

# Up-to-date survival estimates from prognostic models using temporal recalibration

Sarah Booth<sup>1</sup>   Mark J. Rutherford<sup>1</sup>   Paul C. Lambert<sup>1,2</sup>

<sup>1</sup>Biostatistics Research Group, Department of Health Sciences, University of Leicester,  
Leicester, UK

<sup>2</sup>Department of Medical Epidemiology and Biostatistics, Karolinska Institutet, Stockholm,  
Sweden

12th September 2018



UNIVERSITY OF  
**LEICESTER**

Nordic and Baltic Stata Users Group Meeting

- Prognostic models for cancer
- Flexible parametric survival models (`stpm2`)
- Period analysis (`stset`)
- Method of temporal recalibration
- Comparison of cohort, recalibrated and period analysis models
- Importance of updating prognostic models

# PREDICT: Prognostic Model for Breast Cancer



[http://www.predict.nhs.uk/predict\\_v2.1/tool](http://www.predict.nhs.uk/predict_v2.1/tool)

Age at diagnosis

Age must be between 25 and 85

Post Menopausal?

ER status

HER2 status

Ki-67 status

Positive means more than 10%

Tumour size (mm)

Tumour grade

Detected by

Positive nodes

Micrometastases

Enabled when positive nodes is zero

dos Reis, F. J. C., Wishart, G. C., Dicks, E. M. et al. (2017), 'An updated PREDICT breast cancer prognostication and treatment benefit prediction model with independent validation', Breast Cancer Research 19(1). PREDICT Version 2.1 tool available from: [http://www.predict.nhs.uk/predict\\_v2.1/](http://www.predict.nhs.uk/predict_v2.1/)

# PREDICT: Prognostic Model for Breast Cancer

Table

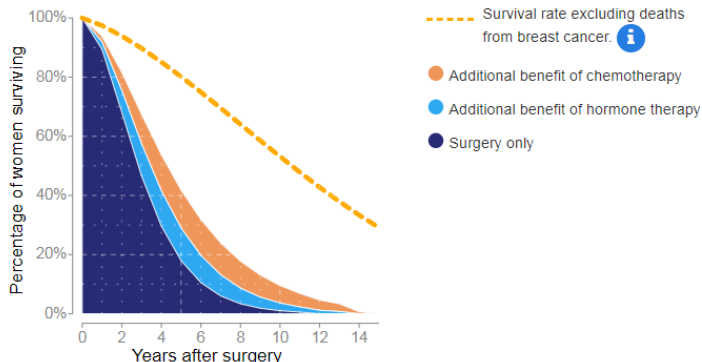
Curves

Chart

Texts

Icons

These results are for women who have already had surgery. This graph shows the percentage of women surviving up to 15 years. These results are based on the inputs and treatments you selected.



dos Reis, F. J. C., Wishart, G. C., Dicks, E. M. et al. (2017), 'An updated PREDICT breast cancer prognostication and treatment benefit prediction model with independent validation', *Breast Cancer Research* 19(1). PREDICT Version 2.1 tool available from: [http://www.predict.nhs.uk/predict\\_v2.1/](http://www.predict.nhs.uk/predict_v2.1/)

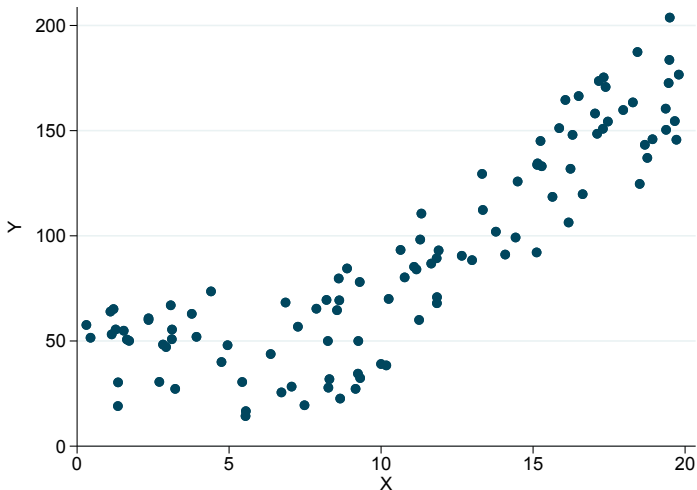
# Flexible Parametric Survival Models

- Unlike the Cox model, parametric models specify the baseline hazard
- The Weibull model requires linearity on the log cumulative hazard scale

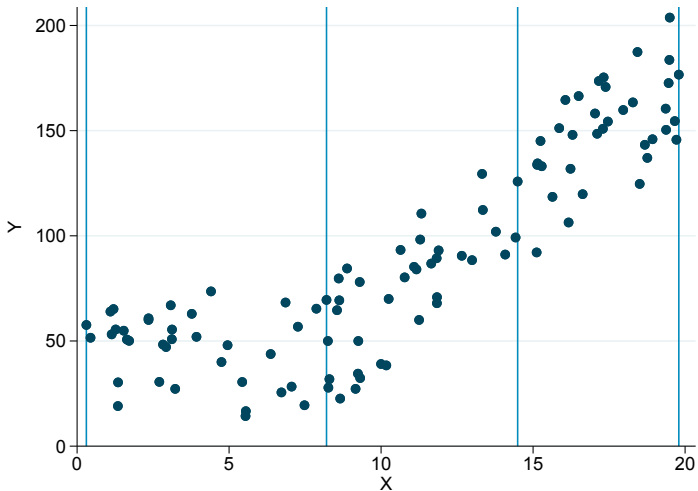
$$\ln[H(t|x_i)] = \ln(\lambda) + \gamma \ln(t) + x_i\beta$$

- Flexible parametric survival models use restricted cubic splines which allow more complex shapes to be captured

