After fitting a Cox model, `stcurve` can be used to plot the estimated survivor, failure, hazard, or cumulative hazard function.

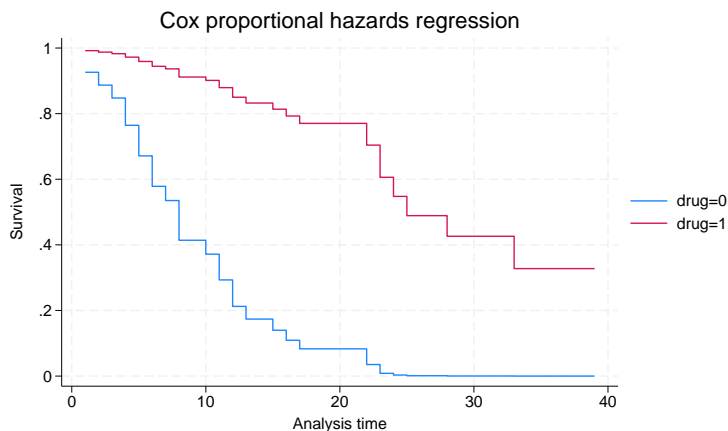
▷ Example 1

```
. use https://www.stata-press.com/data/r18/drugtr
(Patient survival in drug trial)
. stcox age drug
(output omitted)
. stcurve, survival
note: function evaluated at overall means of covariates.
```



By default, the curve is evaluated at the mean values of all the predictors, but we can specify other values if we wish.

```
. stcurve, survival at1(drug=0) at2(drug=1)
note: function evaluated at specified values of selected covariates and
      overall means of other covariates (if any).
```



Alternatively, you can obtain the same plot by typing the following:

```
. stcurve, survival at(drug=(0 1))
```

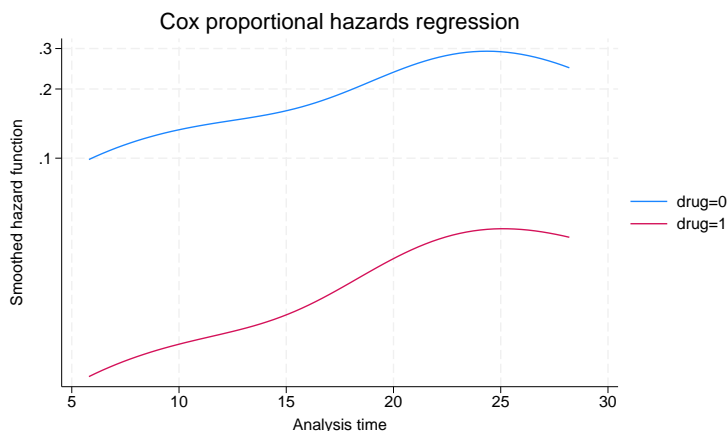
In this example, we asked for two plots, one for the placebo group and one for the treatment group. For both groups, the value of `age` was held at its mean value for the overall estimation sample.

See [Cefalu \(2011\)](#) for a Stata command to plot the survivor or cumulative hazard function with pointwise confidence intervals.

▷ Example 2

stcurve can also be used to plot estimated hazard functions. The hazard function is estimated by a kernel smooth of the estimated hazard contributions; see [ST] [sts graph](#) for details. We can thus customize the smooth as we would any other; see [R] [kdensity](#) for details.

```
. stcurve, hazard at(drug=(0 1)) kernel(gauss) yscale(log)
note: function evaluated at specified values of selected covariates and
      overall means of other covariates (if any).
```



For the hazard plot, we plotted on a log scale to demonstrate the proportionality of hazards under this model; see the technical note below on smoothed hazards.



□ Technical note

For survivor or cumulative hazard estimation, stcurve works by first estimating the baseline function and then modifying it to adhere to the specified (or by default, mean) covariate patterns. As mentioned previously, *baseline* (when all covariates are equal to zero) must correspond to something that is meaningful and preferably in the range of your data. Otherwise, stcurve could encounter numerical difficulties. We ignored our own advice above and left age unchanged. Had we encountered numerical problems, or funny-looking graphs, we would have known to try shifting age so that age==0 was in the range of our data.

