

Analysing competing risks data using flexible parametric survival models: what tools are available in Stata, which ones to use and when?

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Overview

1. Introduction to survival analysis & competing risks
2. Fundamental relationships
3. Modelling on the cause-specific hazards scale
 - Cause-specific Cox PH model
 - Flexible parametric models (log-cumulative cause-specific hazards)
4. Modelling directly on the cause-specific cumulative incidence
 - Fine & Gray model
 - Flexible parametric models (log-cumulative subdistribution hazards)
5. Which scale is most appropriate?
6. Summary

Survival analysis: the fundamentals

Key components of a survival analysis

The study of time to a particular event of interest:

- Engineering e.g. time to failure of a component
- Economics e.g. duration of unemployment
- Medical e.g. time to death (survival time) of a cancer patient

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Censoring:

- Right censoring: survival time $>$ follow-up time
 - Emigration
 - Administrative (most common)
- Non-informative censoring: Loss to follow-up is not associated with factors related to the study

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 - Emigration *informative?*
 - Administrative (most common) *non-informative*
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Censoring:

- Right censoring: survival time $>$ follow-up time
 - Emigration
 - Administrative (most common)
- Non-informative censoring: Loss to follow-up is not associated with factors related to the study
- Independent and identically distributed (i.i.d) censoring: independence between survival time and censoring time (untestable)

Some important notation

Let T be a non-negative random variable that denotes observed survival time:

(All-cause) Survival function

$$S(t) = P(T \geq t)$$

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Let T be a non-negative random variable that denotes observed survival time:

(All-cause) Survival function

$$S(t) = P(T \geq t) = 1 - F(t)$$

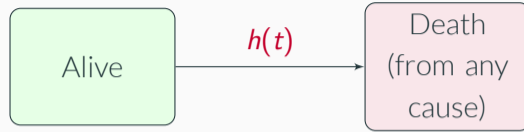
(All-cause) Cumulative incidence function (CIF)

$$F(t) = P(T < t)$$

A typical survival analysis: two-state model



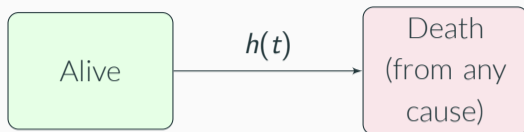
A typical survival analysis: two-state model



(All-cause) Hazard rate, $h(t)$

Instantaneous mortality (failure) rate from any cause, given that the individual is still alive up to time t

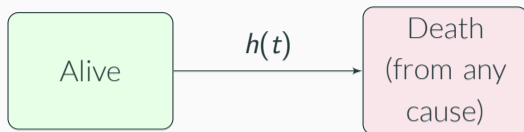
A typical survival analysis: two-state model



(All-cause) Hazard rate, $h(t)$

$$h(t) = \lim_{\Delta t \rightarrow 0} \frac{P(t \leq T < t + \Delta t \mid T \geq t)}{\Delta t}$$

A typical survival analysis: two-state model



(All-cause) Hazard rate, $h(t)$

$$h(t) = \lim_{\Delta t \rightarrow 0} \frac{P(t \leq T < t + \Delta t \mid T \geq t)}{\Delta t}$$

(All-cause) Survival function, $S(t)$

$$S(t) = \exp\left(-\int_0^t h(u)du\right)$$

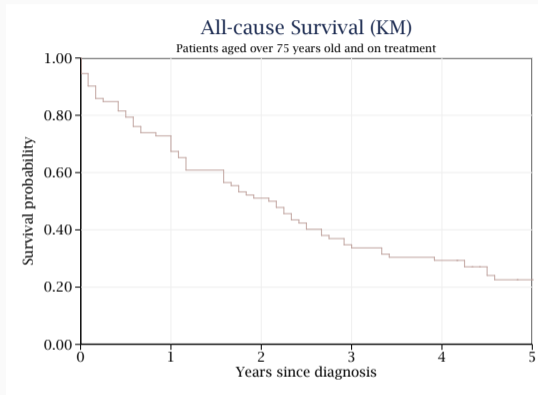
Example dataset

Load public-use prostate cancer dataset:

```
. use "http://www.stata-journal.com/software/sj4-2/st0059/prostatecancer", clear  
. tab status
```

status	Freq.	Percent	Cum.
Censor	150	29.64	29.64
Cancer	155	30.63	60.28
CVD	141	27.87	88.14
Other	60	11.86	100.00
Total	506	100.00	

The Kaplan-Meier estimator



```
. stset time, f(status==1,2,3) id(id) exit(time 60) scale(12)  
. sts graph if agegrp == 1 & treatment == 1, ...
```

What are competing risks?

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Competing risks = when a patient dies from other causes that exclude the disease under study.

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- Death from "competing" causes may be due to adverse effects of treatment for disease

Competing risks

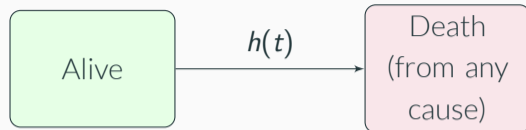
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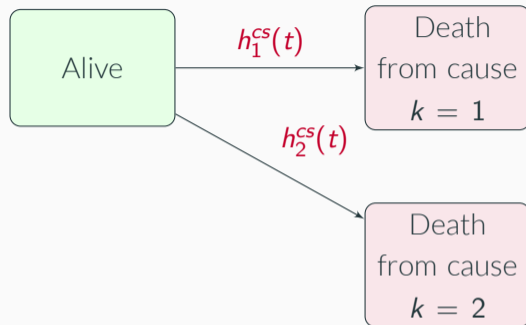
- Not valid under competing risks
- Death from "competing" causes may be due to adverse effects of treatment for disease

Due to informative censoring - specialised competing risks methods are required to avoid biased estimation.

No competing risks



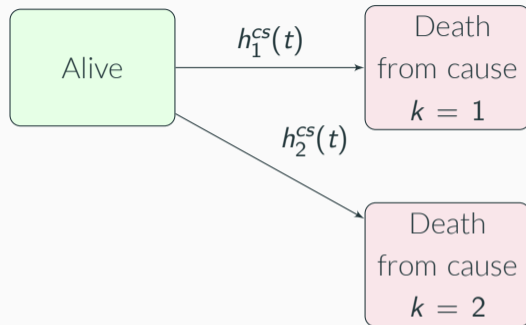
With competing risks



Cause-specific hazard (CSH) rate, $h_k^{CS}(t)$

Instantaneous mortality (failure) rate from **cause k** , given that the individual is still alive up to time t

With competing risks



Cause-specific hazard (CSH) rate, $h_k^{CS}(t)$

$$h_k^{CS}(t) = \lim_{\Delta t \rightarrow 0} \frac{P(t < T \leq t + \Delta t, D = k | T > t)}{\Delta t}$$

The cause-specific CIF (transition probability)