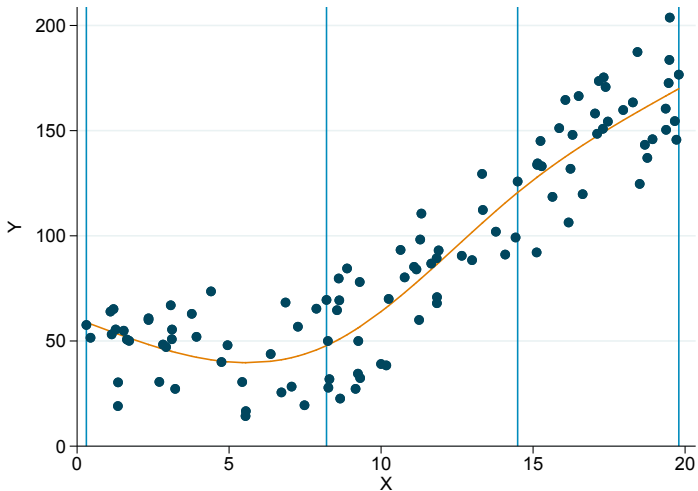
# Restricted Cubic Splines



# Restricted Cubic Splines



# Restricted Cubic Splines





$$\ln[H(t|x_i)] = \gamma_0 + \gamma_1 z_{1i} + \gamma_2 z_{2i} + \gamma_3 z_{3i} + \dots + x_i \beta$$

- $z_i$  = derived variables for the restricted cubic splines
- $x_i \beta$  = linear predictor = prognostic index
- `stpm2` command in Stata

# Cohort vs Period Analysis

Participant	Follow-Up											
	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007
A	1	2	3	4	5	6	7	8	9	10	11	
B		1	2	3	4	5						
C						1	2	3	4	5	6	7
D									1	2	3	

## Cohort Analysis

- All 4 participants would be included in cohort analysis
- Referred to as “complete analysis” by Brenner et al. (2009)

# Cohort vs Period Analysis

Participant	Follow-Up											
	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007
A	1	2	3	4	5	6	7	8	9	10	11	
B		1	2	3	4	5			-	-		
C						1	2	3	4	5	6	7
D									1	2	3	

# Cohort vs Period Analysis

Participant	Follow-Up											
	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007
A	1	2	3	4	5	6	7	8	9	10	11	
B		1	2	3	4	5			-	-		
C						1	2	3	4	5	6	7
D									1	2	3	

## Advantages of Period Analysis

- Creates more up-to-date survival estimates because people diagnosed many years ago only contribute to long-term survival estimates

# Cohort vs Period Analysis

Participant	Follow-Up											
	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007
A	1	2	3	4	5	6	7	8	9	10	11	
B		1	2	3	4	5			-	-		
C						1	2	3	4	5	6	7
D									1	2	3	

## Advantages of Period Analysis

- Creates more up-to-date survival estimates because people diagnosed many years ago only contribute to long-term survival estimates

## Disadvantages of Period Analysis

- Reduces sample size

# Temporal Recalibration

Participant	Follow-Up											
	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007
A	1	2	3	4	5	6	7	8	9	10	11	
B		1	2	3	4	5			-	-		
C						1	2	3	4	5	6	7
D									1	2	3	

## Method

- Fit a cohort model
- Use a period analysis sample to recalibrate the model
- The covariate effects are constrained to be the same
- The baseline hazard function is allowed to vary which can capture any improvements in survival

- Colon cancer data from Surveillance, Epidemiology, and End Results Program (SEER) database
- National Cancer Institute: Data collected from the United States
- Variables used in this analysis are: age at diagnosis, sex, ethnicity
- Survival times measured in months but for period analysis dates are required

- Colon cancer data from Surveillance, Epidemiology, and End Results Program (SEER) database
- National Cancer Institute: Data collected from the United States
- Variables used in this analysis are: age at diagnosis, sex, ethnicity
- Survival times measured in months but for period analysis dates are required

```
. gen dx = mdy(mmdx,1,yydx)
. format dx %td
. gen exit = dx+survmm*30.5
. format exit %td
```

- **mmdx**: month of diagnosis
- **yydx**: year of diagnosis
- **survmm**: survival time in months
- **dx**: date of diagnosis
- **exit**: date of death or censoring



# Data Used for Each Model

Type of Analysis	Dates of Diagnosis & Follow-Up					Follow-Up Only
	1996-2002	2003	2004	2005	2006	2007-2015
Cohort	█					
Recalibration			█			
Period Analysis			█			
Observed					█	

- **Cause-specific survival:** deaths due to colon cancer
- **Proportional hazards models:** for simplicity but also possible with time-dependent effects
- **Cohort:** 63,223 participants, 22,119 deaths
- **Period Analysis:** 39,743 participants, 4,889 deaths
- **Observed:** 6,300 participants, 2,474 deaths

```
. stset exit, origin(dx) fail(cancer==1) scale(365.24) ///  
> exit(time min(dx+10*365.25,mdy(12,31,2005)))  
  
      id: id  
      failure event: cancer == 1  
obs. time interval: (exit[_n-1], exit]  
exit on or before: time min(dx+10*365.25,mdy(12,31,2005))  
t for analysis: (time-origin)/365.24  
origin: time dx
```

---

```
124,579 total observations  
61,356 observations begin on or after exit
```

---

```
63,223 observations remaining, representing  
63,223 subjects  
22,119 failures in single-failure-per-subject data  
184,050.03 total analysis time at risk and under observation  
                                     at risk from t =          0  
earliest observed entry t =          0  
last observed exit t = 9.998905
```

**exit:** date of death or censoring

```
. stset exit, origin(dx) fail(cancer==1) scale(365.24) ///  
> exit(time min(dx+10*365.25,mdy(12,31,2005)))  
  
      id: id  
      failure event: cancer == 1  
obs. time interval: (exit[_n-1], exit]  
exit on or before: time min(dx+10*365.25,mdy(12,31,2005))  
  t for analysis: (time-origin)/365.24  
      origin: time dx
```