For hazard estimation, stcurve works by first transforming the estimated hazard contributions to adhere to the necessary covariate pattern and then applying the smooth. When you plot multiple curves, each is smoothed independently, although the same bandwidth is used for each.

The smoothing takes place in the hazard scale and not in the log hazard-scale. As a result, the resulting curves will look nearly, but not exactly, parallel when plotted on a log scale. This inexactitude is a product of the smoothing and should not be interpreted as a deviation from the proportional-hazards assumption; stcurve (after stcox) assumes proportionality of hazards and will reflect this in the produced plots. If smoothing were a perfect science, the curves would be parallel when plotted on a log scale. If you encounter estimated hazards exhibiting severe disproportionality, this may signal a numerical problem as described above. Try recentering your covariates so that baseline is more reasonable.



stcurve after streg

`stcurve` is used after `streg` to plot the fitted survivor, failure, hazard, or cumulative hazard function. By default, `stcurve` computes the means of the covariates and evaluates the functions at each time in the data, censored or uncensored. The resulting plot is therefore the survival experience of a subject with a covariate pattern equal to the average covariate pattern in the study. You can produce the plot at other values of the covariates by using the `at()` option or specify a time range by using the `range()` option.

► Example 3

We pick up where [example 6](#) of [ST] `streg` left off. The cancer dataset we are using has three values for variable `drug`: 1 corresponds to placebo, and 2 and 3 correspond to two alternative treatments. Using the cancer data with `drug` remapped to form an indicator of treatment, let's fit a loglogistic regression model and plot its survival curves. We can perform a loglogistic regression by issuing the following commands:

```
. use https://www.stata-press.com/data/r18/cancer
(Patient survival in drug trial)
. replace drug = drug==2 | drug==3           // 0, placebo : 1, nonplacebo
(48 real changes made)
. stset studytime, failure(died)
(output omitted)
. streg age drug, distribution(llogistic) nolog
      Failure _d: died
      Analysis time _t: studytime
Loglogistic AFT regression
No. of subjects = 48                Number of obs = 48
No. of failures = 31
Time at risk   = 744
LR chi2(2)     = 35.14
Log likelihood = -43.21698          Prob > chi2    = 0.0000
```

| _t | Coefficient | Std. err. | z | P> z | [95% conf. interval] | |
|----------|-------------|-----------|-------|-------|----------------------|-----------|
| age | -.0803289 | .0221598 | -3.62 | 0.000 | -.1237614 | -.0368964 |
| drug | 1.420237 | .2502148 | 5.68 | 0.000 | .9298251 | 1.910649 |
| _cons | 6.446711 | 1.231914 | 5.23 | 0.000 | 4.032204 | 8.861218 |
| /lngamma | -.8456552 | .1479337 | -5.72 | 0.000 | -1.1356 | -.5557105 |
| gamma | .429276 | .0635044 | | | .3212293 | .5736646 |

Now, we wish to plot the survivor and the hazard functions:

```
. stcurve, survival ylabel(0 .5 1)
note: function evaluated at overall means of covariates.
```

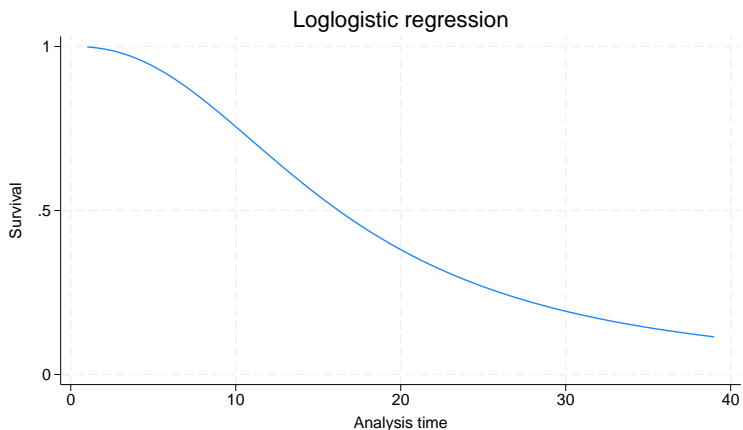


Figure 3. Loglogistic survival distribution at mean value of all covariates

```
. stcurve, hazard
note: function evaluated at overall means of covariates.
```