Estimating the cause-specific CIF is of interest:

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- Those who die from competing causes are removed from risk-set

The cause-specific CIF (transition probability)

Estimating the cause-specific CIF is of interest:

- Awkward interpretation on survival scale - what does it mean?
- The cause-specific survival function does not account for those who die from other competing causes before time t
- Those who die from competing causes are removed from risk-set
- Better interpretation on mortality scale

Cause-specific CIF, $F_k(t)$

Probability a patient will die from cause $D = k$ by time t whilst also being at risk of dying from other competing causes of death

CSH relationship with cause-specific CIF

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$$F_k(t) = \int_0^t S(u) h_k^{cs}(u) du$$

$$S(t) = \prod_{k=1}^K S_k^{cs}(t) = \exp \left(- \sum_{k=1}^K \int_0^t h_k^{cs}(u) du \right)$$

CSH relationship with cause-specific CIF

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Note

$$S_k^{cs}(t) = \exp \left(- \int_0^t h_k^{cs}(u) du \right) \neq 1 - F_k(t)$$

Obtaining Aalen-Johansen (AJ) estimates of the cause-specific CIF

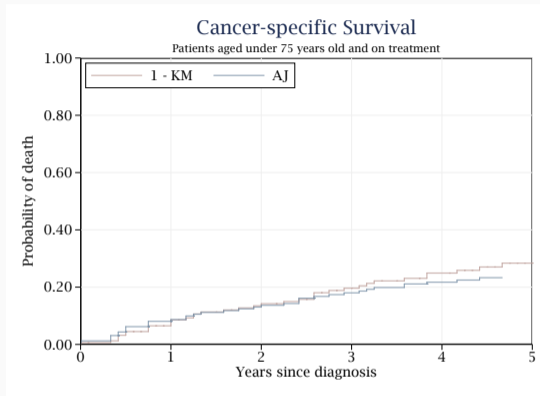
Non-parametric estimates of cause-specific CIFs obtained using `stcompet`:

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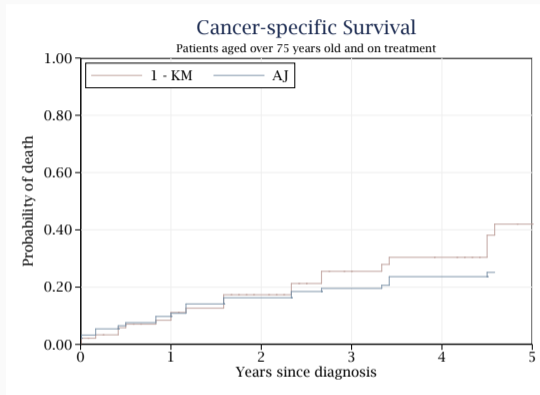
```
. stset time, f(status==1) id(id) exit(time 60) scale(12)
. stcompet CIF1 = ci if agegrp == 0 & treatment == 1, compet1(2) compet2(3)
. stcompet CIF2 = ci if agegrp == 1 & treatment == 1, compet1(2) compet2(3)
```

Comparing AJ with 1 - KM estimates of the cancer-specific CIF



```
. stset time, f(status==1) id(id) exit(time 60) scale(12)
. sts graph if agegrp == 0 & treatment == 1, failure ///
> addplot(line CIF1 _t if status == 1, sort connect(stepstair)) ...
```

Comparing AJ with 1 - KM estimates of the cancer-specific CIF



```
. stset time, f(status==1) id(id) exit(time 60) scale(12)  
. sts graph if agegrp == 1 & treatment == 1, failure ///  
> addplot(line CIF2 _t if status == 1, sort connect(stepstair)) ...
```

Approaches for modelling (all) CSHs in Stata

Standard approach: cause-specific Cox model

A common approach for modelling CSH function is by assuming proportional hazards (PH) using the Cox model.

Cause-specific Cox PH model

$$h_k^{cs}(t | \mathbf{x}_k) = h_{0k} \exp(\boldsymbol{\beta}_k^{cs} \mathbf{x}_k)$$

$\boldsymbol{\beta}_k^{cs}$: row vector of coefficients/log-CSH ratio for cause k

\mathbf{x}_k : column vector of covariates for cause k

h_{0k} : the baseline CSH function

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$\boldsymbol{\beta}_k^{CS}$: row vector of coefficients/log-CSH ratio for cause k

\mathbf{x}_k : column vector of covariates for cause k

h_{0k} : the baseline CSH function

CHR = association on the effect of a covariate on rate of dying from cause k

```
. stset time, failure(status == 1) id(id) scale(12) exit(time 60)
. stcox treatment, nolog noshow
```

Cox regression -- Breslow method for ties

```
No. of subjects =          506      Number of obs   =          506
No. of failures =          145
Time at risk    = 1457.966667
Log likelihood  = -834.85419      LR chi2(1)     =          6.14
                                      Prob > chi2    =          0.0132
```

_t	Haz. Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
treatment	.6602897	.1116672	-2.45	0.014	.4740025	.9197894

```
. predict h0_cancer, basehc
. gsort _t -_d
. by _t: replace h0_cancer = . if _n > 1
. gen h_cancer_trt0 = h0_cancer
. gen h_cancer_trt1 = h0_cancer*exp(_b[treatment])
```

```
. stset time, failure(status == 2) id(id) scale(12) exit(time 60)
```

```
. stcox treatment, nolog noshow
```

Cox regression -- Breslow method for ties

```
No. of subjects =          506          Number of obs   =          506
No. of failures =          140
Time at risk    = 1457.966667
Log likelihood  = -806.46297          LR chi2(1)        =          1.19
                                          Prob > chi2      =          0.2755
```

_t	Haz. Ratio	Std. Err.	z	P> z	[95% Conf. Interval]
treatment	1.20334	.2048509	1.09	0.277	.8619538 1.679937

```
. predict h0_cvd, basehc
```

```
. gsort _t -_d
```

```
. by _t: replace h0_cvd = . if _n > 1
```

```
. gen h_cvd_trt0 = h0_cvd
```

```
. gen h_cvd_trt1 = h0_cvd*exp(_b[treatment])
```



```
. stset time, failure(status == 3) id(id) scale(12) exit(time 60)
```

```
. stcox treatment, nolog noshow
```

Cox regression -- Breslow method for ties

```

No. of subjects =          506          Number of obs   =          506
No. of failures =           57
Time at risk    = 1457.966667
Log likelihood  = -324.95951          LR chi2(1)       =          2.67
                                          Prob > chi2     =          0.1023

```

_t	Haz. Ratio	Std. Err.	z	P> z	[95% Conf. Interval]
treatment	.6460519	.1745103	-1.62	0.106	.3804893 1.096964

```
. predict h0_other, basehc
```