---

```
124,579 total observations  
61,356 observations begin on or after exit
```

---

```
63,223 observations remaining, representing  
63,223 subjects  
22,119 failures in single-failure-per-subject data  
184,050.03 total analysis time at risk and under observation  
                                     at risk from t =          0  
earliest observed entry t =          0  
last observed exit t = 9.998905
```

**origin:** when people become at risk, **dx** date of diagnosis

```
. stset exit, origin(dx) fail(cancer==1) scale(365.24) ///  
> exit(time min(dx+10*365.25,mdy(12,31,2005)))  
  
      id: id  
      failure event: cancer == 1  
obs. time interval: (exit[_n-1], exit]  
exit on or before: time min(dx+10*365.25,mdy(12,31,2005))  
t for analysis: (time-origin)/365.24  
origin: time dx
```

---

```
124,579 total observations  
61,356 observations begin on or after exit
```

---

```
63,223 observations remaining, representing  
63,223 subjects  
22,119 failures in single-failure-per-subject data  
184,050.03 total analysis time at risk and under observation  
                                     at risk from t = 0  
earliest observed entry t = 0  
last observed exit t = 9.998905
```

**scale(365.24):** convert to survival time in years

```
. stset exit, origin(dx) fail(cancer==1) scale(365.24) ///  
> exit(time min(dx+10*365.25,mdy(12,31,2005)))  
  
      id: id  
      failure event: cancer == 1  
obs. time interval: (exit[_n-1], exit]  
exit on or before: time min(dx+10*365.25,mdy(12,31,2005))  
t for analysis: (time-origin)/365.24  
origin: time dx
```

---

```
124,579 total observations  
61,356 observations begin on or after exit
```

---

```
63,223 observations remaining, representing  
63,223 subjects  
22,119 failures in single-failure-per-subject data  
184,050.03 total analysis time at risk and under observation  
                                     at risk from t =          0  
earliest observed entry t =          0  
last observed exit t = 9.998905
```

**fail:** event indicator, **cancer==1:** death due to colon cancer

```
. stset exit, origin(dx) fail(cancer==1) scale(365.24) ///  
> exit(time min(dx+10*365.25,mdy(12,31,2005)))  
  
      id: id  
      failure event: cancer == 1  
obs. time interval: (exit[_n-1], exit]  
exit on or before: time min(dx+10*365.25,mdy(12,31,2005))  
t for analysis: (time-origin)/365.24  
      origin: time dx
```

---

```
124,579 total observations  
61,356 observations begin on or after exit
```

---

```
63,223 observations remaining, representing  
63,223 subjects  
22,119 failures in single-failure-per-subject data  
184,050.03 total analysis time at risk and under observation  
                                     at risk from t =          0  
earliest observed entry t =          0  
last observed exit t = 9.998905
```

**exit():** follow-up until end of 2005 or for a maximum of 10 years

# Model: Cohort

```
. stpm2 agercs* female black, scale(hazard) df(5) noorthog eform  
Log likelihood = -73439.283                Number of obs   =    63,223
```

	exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]	
xb						
agercs1	1.012557	.0025474	4.96	0.000	1.007577	1.017563
agercs2	1.00005	7.46e-06	6.68	0.000	1.000035	1.000064
agercs3	.9999177	8.99e-06	-9.15	0.000	.9999001	.9999353
female	.9098671	.0125303	-6.86	0.000	.8856366	.9347606
black	1.403117	.0286116	16.61	0.000	1.348145	1.46033
_rcs1	12.69938	.6035658	53.48	0.000	11.56984	13.93919
_rcs2	1.150777	.0046616	34.67	0.000	1.141677	1.15995
_rcs3	.8279092	.0097947	-15.96	0.000	.8089329	.8473307
_rcs4	1.009746	.0174485	0.56	0.575	.9761203	1.04453
_rcs5	1.113578	.0115556	10.37	0.000	1.091159	1.136459
_cons	308.5041	53.719	32.92	0.000	219.3025	433.9887

```
. estimates store cohort  
. range timevar10 0 10 1000  
. predict cohort2006 if yydx==2006, timevar(timevar10) meansurv
```

**agercs\* female black:** covariates in the model

# Model: Cohort

```
. stpm2 agercs* female black, scale(hazard) df(5) noorthog eform  
Log likelihood = -73439.283                Number of obs   =    63,223
```

	exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]
xb					
agercs1	1.012557	.0025474	4.96	0.000	1.007577 1.017563
agercs2	1.000005	7.46e-06	6.68	0.000	1.000035 1.000064
agercs3	.9999177	8.99e-06	-9.15	0.000	.9999001 .9999353
female	.9098671	.0125303	-6.86	0.000	.8856366 .9347606
black	1.403117	.0286116	16.61	0.000	1.348145 1.46033
_rcs1	12.69938	.6035658	53.48	0.000	11.56984 13.93919
_rcs2	1.150777	.0046616	34.67	0.000	1.141677 1.15995
_rcs3	.8279092	.0097947	-15.96	0.000	.8089329 .8473307
_rcs4	1.009746	.0174485	0.56	0.575	.9761203 1.04453
_rcs5	1.113578	.0115556	10.37	0.000	1.091159 1.136459
_cons	308.5041	53.719	32.92	0.000	219.3025 433.9887

```
. estimates store cohort  
. range timevar10 0 10 1000  
. predict cohort2006 if yydx==2006, timevar(timevar10) meansurv
```