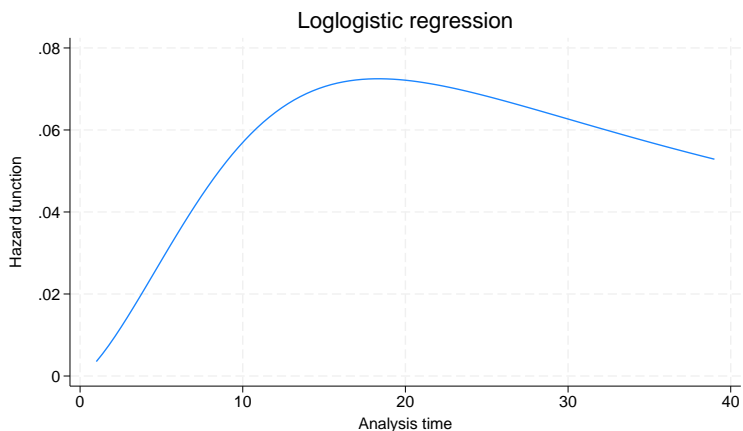


Figure 4. Loglogistic hazard distribution at mean value of all covariates

These plots show the fitted survivor and hazard functions evaluated for a cancer patient of average age receiving the average drug. Of course, the “average drug” has no meaning here because `drug` is an indicator variable. It makes more sense to plot the curves at a fixed value (level) of the drug. We can do this with the `at` option. For example, we may want to compare the average-age patient’s survival curve under placebo (`drug==0`) and under treatment (`drug==1`).

We can plot both curves on the same graph:

```
. stcurve, survival at(drug=(0 1)) ylabel(0 .5 1)
note: function evaluated at specified values of selected covariates and
overall means of other covariates (if any).
```

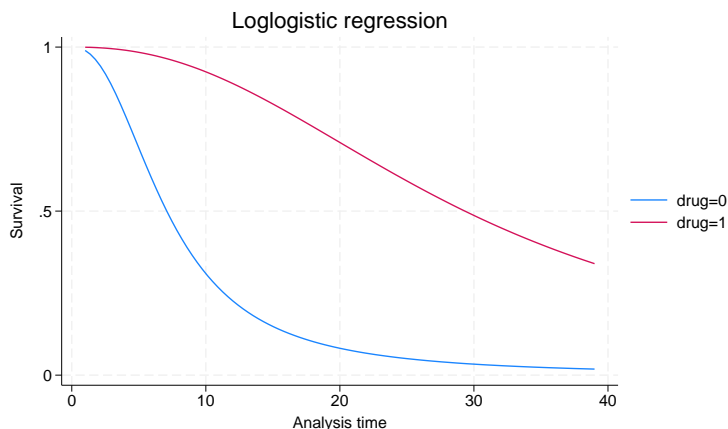


Figure 5. Loglogistic survival distribution at mean age for placebo

In the plot, we can see from the loglogistic model that the survival experience of an average-age patient receiving the placebo is worse than the survival experience of that same patient receiving treatment. We can also see the accelerated-failure-time feature of the loglogistic model. The survivor function for treatment is a time-decelerated (stretched-out) version of the survivor function for placebo. ◀

▷ Example 4

In our discussion of frailty models in [ST] **streg**, we emphasize the distinction between the individual hazard (or survivor) function and the hazard (survivor) function for the population. When significant frailty is present, the population hazard will tend to begin falling past a certain point, regardless of the shape of the individual hazard. This is due to the frailty effect—as time passes, the frailer individuals will fail, leaving a more homogeneous population comprising only the most robust individuals.

The frailty effect may be demonstrated using **stcurve** to plot the estimated hazard (both individual and population) after fitting a frailty model. Use the **alpha1** option to specify the individual hazard ($\alpha = 1$) and the **unconditional** option to specify the population hazard. Applying this to the Weibull/inverse-Gaussian shared-frailty model on the kidney data of example 11 of [ST] **streg**,

```
. use https://www.stata-press.com/data/r18/catheter, clear
(Kidney data, McGilchrist and Aisbett, Biometrics, 1991)
. stset time infect
  (output omitted)
. quietly streg age female, distribution(weibull) frailty(invgauss) shared(patient)
```

```
. stcurve, hazard at(female=1) alpha1
note: function evaluated at specified values of selected covariates and
      overall means of other covariates (if any).
```