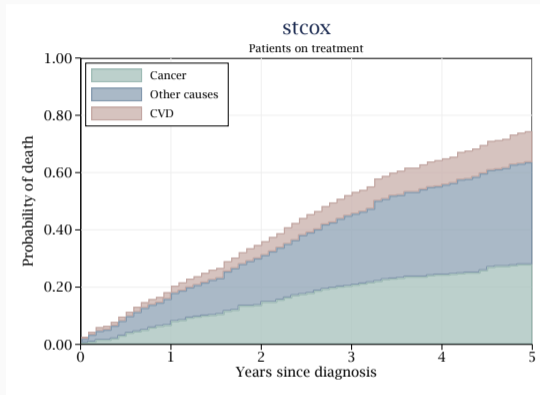
```
. gsort _t -_d
```

```
. by _t: replace h0_other = . if _n > 1
```

```
. gen h_other_trt0 = h0_other
```

```
. gen h_other_trt1 = h0_other*exp(_b[treatment])
```

```
. drop if missing(h0_cancer) & missing(h0_other) & missing(h0_cvd)
. foreach i in cancer other cvd {
  2.     replace h0_`i' = 0 if missing(h0_`i')
  3.     replace h_`i'_trt0 = 0 if missing(h_`i'_trt0)
  4.     replace h_`i'_trt1 = 0 if missing(h_`i'_trt1)
  5. }
. sort _t
. gen S_1 = exp(sum(log(1- h_cancer_trt0 - h_other_trt0 - h_other_trt0)))
. gen S_2 = exp(sum(log(1- h_cancer_trt1 - h_other_trt1 - h_other_trt1)))
. foreach i in cancer other cvd {
  2.     gen cif_trt0_`i' = sum(S_1[_n-1]*h_`i'_trt0)
  3.     gen cif_trt1_`i' = sum(S_2[_n-1]*h_`i'_trt1)
  4. }
. foreach i in trt0 trt1 {
  2.     gen totcif2_`i' = cif_`i'_cancer + cif_`i'_cvd
  3.     gen totcif3_`i' = totcif2_`i' + cif_`i'_other
  4. }
```



```
. tw (rarea totcif3_trt1 totcif2_trt1 _t, sort connect(stepstair) ...) ///  
> (rarea cif_trt1_cancer totcif2_trt1 _t, ...) ///  
> (rarea zeros cif_trt1_cancer _t, ...), ...
```

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- For a smooth function, further smoothing techniques must be applied

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 - Conditional and absolute measures
 - Cause-specific CIF in presence of competing risks
- To obtain such measures baseline hazard can be estimated non-parametrically as described by Breslow (1972)
- For a smooth function, further smoothing techniques must be applied
- Computationally intensive methods such as bootstrapping is required for SEs/CIs

Flexible parametric survival models (FPMs) [Royston and Parmar, 2002]

- Models and more accurately captures complex shapes of the (log-cumulative) baseline hazard function
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Cause-specific log-cumulative PH FPM

$$\ln(H_k^{CS}(t | \mathbf{x}_k)) = s_k(\ln t; \boldsymbol{\gamma}_k, \mathbf{m}_{0k}) + \boldsymbol{\beta}_k^{CS} \mathbf{x}_k$$

$s_k(\ln t; \boldsymbol{\gamma}_k, \mathbf{m}_{0k})$: baseline restricted cubic spline function on log-time

Flexible parametric survival models (FPMs) [Royston and Parmar, 2002]

- Models and more accurately captures complex shapes of the (log-cumulative) baseline hazard function
- A generalisation of the Weibull distribution is used with restricted cubic splines (RCS) that allows for more flexibility
- Can also easily include time-dependent effects (TDE)

Cause-specific log-cumulative non-PH FPM

$$\ln(H_k^{CS}(t | \mathbf{x}_k)) = s_k(\ln t; \gamma_k, \mathbf{m}_{0k}) + \beta_k^{CS} \mathbf{x}_k + \sum_{l=1}^E s_k(\ln t; \alpha_{lk}, \mathbf{m}_{lk}) \mathbf{x}_{lk}$$

$s_k(\ln t; \alpha_{lk}, \mathbf{m}_{lk}) \mathbf{x}_{lk}$: interaction between spline variables and covariates for TDEs

stpm2 [Lambert and Royston, 2009]

```
. stset time, failure(status == 1) id(id) scale(12) exit(time 60)
. stpm2 treatment, scale(hazard) df(4) eform nolog
Log likelihood = -440.316          Number of obs   =          506
```

	exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]	
xb						
treatment	.6594084	.111509	-2.46	0.014	.4733827	.9185368
_rcs1	3.389716	.4258797	9.72	0.000	2.649838	4.336179
_rcs2	.8879662	.0724157	-1.46	0.145	.7567963	1.041871
_rcs3	1.06315	.0411503	1.58	0.114	.9854806	1.146942
_rcs4	1.016818	.0199075	0.85	0.394	.9785387	1.056594
_cons	.229559	.0272468	-12.40	0.000	.1819129	.2896844

Note: Estimates are transformed only in the first equation.

```
. stcox treatment, nolog noSHOW
Cox regression -- Breslow method for ties
```

_t	Haz. Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
treatment	.6602897	.1116672	-2.45	0.014	.4740025	.9197894

stpm2 [Lambert and Royston, 2009]

```
. stset time, failure(status == 2) id(id) scale(12) exit(time 60)
. stpm2 treatment, scale(hazard) df(4) eform nolog
Log likelihood = -448.73758                Number of obs   =           506
```

	exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]	
xb						
treatment	1.202808	.2047249	1.08	0.278	.8616223	1.679097
_rcs1	2.82908	.2642265	11.13	0.000	2.355841	3.397384
_rcs2	.8685486	.0544436	-2.25	0.025	.7681357	.9820878
_rcs3	.9529595	.0319403	-1.44	0.151	.8923696	1.017663
_rcs4	1.027927	.0213538	1.33	0.185	.986915	1.070644
_cons	.17767	.0237024	-12.95	0.000	.1367912	.2307651

Note: Estimates are transformed only in the first equation.

```
. stcox treatment, nolog noshow
```

_t	Haz. Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
treatment	1.20334	.2048509	1.09	0.277	.8619538	1.679937

stpm2 [Lambert and Royston, 2009]

```
. stset time, failure(status == 3) id(id) scale(12) exit(time 60)
. stpm2 treatment, scale(hazard) df(4) eform nolog
Log likelihood = -231.45608                Number of obs   =           506
```

	exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]	
xb						
treatment	.6432149	.1737196	-1.63	0.102	.3788467	1.092066
_rcs1	2.638735	.3351586	7.64	0.000	2.057219	3.384628
_rcs2	.7913665	.0590788	-3.13	0.002	.683647	.9160589
_rcs3	.9369818	.0467358	-1.30	0.192	.8497164	1.033209
_rcs4	1.029843	.031817	0.95	0.341	.9693337	1.09413
_cons	.097687	.0179093	-12.69	0.000	.0681998	.1399235