**scale(hazard):** scale used e.g. hazards, odds



# Model: Cohort

```
. stpm2 agercs* female black, scale(hazard) df(5) noorthog eform  
Log likelihood = -73439.283                Number of obs   =    63,223
```

	exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]
xb					
agercs1	1.012557	.0025474	4.96	0.000	1.007577 1.017563
agercs2	1.000005	7.46e-06	6.68	0.000	1.000035 1.000064
agercs3	.9999177	8.99e-06	-9.15	0.000	.9999001 .9999353
female	.9098671	.0125303	-6.86	0.000	.8856366 .9347606
black	1.403117	.0286116	16.61	0.000	1.348145 1.46033
_rcs1	12.69938	.6035658	53.48	0.000	11.56984 13.93919
_rcs2	1.150777	.0046616	34.67	0.000	1.141677 1.15995
_rcs3	.8279092	.0097947	-15.96	0.000	.8089329 .8473307
_rcs4	1.009746	.0174485	0.56	0.575	.9761203 1.04453
_rcs5	1.113578	.0115556	10.37	0.000	1.091159 1.136459
_cons	308.5041	53.719	32.92	0.000	219.3025 433.9887

```
. estimates store cohort  
. range timevar10 0 10 1000  
. predict cohort2006 if yydx==2006, timevar(timevar10) meansurv
```

**df(5):** degrees of freedom for modelling the baseline

# Model: Cohort

```
. stpm2 agercs* female black, scale(hazard) df(5) noorthog eform  
Log likelihood = -73439.283                Number of obs   =      63,223
```

	exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]	
xb						
agercs1	1.012557	.0025474	4.96	0.000	1.007577	1.017563
agercs2	1.000005	7.46e-06	6.68	0.000	1.000035	1.000064
agercs3	.9999177	8.99e-06	-9.15	0.000	.9999001	.9999353
female	.9098671	.0125303	-6.86	0.000	.8856366	.9347606
black	1.403117	.0286116	16.61	0.000	1.348145	1.46033
_rcs1	12.69938	.6035658	53.48	0.000	11.56984	13.93919
_rcs2	1.150777	.0046616	34.67	0.000	1.141677	1.15995
_rcs3	.8279092	.0097947	-15.96	0.000	.8089329	.8473307
_rcs4	1.009746	.0174485	0.56	0.575	.9761203	1.04453
_rcs5	1.113578	.0115556	10.37	0.000	1.091159	1.136459
_cons	308.5041	53.719	32.92	0.000	219.3025	433.9887

```
. estimates store cohort  
. range timevar10 0 10 1000  
. predict cohort2006 if yydx==2006, timevar(timevar10) meansurv
```

**noorthog:** splines are not orthogonalised (simplifies recalibration)

# Model: Cohort

```
. stpm2 ageracs* female black, scale(hazard) df(5) noorthog eform
```

```
Log likelihood = -73439.283                Number of obs   =    63,223
```

	exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]	
xb						
ageracs1	1.012557	.0025474	4.96	0.000	1.007577	1.017563
ageracs2	1.000005	7.46e-06	6.68	0.000	1.000035	1.000064
ageracs3	.9999177	8.99e-06	-9.15	0.000	.9999001	.9999353
female	.9098671	.0125303	-6.86	0.000	.8856366	.9347606
black	1.403117	.0286116	16.61	0.000	1.348145	1.46033
_rcs1	12.69938	.6035658	53.48	0.000	11.56984	13.93919
_rcs2	1.150777	.0046616	34.67	0.000	1.141677	1.15995
_rcs3	.8279092	.0097947	-15.96	0.000	.8089329	.8473307
_rcs4	1.009746	.0174485	0.56	0.575	.9761203	1.04453
_rcs5	1.113578	.0115556	10.37	0.000	1.091159	1.136459
_cons	308.5041	53.719	32.92	0.000	219.3025	433.9887

```
. estimates store cohort
```

```
. range timevar10 0 10 1000
```

```
. predict cohort2006 if yydx==2006, timevar(timevar10) meansurv
```

**eform:** display the hazard ratios instead of log hazard ratios

# Model: Cohort

```
. stpm2 agercs* female black, scale(hazard) df(5) noorthog eform  
Log likelihood = -73439.283                Number of obs   =    63,223
```

	exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]	
xb						
agercs1	1.012557	.0025474	4.96	0.000	1.007577	1.017563
agercs2	1.00005	7.46e-06	6.68	0.000	1.000035	1.000064
agercs3	.9999177	8.99e-06	-9.15	0.000	.9999001	.9999353
female	.9098671	.0125303	-6.86	0.000	.8856366	.9347606
black	1.403117	.0286116	16.61	0.000	1.348145	1.46033
_rcs1	12.69938	.6035658	53.48	0.000	11.56984	13.93919
_rcs2	1.150777	.0046616	34.67	0.000	1.141677	1.15995
_rcs3	.8279092	.0097947	-15.96	0.000	.8089329	.8473307
_rcs4	1.009746	.0174485	0.56	0.575	.9761203	1.04453
_rcs5	1.113578	.0115556	10.37	0.000	1.091159	1.136459
_cons	308.5041	53.719	32.92	0.000	219.3025	433.9887

```
. estimates store cohort  
. range timevar10 0 10 1000  
. predict cohort2006 if yydx==2006, timevar(timevar10) meansurv
```

# Model: Cohort

```
. stpm2 ageracs* female black, scale(hazard) df(5) noorthog eform  
Log likelihood = -73439.283                Number of obs   =    63,223
```

	exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]	
xb						
ageracs1	1.012557	.0025474	4.96	0.000	1.007577	1.017563
ageracs2	1.000005	7.46e-06	6.68	0.000	1.000035	1.000064
ageracs3	.9999177	8.99e-06	-9.15	0.000	.9999001	.9999353
female	.9098671	.0125303	-6.86	0.000	.8856366	.9347606
black	1.403117	.0286116	16.61	0.000	1.348145	1.46033
_rcs1	12.69938	.6035658	53.48	0.000	11.56984	13.93919
_rcs2	1.150777	.0046616	34.67	0.000	1.141677	1.15995
_rcs3	.8279092	.0097947	-15.96	0.000	.8089329	.8473307
_rcs4	1.009746	.0174485	0.56	0.575	.9761203	1.04453
_rcs5	1.113578	.0115556	10.37	0.000	1.091159	1.136459
_cons	308.5041	53.719	32.92	0.000	219.3025	433.9887

```
. estimates store cohort  
. range timevar10 0 10 1000  
. predict cohort2006 if yydx==2006, timevar(timevar10) meansurv
```