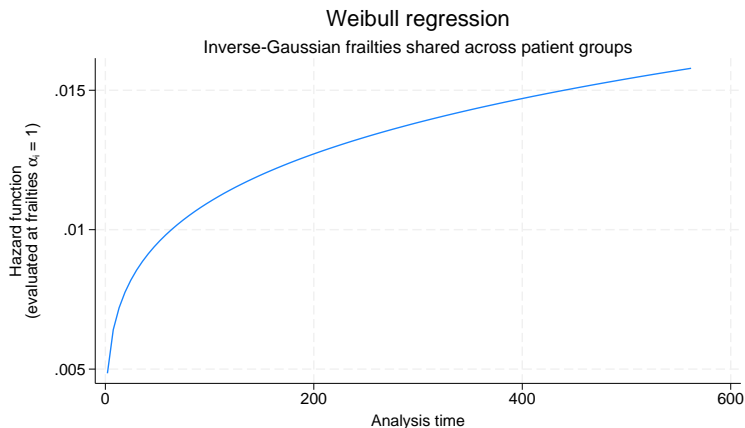


Figure 6. Individual hazard for females at mean age

Compare with

```
. stcurve, hazard at(female=1) unconditional
note: function evaluated at specified values of selected covariates and
      overall means of other covariates (if any).
```

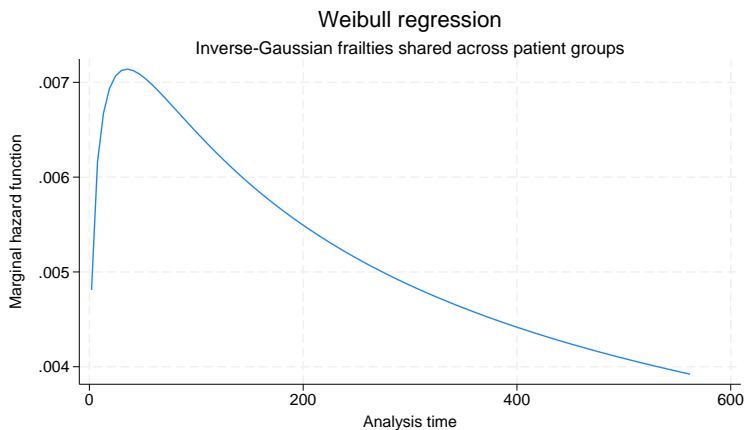


Figure 7. Population hazard for females at mean age

stcurve after `stcrreg`

► Example 5

In [ST] `stcrreg`, we analyzed data from 109 patients with primary cervical cancer, treated at a cancer center between 1994 and 2000. We fit a competing-risks regression model where local relapse was the failure event (`failtype == 1`), distant relapse with no local relapse was the competing risk event (`failtype == 2`), and we were interested primarily in the effect of interstitial fluid pressure (`ifp`) while controlling for tumor size and pelvic node involvement.

After fitting the competing-risks regression model, we can use `stcurve` to plot the estimated cumulative incidence of local relapses in the presence of the competing risk. We wish to compare the cumulative incidence curves for `ifp == 5` versus `ifp == 20`, assuming positive pelvic node involvement (`pelnode == 0`) and a tumor size that is the average over the data.

```
. use https://www.stata-press.com/data/r18/hypoxia
(Hypoxia study)
. stset dftime, fail(failtype==1)
(output omitted)
. stcrreg ifp tumsz pelnode, compete(failtype==2)
(output omitted)
. stcurve, cif at(ifp=(5 20) pelnode=0)
note: function evaluated at specified values of selected covariates and
overall means of other covariates (if any).
```