Note: Estimates are transformed only in the first equation.

```
. stcox treatment, nolog noshow
```

_t	Haz. Ratio	Std. Err.	z	P> z	[95% Conf. Interval]	
treatment	.6460519	.1745103	-1.62	0.106	.3804893	1.096964

stpm2 [Lambert and Royston, 2009]

```
. stset time, failure(status == 3) id(id) scale(12) exit(time 60)
. stpm2 treatment, scale(hazard) df(4) tvc(treatment) dftvc(2) eform nolog
Log likelihood = -230.90611                Number of obs   =          506
```

	exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]	
xb						
treatment	.711078	.2158501	-1.12	0.261	.3922222	1.289147
_rcs1	2.805675	.4977957	5.81	0.000	1.981588	3.972477
_rcs2	.7487466	.0683538	-3.17	0.002	.6260772	.895451
_rcs3	.9426525	.0484762	-1.15	0.251	.8522722	1.042617
_rcs4	1.032005	.0318598	1.02	0.308	.9714123	1.096377
_rcs_treatment1	.9101003	.2468771	-0.35	0.728	.5347974	1.548778
_rcs_treatment2	1.161785	.1848084	0.94	0.346	.8505949	1.586824
_cons	.0931347	.0183948	-12.02	0.000	.0632401	.1371608

Note: Estimates are transformed only in the first equation.

Estimating cause-specific CIFs after fitting FPMs

Cause-specific CIF, $F_k(t)$

$$F_k(t) = \int_0^t \exp\left(-\sum_{k=1}^K \int_0^u h_k^{CS}(v)dv\right) h_k^{CS}(u)du$$

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Cause-specific CIF, $F_k(t)$

$$F_k(t) = \int_0^t \exp\left(-\sum_{k=1}^K \int_0^u h_k^{CS}(u) du\right) h_k^{CS}(u) du$$

Must be obtained by numerical approximation:

- Trapezoid method - `stpm2cif` [Hinchliffe and Lambert, 2013]
- Gauss-Legendre quadrature - `stpm2cr` [Mozumder et al., 2017]

stpm2cif: Data setup

```
. local knotstvc_opt
. local bknotstvc_opt
. local k = 1
. foreach cause in _cancer _cvd _other {
2.     stset time, failure(status == `k') exit(time 60) scale(12)
3.     cap stpm2 treatment, df(4) scale(h) eform nolog
4.     estimates store stpm2`cause'
5.     local bhknots`cause' `e(bhknots)´
6.     local boundknots`cause' `e(boundary_knots)´
7.     local knotstvc_opt `knotstvc_opt´ `cause´ `bhknots`cause´´
8.     local bknotstvc_opt `bknotstvc_opt´ `cause´ `boundknots`cause´´
9.     local k = `k´ + 1
10. }
```

stpm2cif: Data setup

```
. expand 3 // augment data k = 3 times
. bysort id: gen _cause=_n
. //create dummy variables for each cause of death
. gen _cvd=_cause==2
. gen _other=_cause==3
. gen _cancer=_cause==1
. //create cause of death event indicator variable
. gen _event=( _cause==status)
. label values _cause status
. foreach cause in _cancer _cvd _other {
2.     gen treatment`cause' = treatment*`cause'
3. }
```

stpm2cif: Data setup

```
. list id status time treatment _cause _event in 1/9, sep(9)
```

	id	status	time	treatm_t	_cause	_event
1.	1	Censor	72	0	1	0
2.	1	Censor	72	0	2	0
3.	1	Censor	72	0	3	0
4.	2	Cancer	1	0	1	1
5.	2	Cancer	1	0	2	0
6.	2	Cancer	1	0	3	0
7.	3	CVD	40	1	1	0
8.	3	CVD	40	1	2	1
9.	3	CVD	40	1	3	0

stpm2cif: Fitting the model

```
. stset time, failure(_event == 1) exit(time 60) scale(12)
. stpm2 treatment_cancer _cancer treatment_cvd _cvd treatment_other _other ///
> , scale(h) knotstvc(`knotstvc_opt`) bknotstvc(`bknotstvc_opt`) ///
> tvc(_cancer _cvd _other) rcsbaseoff nocons eform nolog
```

Log likelihood = -1120.5192 Number of obs = 1,518

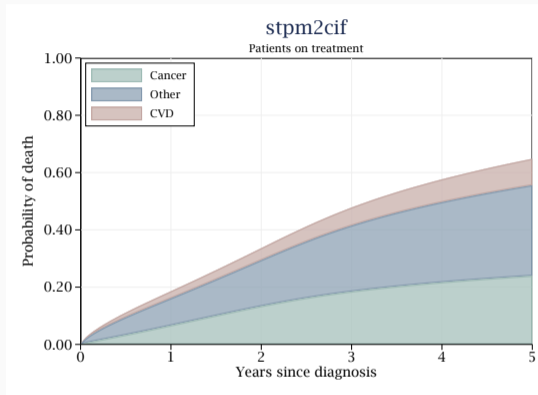
	exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]	
xb						
treatment_cancer	.6593781	.111504	-2.46	0.014	.4733607	.9184951
_cancer	.2295677	.0272475	-12.40	0.000	.1819204	.2896945
treatment_cvd	1.202808	.2047249	1.08	0.278	.8616223	1.679097
_cvd	.17767	.0237024	-12.95	0.000	.1367912	.2307651
treatment_other	.6432149	.1737196	-1.63	0.102	.3788467	1.092066
_other	.097687	.0179093	-12.69	0.000	.0681998	.1399235
<i>(output omitted)</i>						

Note: Estimates are transformed only in the first equation.

stpm2cif: Post-estimation

```
. stpm2cif cancer cvd other, cause1(treatment_cancer 1 _cancer 1) ///  
> cause2(treatment_cvd 1 _cvd 1) cause3(treatment_other 1 _other 1) ci  
  
. gen _totcif2_trt1 = CIF_cancer + CIF_cvd  
. gen _totcif3_trt1 = _totcif2_trt1 + CIF_other
```

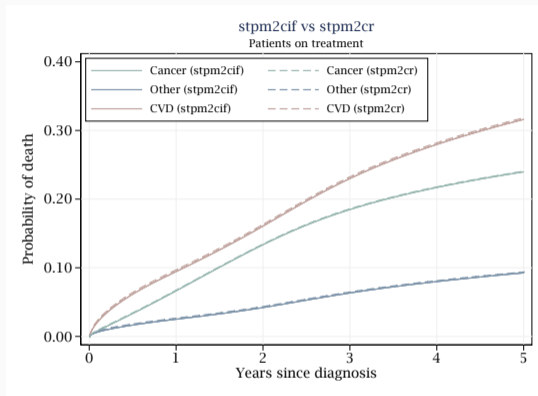
stpm2cif: Post-estimation



```
. gen zeros = 0  
. tw (rarea _totcif3_trt1 _totcif2_trt1 _newt, sort color(eros%80)) ///  
> (rarea CIF_cancer _totcif2_trt1 _newt, sort color(emidblue%80)) ///  
> (rarea zeros CIF_cancer _newt, sort color(eltgreen%80)), ...
```