# Model: Cohort

```
. stpm2 ageracs* female black, scale(hazard) df(5) noorthog eform  
Log likelihood = -73439.283                Number of obs   =    63,223
```

	exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]	
xb						
ageracs1	1.012557	.0025474	4.96	0.000	1.007577	1.017563
ageracs2	1.000005	7.46e-06	6.68	0.000	1.000035	1.000064
ageracs3	.9999177	8.99e-06	-9.15	0.000	.9999001	.9999353
female	.9098671	.0125303	-6.86	0.000	.8856366	.9347606
black	1.403117	.0286116	16.61	0.000	1.348145	1.46033
_rcs1	12.69938	.6035658	53.48	0.000	11.56984	13.93919
_rcs2	1.150777	.0046616	34.67	0.000	1.141677	1.15995
_rcs3	.8279092	.0097947	-15.96	0.000	.8089329	.8473307
_rcs4	1.009746	.0174485	0.56	0.575	.9761203	1.04453
_rcs5	1.113578	.0115556	10.37	0.000	1.091159	1.136459
_cons	308.5041	53.719	32.92	0.000	219.3025	433.9887

```
. estimates store cohort  
. range timevar10 0 10 1000  
. predict cohort2006 if ydx==2006, timevar(timevar10) meansurv
```

# stset: Temporal Recalibration & Period Analysis

```
. stset exit, origin(dx) fail(cancer==1) scale(365.24) ///
> entry(time mdy(1,1,2004)) exit(time min(dx+10*365.25,mdy(12,31,2005)))

      id: id
      failure event: cancer == 1
obs. time interval: (exit[_n-1], exit]
enter on or after: time mdy(1,1,2004)
exit on or before: time min(dx+10*365.25,mdy(12,31,2005))
t for analysis: (time-origin)/365.24
origin: time dx
```

---

```
124,579 total observations
23,480 observations end on or before enter()
61,356 observations begin on or after exit
```

---

```
39,743 observations remaining, representing
39,743 subjects
4,889 failures in single-failure-per-subject data
59,904.493 total analysis time at risk and under observation
                                at risk from t = 0
                                earliest observed entry t = 0
                                last observed exit t = 9.998905
```

# Constraints: Temporal Recalibration

```
. estimates restore cohort
(results cohort are active now)
. local ageracs1 = _b[ageracs1]
. local ageracs2 = _b[ageracs2]
. local ageracs3 = _b[ageracs3]
. local female = _b[female]
. local black = _b[black]
. constraint 1 _b[ageracs1] = `ageracs1`
. constraint 2 _b[ageracs2] = `ageracs2`
. constraint 3 _b[ageracs3] = `ageracs3`
. constraint 4 _b[female] = `female`
. constraint 5 _b[black] = `black`
. local knots = e(bhknots)
. local bknots = e(boundary_knots)
```



# Constraints: Temporal Recalibration

```
. estimates restore cohort
(results cohort are active now)
. local ageracs1 = _b[ageracs1]
. local ageracs2 = _b[ageracs2]
. local ageracs3 = _b[ageracs3]
. local female = _b[female]
. local black = _b[black]
. constraint 1 _b[ageracs1] = `ageracs1`
. constraint 2 _b[ageracs2] = `ageracs2`
. constraint 3 _b[ageracs3] = `ageracs3`
. constraint 4 _b[female] = `female`
. constraint 5 _b[black] = `black`
. local knots = e(bhknots)
. local bknots = e(boundary_knots)
```

# Constraints: Temporal Recalibration

```
. estimates restore cohort
(results cohort are active now)
. local agercs1 = _b[agercs1]
. local agercs2 = _b[agercs2]
. local agercs3 = _b[agercs3]
. local female = _b[female]
. local black = _b[black]
. constraint 1 _b[agercs1] = `agercs1`
. constraint 2 _b[agercs2] = `agercs2`
. constraint 3 _b[agercs3] = `agercs3`
. constraint 4 _b[female] = `female`
. constraint 5 _b[black] = `black`
. local knots = e(bhknots)
. local bknots = e(boundary_knots)
```







# Model: Period Analysis

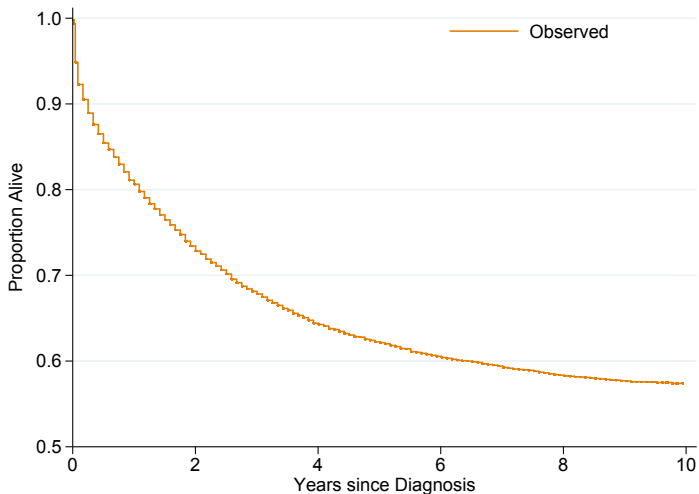
```
. stpm2 agercs* female black, scale(hazard) df(5) eform  
note: delayed entry models are being fitted
```

```
Log likelihood = -16080.35                Number of obs   =    39,743
```