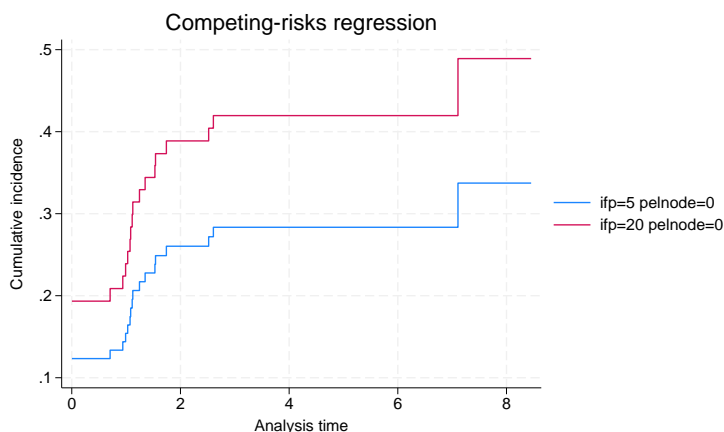


Figure 8. Comparative cumulative incidence functions

Specifying `ifp=(5 20)` in the `at()` option is the same as specifying the following `at#()` options:

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

stcurve after stintreg and stintcox

stcurve can be used after stintreg or stintcox to plot the fitted survivor, failure, hazard, or cumulative hazard function. For [single-record interval-censored data](#), these functions can be evaluated at a lower or upper time endpoint of time intervals. stcurve after stintreg uses the lower and upper time endpoints to determine the range for the plotted functions. stcurve after stintcox plots the functions at the distinct time points formed by combining the lower and upper time endpoints. By default, without the at() option, stcurve computes the overall means of the covariates and evaluates the function at the overall means and at each time in the data, censored or uncensored. The resulting plot is therefore the survival experience of a subject with a covariate pattern equal to the average covariate pattern in the study. You can produce the plot at other values of the covariates by using the at() option or specify a time range by using the range() option. stcurve after stintcox can also be used to plot functions that allow covariates to vary over time; see [Remarks and examples in \[ST\] stintcox postestimation](#).

► Example 6

We continue with [example 1](#) of [\[ST\] stintreg](#), which studies the effect of treatment on breast retraction for breast cancer patients. In that example, we compared the cosmetic effects of two cancer treatments, radiotherapy alone versus radiotherapy plus adjuvant chemotherapy, by fitting a Weibull proportional hazards model:

```
. use https://www.stata-press.com/data/r18/cosmesis, clear
(Cosmetic deterioration of breast cancer patients)
. stintreg i.treat, interval(ltime rtime) distribution(weibull)
  (iteration log omitted)
Weibull PH regression
```

| | | | |
|--|----------------|---|--------|
| | Number of obs | = | 94 |
| | Uncensored | = | 0 |
| | Left-censored | = | 5 |
| | Right-censored | = | 38 |
| | Interval-cens. | = | 51 |
| | LR chi2(1) | = | 10.93 |
| | Prob > chi2 | = | 0.0009 |

```
Log likelihood = -143.19228
```

| | Haz. ratio | Std. err. | z | P> z | [95% conf. interval] | |
|-------------|------------|-----------|-------|-------|----------------------|----------|
| treat | | | | | | |
| Radio+Chemo | 2.498526 | .7069467 | 3.24 | 0.001 | 1.434961 | 4.350383 |
| _cons | .0018503 | .0013452 | -8.66 | 0.000 | .000445 | .007693 |
| /ln_p | .4785786 | .1198972 | 3.99 | 0.000 | .2435844 | .7135729 |
| p | 1.613779 | .1934876 | | | 1.275814 | 2.041271 |
| 1/p | .6196635 | .0742959 | | | .4898907 | .7838134 |

Note: **_cons** estimates baseline hazard.

Now, we wish to compare the average patient's survival curve under radiotherapy only (`treat == 0`) and under radiotherapy plus chemotherapy (`treat == 1`):

```
. stcurve, survival at(treat=(0 1))
note: function evaluated at specified covariate values.
```

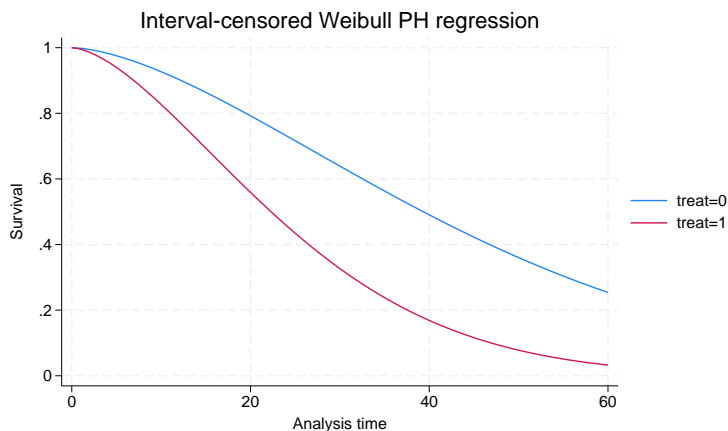


Figure 9. Treatment-specific survivor functions for Weibull proportional hazards model

From figure 9, we see that the risk of developing breast retraction for an average patient receiving the radiotherapy-plus-chemotherapy treatment is higher than that for the same patient receiving radiotherapy-only treatment. In other words, the adjuvant chemotherapy increases the risk of breast retraction.