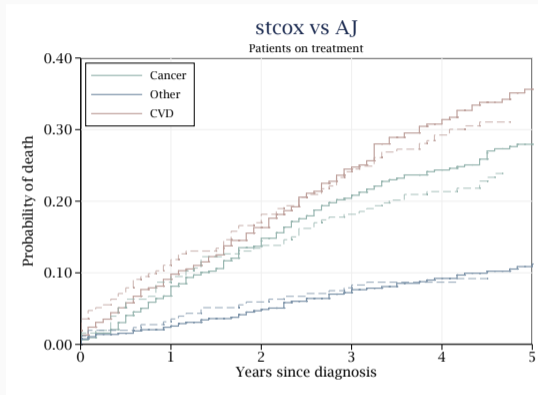
```
. stset time, failure(status == 1,2,3) exit(time 60) scale(12)
. stpm2cr [cancer: treatment, scale(hazard) df(4)] ///
> [cvd: treatment, scale(hazard) df(4)] ///
> [other: treatment, scale(hazard) df(4)], ///
> events(status) cause(1 2 3) cens(0) eform model(csh)
```


stpm2cr: Post-estimation

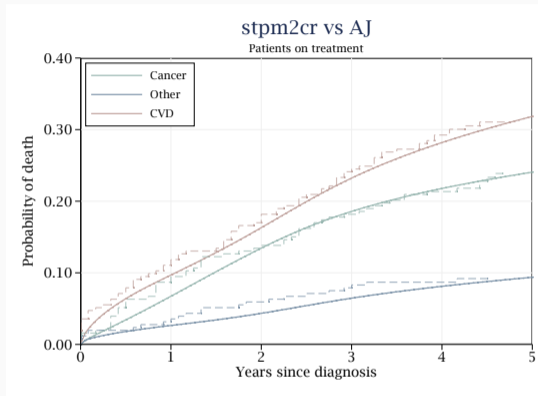


```
. range newt 0 5 100  
. predict cifg_trt1, cif at(treatment 1) timevar(newt) ci
```

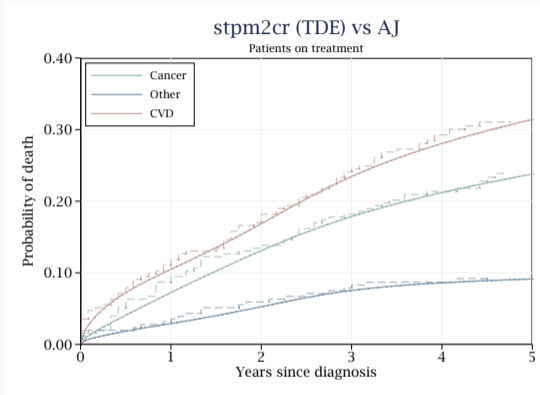
Comparison with AJ estimates



Comparison with AJ estimates



Comparison with AJ estimates



```
. stpm2cr [cancer: treatment, scale(hazard) df(4) tvc(treatment) dftvc(3)] ///  
> [cvd: treatment, scale(hazard) df(4) tvc(treatment) dftvc(3)] ///  
> [other: treatment, scale(hazard) df(4) tvc(treatment) dftvc(3)], ///  
> events(status) cause(1 2 3) cens(0) eform model(csh)
```

Note on computational time

```
. expand 500 //now 253,000 observations
. replace time = time + runiform()*0.0001
. replace id = _n
variable id was int now long
```

	Time (secs)
stpm2cr model	52.60
stpm2 (stacked data)	76.59
stpm2cr predict (w/ CIs)	2.56
stpm2cif (w/ CIs)	11.10

- Restricted mean lifetime (RML) [Royston and Parmar, 2013; Andersen, 2013]
- Absolute & relative CIF measures
- Subdistribution hazard [Beyersmann et al., 2009]
- *Standardisation (to come)*

- Restricted mean lifetime (RML) [Royston and Parmar, 2013; Andersen, 2013] - double integration
- Absolute & relative CIF measures
- Subdistribution hazard [Beyersmann et al., 2009]
- *Standardisation (to come)*- predict for and average over every individual in study population

Using the multistate package

multistate [Crowther and Lambert, 2017]

- Written mainly by Michael (& Paul) for more complex multi-state models e.g. illness-death models
- Competing risks is a special case of multi-state models
- Can use **multistate** package to obtain equivalent non-parametric estimates and fit parametric models in presence of competing risks
- Uses a simulation approach for calculating transition probabilities i.e. cause-specific CIFs

```

. tab status, gen(cause)
. rename cause2 _cancer
. rename cause3 _cvd
. rename cause4 _other
. msset, id(id) states(_cancer _cvd _other) times(time time time) cr
. li id treatment status time _from _to _trans _start _stop _status _flag in 1/9, sep(9) noobs

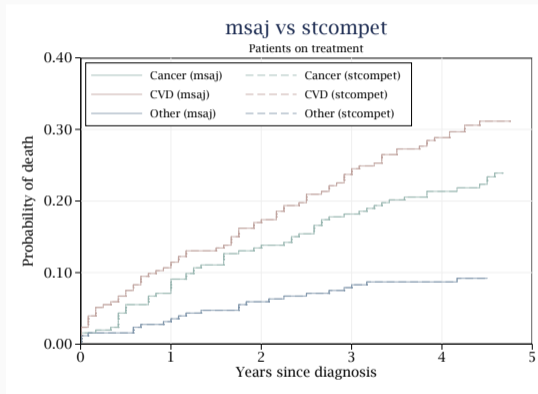
```

id	treatm_t	status	time	_from	_to	_trans	_start	_stop	_status	_flag
1	0	Censor	72.0024	1	2	1	0	72.002434	0	0
1	0	Censor	72.0024	1	3	2	0	72.002434	0	0
1	0	Censor	72.0024	1	4	3	0	72.002434	0	0
2	0	Cancer	1.00301	1	2	1	0	1.0030106	1	0
2	0	Cancer	1.00301	1	3	2	0	1.0030106	0	0
2	0	Cancer	1.00301	1	4	3	0	1.0030106	0	0
3	1	CVD	40.008	1	2	1	0	40.007992	0	0
3	1	CVD	40.008	1	3	2	0	40.007992	1	0
3	1	CVD	40.008	1	4	3	0	40.007992	0	0

```
. stset _stop, failure(_status == 1) scale(12) exit(time 60)
. msaj if treatment == 1, cr //ci
. sort _t
. li id status _trans _d _t P_AJ_1 P_AJ_2 P_AJ_3 P_AJ_4
```