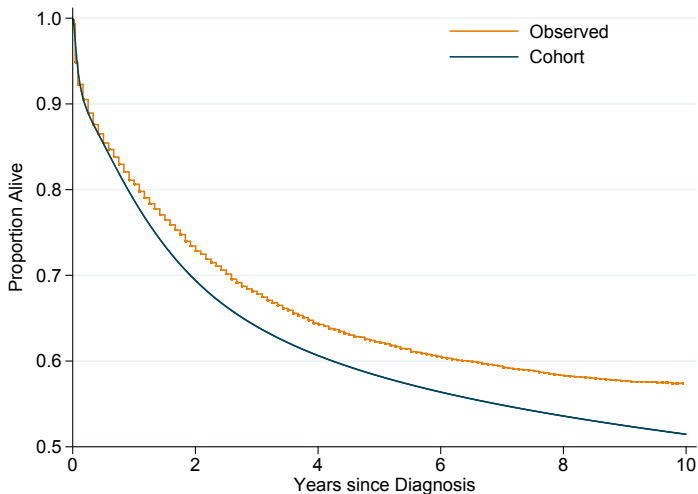
	exp(b)	Std. Err.	z	P> z	[95% Conf. Interval]
xb					
agercs1	1.004674	.0051795	0.90	0.366	.9945736 1.014877
agercs2	1.000028	.0000157	1.80	0.072	.9999974 1.000059
agercs3	.9999383	.000019	-3.24	0.001	.999901 .9999756
female	.9084784	.0266046	-3.28	0.001	.8578025 .962148
black	1.441617	.0606779	8.69	0.000	1.327464 1.565587
_rcs1	2.014562	.0187427	75.28	0.000	1.97816 2.051634
_rcs2	1.124344	.0079382	16.60	0.000	1.108892 1.14001
_rcs3	.9535394	.0044961	-10.09	0.000	.9447678 .9623925
_rcs4	1.069052	.003847	18.56	0.000	1.061538 1.076618
_rcs5	1.008206	.0025619	3.22	0.001	1.003198 1.01324
_cons	.3234849	.0094079	-38.81	0.000	.3055615 .3424596

```
. predict period2006 if yydx==2006, timevar(timevar10) meansurv
```

# 10 Year Marginal Survival

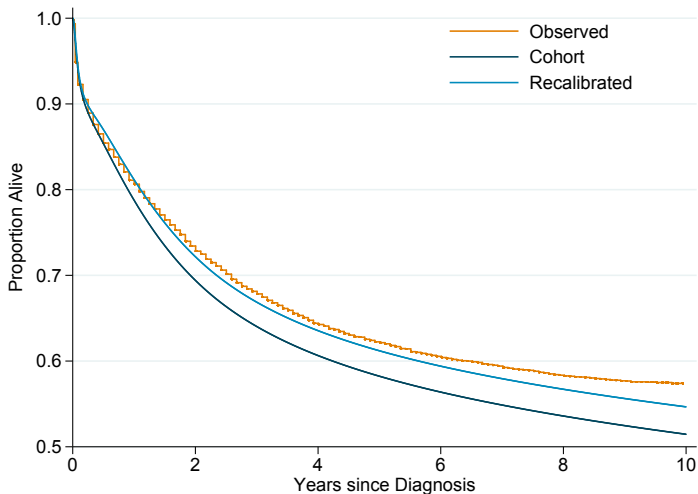


# 10 Year Marginal Survival

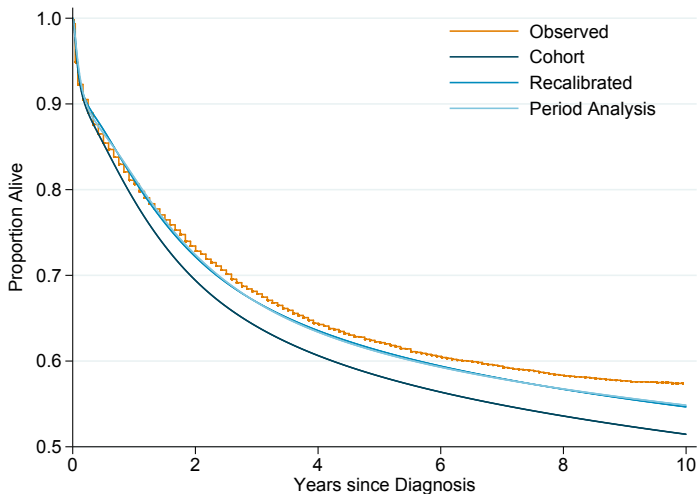




# 10 Year Marginal Survival

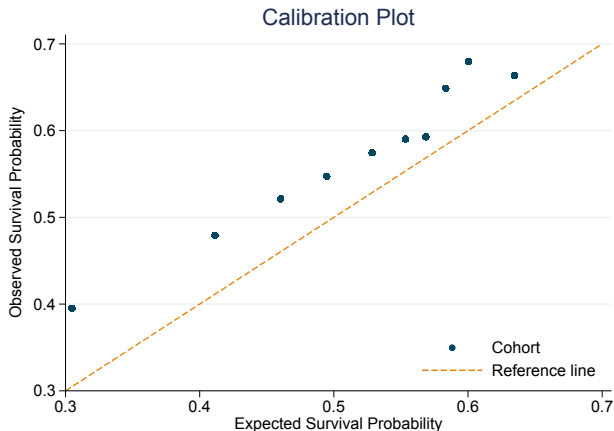


# 10 Year Marginal Survival



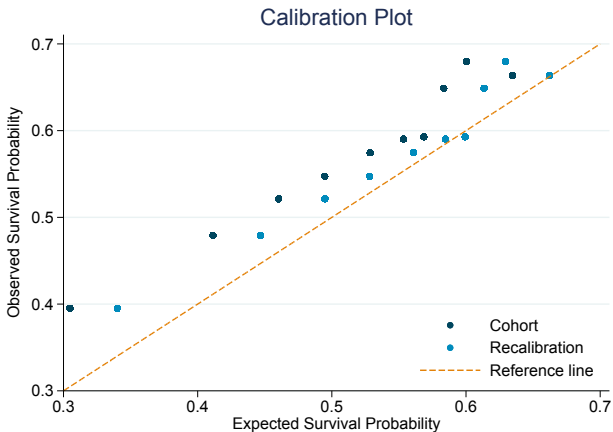
# Calibration of Models

- . predict prognosticindex, xbnobaseline
- . xtile calibrationgroup = prognosticindex, n(10)