Let's now use `stintcox` to fit a semiparametric Cox model that relaxes the distributional assumption about the event-time distribution. To speed up execution, we will use the `favorspeed` option in this demonstration.

```
. stintcox i.treat, interval(ltime rtime) favorspeed
note: using fixed step size with a multiplier of 5 to compute derivatives.
note: using EM and VCE tolerances of 0.0001.
note: option noemhstolerance assumed.
Performing EM optimization (showing every 100 iterations):
Iteration 0:   Log likelihood = -150.52924
Iteration 36: Log likelihood = -133.02071
Computing standard errors: ... done
Interval-censored Cox regression                               Number of obs   =   94
Baseline hazard: Reduced intervals                            Uncensored      =    0
                                                                Left-censored   =    5
Event-time interval:                                        Right-censored  =   38
  Lower endpoint: ltime                                    Interval-cens. =   51
  Upper endpoint: rtime
                                                                Wald chi2(1)    =    8.34
Log likelihood = -133.02071                                Prob > chi2     =  0.0039
```

| | OPG | | z | P> z | [95% conf. interval] | |
|-------------|------------|-----------|------|-------|----------------------|----------|
| | Haz. ratio | std. err. | | | | |
| treat | | | | | | |
| Radio+Chemo | 2.229089 | .6188939 | 2.89 | 0.004 | 1.293589 | 3.841127 |

Note: Standard error estimates may be more variable for small datasets and datasets with low proportions of interval-censored observations.

And we now compare the survivor functions of the two treatment groups:

```
. stcurve, survival at(treat=(0 1))
note: function evaluated at specified covariate values.
```

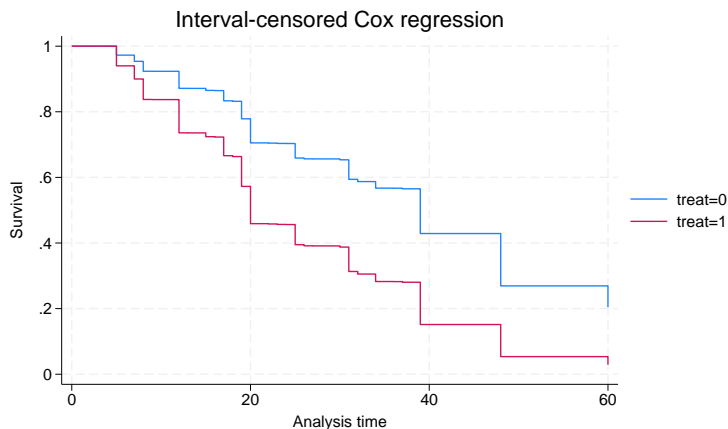


Figure 10. Treatment-specific survivor functions for Cox proportional hazards model

The survivor functions for the semiparametric Cox model are step functions but they look similar to the Weibull survivor functions from figure 9.

◀

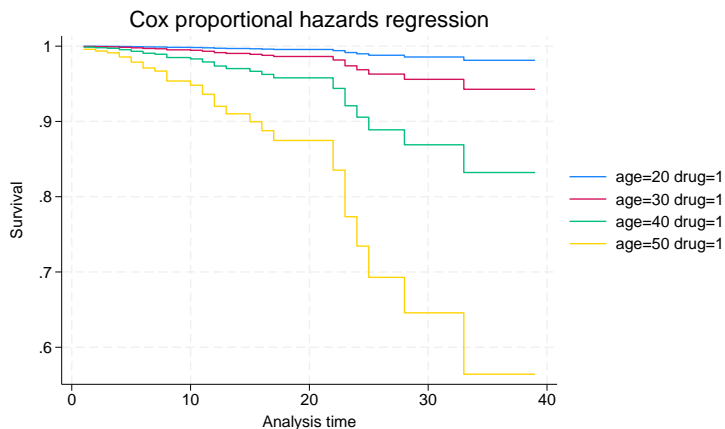
Using at() with stcurve

`stcurve`, by default, evaluates the function by setting each covariate to its mean value. The `at()` option specifies that the function be evaluated at the values of the covariates listed in `at()` and at the means of all unlisted covariates. You can repeat the `at()` option to produce multiple curves corresponding to different sets of covariate values.