id	status	_trans	_d	_t	P_AJ_1	P_AJ_2	P_AJ_3	P_AJ_4
202	Cancer	1	1	.00841895	.99604743	.00395257	0	0
105	CVD	2	1	.00854265	.99209486	.00395257	.00395257	0
151	Other	3	1	.00855531	.98814229	.00395257	.00395257	.00395257
382	CVD	2	1	.00866204	.98418972	.00395257	.00790514	.00395257
437	CVD	2	1	.00869011	.98023715	.00395257	.01185771	.00395257
120	Cancer	1	1	.00869888	.97628458	.00790514	.01185771	.00395257
502	Cancer	1	1	.00881231	.97233202	.01185771	.01185771	.00395257
464	CVD	2	1	.00886007	.96837945	.01185771	.01581028	.00395257
93	Other	3	1	.00898155	.96442688	.01185771	.01581028	.00790514
492	CVD	2	1	.00904977	.96047431	.01185771	.01976285	.00790514

```
. bysort P_AJ_2 (_t): gen first1 = _n==1
. bysort P_AJ_3 (_t): gen first2 = _n==1
. bysort P_AJ_4 (_t): gen first3 = _n==1
```



```
. stpm2 treatment if _trans==1, df(4) scale(h) eform nolog
. estimates store m1

. stpm2 treatment if _trans==2, df(4) scale(h) eform nolog
. estimates store m2

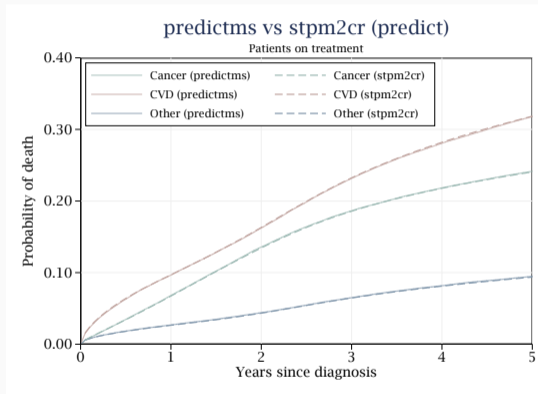
. stpm2 treatment if _trans==3, df(4) scale(h) eform nolog
. estimates store m3

. range tempt 0 5 100

. predictms , cr timevar(tempt) models(m1 m2 m3) at1(treatment 1)
```

predictms - without msset

```
. forvalues k = 1/3 {  
  2.      stset time, failure(status == `k') id(id) scale(12) exit(time 60)  
  3.      stpm2 treatment, df(4) scale(h) eform nolog  
  4.      estimates store m`k'  
  5. }  
  
. range tempt 0 5 100  
  
. predictms , cr timevar(tempt) models(m1 m2 m3) at1(treatment 1)
```



Summary of FPM tools for estimating cause-specific CIFs using CSHs

- Post-estimation command, `stpm2cif`
 - Requires augmenting data before `stpm2`
 - Fitting a single model means interpretation is difficult and more room for errors
 - Uses a basic numerical integration method - slow for larger datasets

Summary of FPM tools for estimating cause-specific CIFs using CSHs

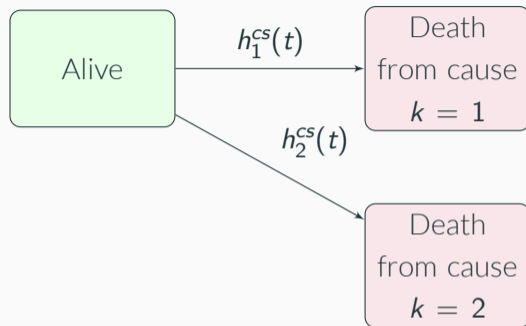
- Post-estimation command, `stpm2cif`
 - Requires augmenting data before `stpm2`
 - Fitting a single model means interpretation is difficult and more room for errors
 - Uses a basic numerical integration method - slow for larger datasets
- Using `stpm2cr` as a wrapper followed by `predict`
 - Fits separate `stpm2` models for each cause of death without data augmentation
 - Uses quicker numerical integration method
 - Can obtain other useful predictions e.g. restricted mean lifetime/comparative predictions

Summary of FPM tools for estimating cause-specific CIFs using CSHs

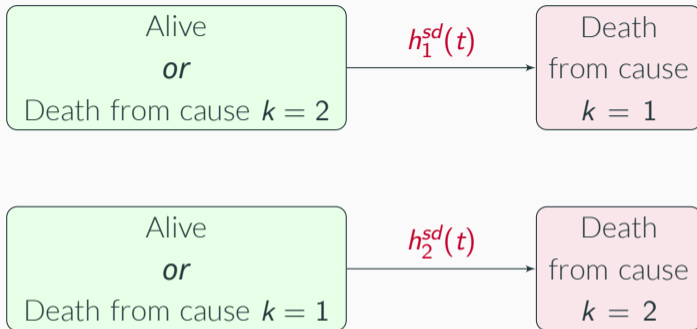
- Via the `predictms` command provided as a part of the `multistate` package
 - Uses a simulation approach. Can alternatively use AJ estimator to save on computational time
 - Can also be used without requiring `msset`
 - Extremely versatile - has some very useful features and post-estimation options

What about modelling covariate effects on the risk of dying from a particular cause?

Cause-specific hazards



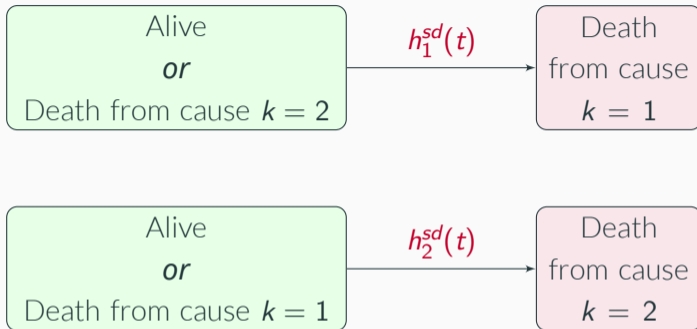
Subdistribution hazards



Subdistribution hazard (SDH) rate, $h_k^{sd}(t)$

The instantaneous rate of failure at time t from cause $D = k$ amongst those who have not died, or have died from any of the other causes, where $D \neq k$

Subdistribution hazards



Subdistribution hazard (SDH) rate, $h_k^{sd}(t)$

$$h_k^{sd}(t) = \lim_{\Delta t \rightarrow 0} \frac{P(t < T \leq t + \Delta t, D = k | T > t \cup (T \leq t \cap D \neq k))}{\Delta t}$$

Cause-specific CIF, $F_k(t)$

$$F_k(t) = 1 - \exp \left[- \int_0^t h_k^{sd}(u) du \right]$$

SDH relationship with cause-specific CIF

Cause-specific CIF, $F_k(t)$

$$F_k(t) = 1 - \exp \left[- \int_0^t h_k^{sd}(u) du \right]$$

Note

$$1 - F_k(t) = P(D \neq k) + S_k^{sd}(t)$$

Standard approach: Fine & Gray model

Derived in a similar way to cause-specific Cox PH model as described by Fine and Gray [1999].