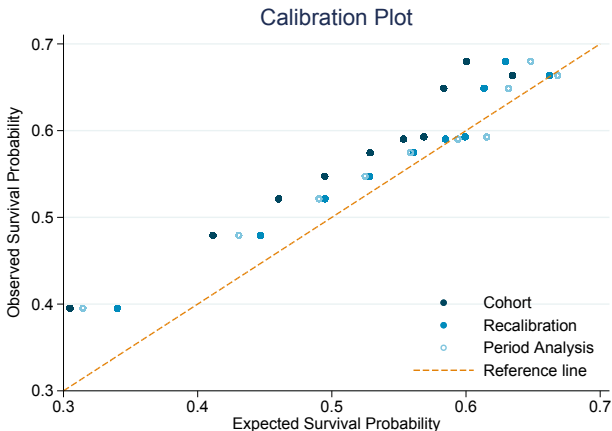
# Calibration of Models

- . predict prognosticindex, xbnobaseline
- . xtile calibrationgroup = prognosticindex, n(10)

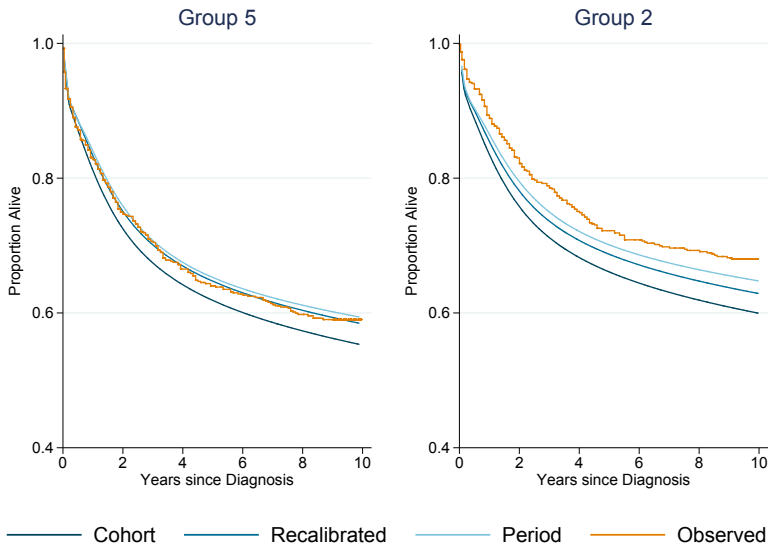


# Calibration of Models

- . predict prognosticindex, xbnobaseline
- . xtile calibrationgroup = prognosticindex, n(10)



# Risk Groups



# Use of New Data

Most Recent Data	Type of Analysis	Dates of Diagnosis & Follow-Up									
		1986	1987	1988-1993	1994	1995	1996	1997	1998-2003	2004	2005
1995	Cohort	█									
	Recalibration					█					
1996	Cohort	█									
	Recalibration					█	█				
1997	Cohort	█									
	Recalibration						█	█			
2005	Cohort	█									
	Recalibration									█	

- Keep the original model from 1986-1995
- Recalibrate using a period window for the 2 most recent years
- ⋮
- Continue until recalibrating with a period window of 2004-2005

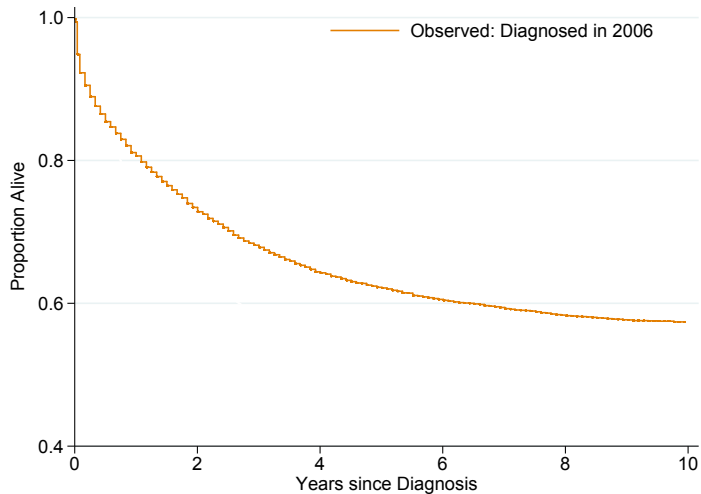
# Use of New Data

Most Recent Data	Type of Analysis	Dates of Diagnosis & Follow-Up									
		1986	1987	1988-1993	1994	1995	1996	1997	1998-2003	2004	2005
1995	Cohort	█									
	Recalibration				█	█					
1996	Cohort		█				█				
	Recalibration				█	█					
1997	Cohort		█			█	█				
	Recalibration					█	█				
2005	Cohort					█	█	█	█	█	█
	Recalibration									█	█