► Example 7

Let's return to [example 1](#). Suppose that we want to compare the survival curves for patients at ages 20, 30, 40, and 50 of the treatment group. The easiest way to do this is to specify multiple values for `age` in `at(numlist)`.

```
. use https://www.stata-press.com/data/r18/drugtr
(Patient survival in drug trial)
. quietly stcox age drug
. stcurve, survival at(age=(20(10)50) drug=1)
note: function evaluated at specified values of selected covariates and
      overall means of other covariates (if any).
```

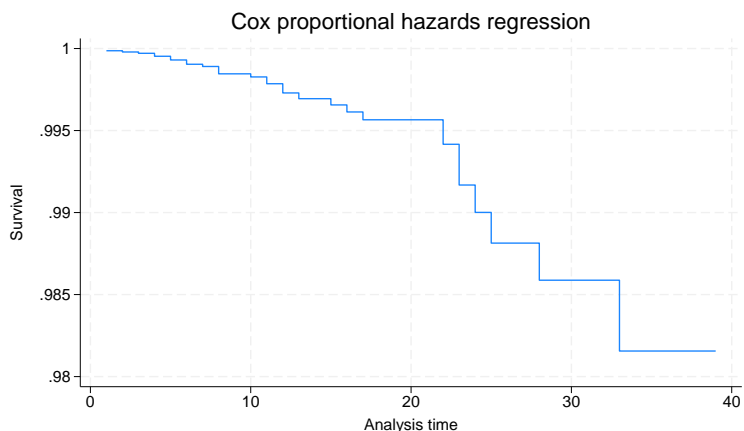


We could have obtained the same plot by specifying the `at#()` options but with more typing:

```
stcurve, survival at1(age=20 drug=1) at2(age=30 drug=1) ///
  at3(age=40 drug=1) at4(age=50 drug=1)
```


The `at()` option provides many other flexible specifications. For example, if we would like to plot the baseline survivor function, we do not need to set every covariate to zero in `at()`. We can set all covariates to zero at once as follows:

```
. stcurve, survival at((zero) _all)
note: function evaluated at specified values of selected covariates and
      overall means of other covariates (if any).
```



For details about the `at()` option, see *Syntax of at()* in [ST] *adjustfor_option*.



References

- Cefalu, M. S. 2011. Pointwise confidence intervals for the covariate-adjusted survivor function in the Cox model. *Stata Journal* 11: 64–81.
- Ruhe, C. 2016. Estimating survival functions after stcox with time-varying coefficients. *Stata Journal* 16: 867–879.

Also see

[ST] **stcox** — Cox proportional hazards model

[ST] **stcox postestimation** — Postestimation tools for **stcox**

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

[ST] **stcrreg postestimation** — Postestimation tools for **stcrreg**

[ST] **stintcox** — Cox proportional hazards model for interval-censored survival-time data

[ST] **stintcox postestimation** — Postestimation tools for **stintcox**

[ST] **stintreg** — Parametric models for interval-censored survival-time data

[ST] **stintreg postestimation** — Postestimation tools for **stintreg**

[ST] **streg** — Parametric survival models

[ST] **streg postestimation** — Postestimation tools for **streg**

[ST] **sts** — Generate, graph, list, and test the survivor and related functions

[ST] **stset** — Declare data to be survival-time data

[ST] **adjustfor_option** — Adjust survivor and related functions for covariates at specific values

[ME] **mestreg** — Multilevel mixed-effects parametric survival models

[ME] **mestreg postestimation** — Postestimation tools for **mestreg**

[XT] **xtstreg** — Random-effects parametric survival models

[XT] **xtstreg postestimation** — Postestimation tools for **xtstreg**

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