SDH Regression Model (Fine & Gray Model)

$$h_k^{sd}(t | \mathbf{x}_k) = h_{0k} \exp(\boldsymbol{\beta}_k^{sd} \mathbf{x}_k)$$

$\boldsymbol{\beta}_k^{sd}$: row vector of coefficients/log-SDH ratio for cause k

\mathbf{x}_k : column vector of covariates for cause k

h_{0k} : the baseline SDH function

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Derived in a similar way to cause-specific Cox PH model as described by Fine and Gray [1999].

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$\boldsymbol{\beta}_k^{sd}$: row vector of coefficients/log-SDH ratio for cause k

\mathbf{x}_k : column vector of covariates for cause k

h_{0k} : the baseline SDH function

SHR = association on the effect of a covariate on risk of dying from cause k

Time-dependent censoring weights

- Need to consider those who have already died from other competing causes of death in risk-set
- Calculate missing censoring times for those that died from other causes by applying time-dependent weights to partial likelihood
- Influence of weights decreases over-time as the probability of being censored increases
- Further details given by Lambert et al. [2017] and Geskus [2011]

stcrreg

```
. *Cancer
. stset time, failure(status == 1) exit(time 60) scale(12)
. stcrreg treatment, compete(status == 2, 3)
      failure _d:  status == 1
      analysis time _t:  time/12
      exit on or before:  time 60

Iteration 0:  log pseudolikelihood = -875.12133
Iteration 1:  log pseudolikelihood = -875.1123
Iteration 2:  log pseudolikelihood = -875.1123

Competing-risks regression                No. of obs      =      506
                                           No. of subjects =      506
Failure event   : status == 1             No. failed      =      145
Competing events: status == 2 3          No. competing   =      197
                                           No. censored    =      164
                                           Wald chi2(1)    =      6.74
Log pseudolikelihood = -875.1123         Prob > chi2     =      0.0094
```

_t	Robust				
	SHR	Std. Err.	z	P> z	[95% Conf. Interval]
treatment	.6454653	.1088223	-2.60	0.009	.463836 .8982171

```
. stcurve, cif at(treatment=1) outfile(cancer1, replace) range(0 5)
```

stcrreg

```
. *CVD
. stset time, failure(status == 2) exit(time 60) scale(12)
. stcrreg treatment, compete(status == 1, 3)
      failure _d:  status == 2
      analysis time _t:  time/12
      exit on or before:  time 60

Iteration 0:  log pseudolikelihood = -848.00112
Iteration 1:  log pseudolikelihood = -847.83627
Iteration 2:  log pseudolikelihood = -847.83627

Competing-risks regression                No. of obs      =      506
                                           No. of subjects =      506
Failure event   : status == 2            No. failed      =      140
Competing events: status == 1 3         No. competing   =      202
                                           No. censored    =      164
                                           Wald chi2(1)    =       2.79
Log pseudolikelihood = -847.83627       Prob > chi2     =      0.0949
```

_t	Robust				
	SHR	Std. Err.	z	P> z	[95% Conf. Interval]
treatment	1.326649	.2245377	1.67	0.095	.9521137 1.848517

```
. stcurve, cif at(treatment=1) outfile(cvd1, replace) range(0 5)
```

stcrreg

```
. *Other causes
. stset time, failure(status == 3) exit(time 60) scale(12)
. stcrreg treatment, compete(status == 1, 2)
      failure _d:  status == 3
      analysis time _t:  time/12
      exit on or before:  time 60

Iteration 0:  log pseudolikelihood = -349.42345
Iteration 1:  log pseudolikelihood = -349.41144
Iteration 2:  log pseudolikelihood = -349.41144

Competing-risks regression                No. of obs      =      506
                                           No. of subjects =      506
Failure event   : status == 3             No. failed      =       57
Competing events: status == 1 2          No. competing   =      285
                                           No. censored    =      164
                                           Wald chi2(1)    =       2.14
                                           Prob > chi2     =      0.1432

Log pseudolikelihood = -349.41144
```

_t	Robust				
	SHR	Std. Err.	z	P> z	[95% Conf. Interval]
treatment	.6736976	.1817566	-1.46	0.143	.3970267 1.143169

```
. stcurve, cif at(treatment=1) outfile(other1, replace) range(0 5)
```

Log-cumulative SDH FPM

$$\ln \left(H_k^{sd}(t | \mathbf{x}_k) \right) = s_k(\ln t; \gamma_k, \mathbf{m}_{0k}) + \beta_k^{sd} \mathbf{x}_k$$

FPMs on (log-cumulative) SDH scale

Log-cumulative non-proportional SDH FPM

$$\ln \left(H_k^{sd}(t | \mathbf{x}_k) \right) = s_k(\ln t; \gamma_k, \mathbf{m}_{0k}) + \beta_k^{sd} \mathbf{x}_k + \sum_{l=1}^E s_k(\ln t; \alpha_{lk}, \mathbf{m}_{lk}) \mathbf{x}_{lk}$$

Log-cumulative non-proportional SDH FPM

$$\ln \left(H_k^{sd}(t \mid \mathbf{x}_k) \right) = s_k(\ln t; \boldsymbol{\gamma}_k, \mathbf{m}_{0k}) + \boldsymbol{\beta}_k^{sd} \mathbf{x}_k + \sum_{l=1}^E s_k(\ln t; \boldsymbol{\alpha}_{lk}, \mathbf{m}_{lk}) \mathbf{x}_{lk}$$

1. Apply time-dependent censoring weights to the likelihood function for each cause k (`stcrprep`) [Lambert et al., 2017]
2. Model all k causes of death simultaneously directly using the full likelihood function (`stpm2cr`) [Mozumder et al., 2017; Jeong and Fine, 2007]

```
. stset time, failure(status == 1,2,3) exit(time 60) scale(12) id(id)
. gen cod2 = cond(_d==0,0,status)
. stcrprep, events(cod2) keep(treatment ) trans(1 2 3) wtstpm2 censcov(treatment) every(1)
. gen event = cod2 == failcode
. stset tstop [iw=weight_c], failure(event) enter(tstart) noshow
  (output omitted)
```

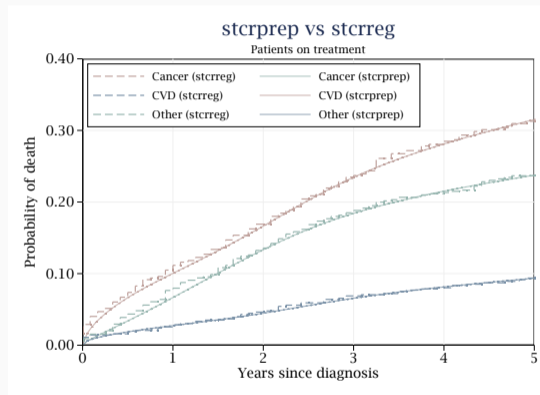
```
. stpm2 treatment_cancer _cancer treatment_cvd _cvd treatment_other _other ///
> , scale(h) knotstvc(`knotstvc_opt`) bknotstvc(`bknotstvc_opt`) ///
> tvc(_cancer _cvd _other) rcsbaseoff nocons eform nolog
note: delayed entry models are being fitted
```

Log likelihood = -1228.025 Number of obs = 3,688

	exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]	
xb						
treatment_cancer	.6408643	.1083623	-2.63	0.009	.4600852	.8926761
_cancer	.3060732	.0335208	-10.81	0.000	.2469463	.3793569
treatment_cvd	1.329932	.2263497	1.68	0.094	.9527038	1.856525
_cvd	.2029639	.0262824	-12.32	0.000	.1574686	.2616034
treatment_other	.6740861	.1819979	-1.46	0.144	.3970979	1.144282
_other	.1034306	.0183681	-12.78	0.000	.0730273	.1464916
<i>(output omitted)</i>						

Note: Estimates are transformed only in the first equation.

```
. predict cif_stcrprep_cancer, at(treatment_cancer 1 _cancer 1) zeros failure timevar(tempt)
. predict cif_stcrprep_cvd, at(treatment_cvd 1 _cvd 1) zeros failure timevar(tempt)
. predict cif_stcrprep_other, at(treatment_other 1 _other 1) zeros failure timevar(tempt)
```



```
. stset time, failure(status == 1,2,3) exit(time 60) scale(12)
. stpm2cr [cancer: treatment, scale(hazard) df(4)] ///
> [cvd: treatment, scale(hazard) df(4)] ///
> [other: treatment, scale(hazard) df(4)], ///
> events(status) cause(1 2 3) cens(0) eform
  (output omitted)

. predict cifgq_trt1, cif at(treatment 1) timevar(tempt)
Calculating predictions for the following causes: 1 2 3
```

```
. stset time, failure(status == 1,2,3) exit(time 60) scale(12)
. stpm2cr [cancer: treatment, scale(hazard) df(4)] ///
> [cvd: treatment, scale(hazard) df(4)] ///
> [other: treatment, scale(hazard) df(4)], ///
> events(status) cause(1 2 3) cens(0) eform
  (output omitted)

. predict cifgq_trt1, cif at(treatment 1) timevar(tempt)
Calculating predictions for the following causes: 1 2 3
```

Above is not comparable with time-dependent censoring weights approach as we assume proportionality for the competing causes of death.

```
. stpm2cr [cancer: treatment, scale(hazard) df(4)] ///
> [cvd: treatment, scale(hazard) df(4) tvc(treatment) dftvc(3)] ///
> [other: treatment, scale(hazard) df(4) tvc(treatment) dftvc(3)], ///
> events(status) cause(1 2 3) cens(0) eform
(output omitted)
```

Log likelihood = -1117.3418 Number of obs = 506

		exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]	
cancer							
	treatment	.647454	.1094638	-2.57	0.010	.464834	.9018201
	(output omitted)						
	_cons	.1889881	.0229604	-13.71	0.000	.1489433	.2397993
	(output omitted)						

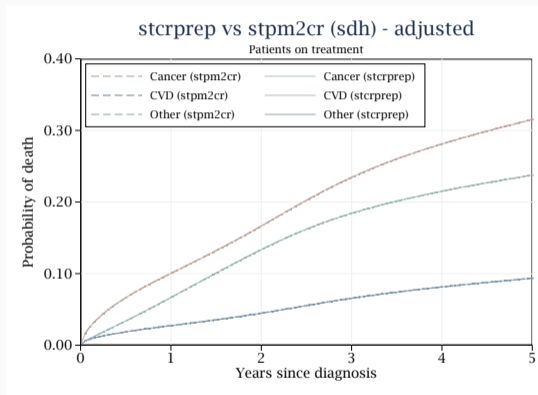
```
. stpm2cr [cancer: treatment, scale(hazard) df(4) tvc(treatment) dftvc(3)] ///
> [cvd: treatment, scale(hazard) df(4)] ///
> [other: treatment, scale(hazard) df(4) tvc(treatment) dftvc(3)], ///
> events(status) cause(1 2 3) cens(0) eform
(output omitted)
```

		exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]	
<i>(output omitted)</i>							
cvd	treatment	1.336129	.2273682	1.70	0.089	.9571939	1.865077
<i>(output omitted)</i>							
	_cons	.1366028	.0187788	-14.48	0.000	.1043385	.178844
<i>(output omitted)</i>							


```
. stpm2cr [cancer: treatment, scale(hazard) df(4) tvc(treatment) dftvc(3)] ///
> [cvd: treatment, scale(hazard) df(4) tvc(treatment) dftvc(3)] ///
> [other: treatment, scale(hazard) df(4)], ///
> events(status) cause(1 2 3) cens(0) eform
(output omitted)
```

	exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]	
<i>(output omitted)</i>						
other						
treatment	.6771057	.1827954	-1.44	0.149	.3988974	1.149349
<i>(output omitted)</i>						
_cons	.0720086	.0138407	-13.69	0.000	.0494056	.1049525

Comparing stcrprep and stpm2cr



Comparison of computational time (to all k causes)

```
. expand 100 //now 50,060 observations
. replace time = time + runiform()*0.0001
. replace id = _n
variable id was int now long
```

	Time
stcrreg (total)	53 mins
stcrprep (total)	1 min
stpm2cr	17 secs

On which scale should we model?

Cause-specific hazards

- Risk-set is defined in usual way - easy to understand

Subdistribution hazards

- Maintains direct relationship with cause-specific CIF

On which scale should we model?

Cause-specific hazards

- Risk-set is defined in usual way - easy to understand
- Infer covariate effects on the **rate** of dying from a cause
 - For research questions on aetiology and causal effects

Subdistribution hazards

- Maintains direct relationship with cause-specific CIF
- Infer covariate effects on the **risk** of dying from a cause
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On which scale should we model?

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Subdistribution hazards

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Many recommend inferences on all CSHs and cause-specific CIFs for a better understanding on the overall impact of cancer [Lambert et al., 2017; Latouche et al., 2013; Beyersmann et al., 2007]

What next?

- Standardisation post-estimation for FPMs on cause-specific log-cumulative hazard scale
- Standardisation post-estimation after `stpm2cr`
- Restricted mean survival time [Royston and Parmar, 2011] for `stpm2cr` and `stcrprep`
- Expected number of life-years lost decomposed by cause of death [Andersen, 2013]

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