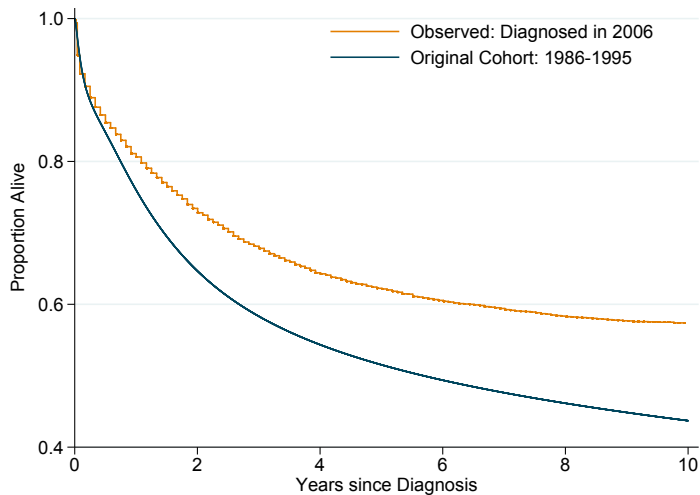
- Refit the model each year using the most recent 10 years of data
- Recalibrate using a period window for the 2 most recent years
- ⋮
- Continue until recalibrating with a period window of 2004-2005



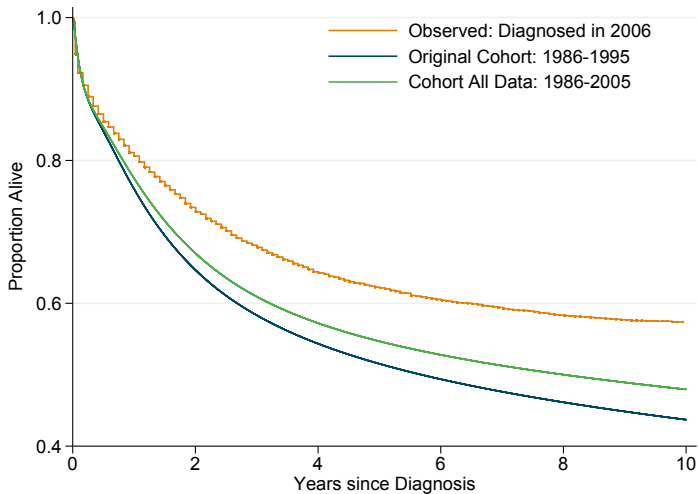
# 10 Year Marginal Survival Predictions



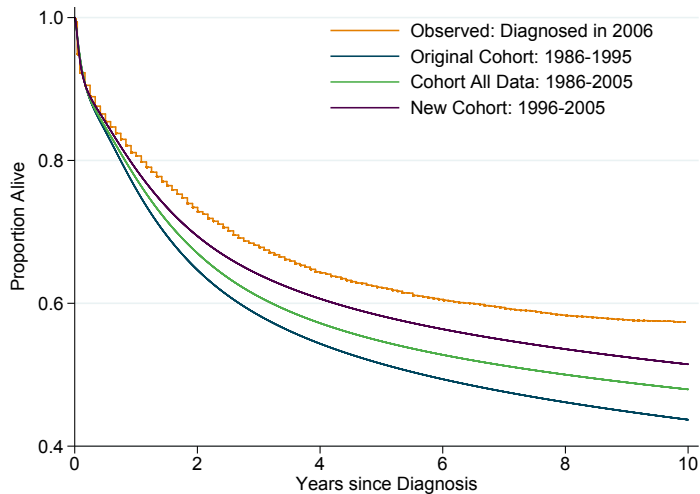
# 10 Year Marginal Survival Predictions



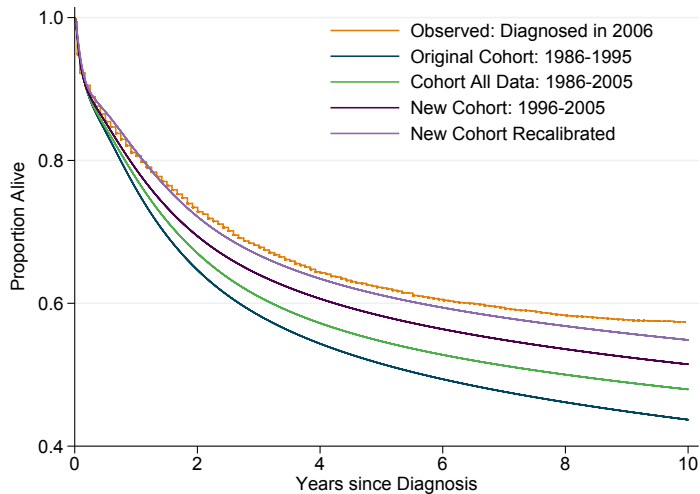
# 10 Year Marginal Survival Predictions



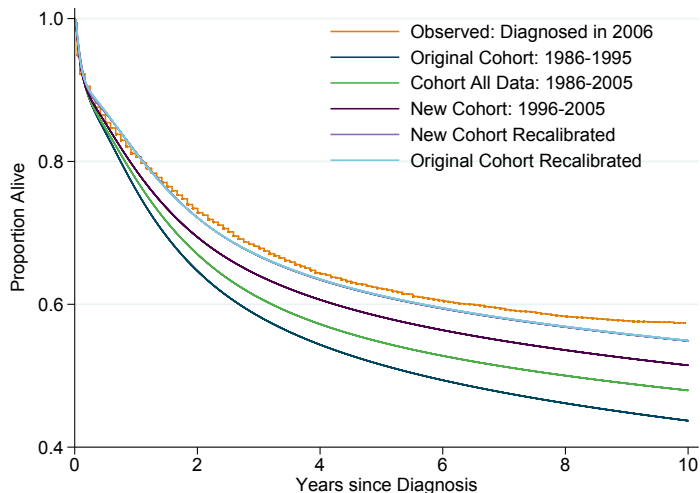
# 10 Year Marginal Survival Predictions



# 10 Year Marginal Survival Predictions



# 10 Year Marginal Survival Predictions



- Cohort models often underestimate survival
- Period analysis uses a subset of data to create more up-to-date survival predictions
- Very similar predictions are produced using temporal recalibration but all the data is used
- Simple to fit these types of models in Stata using `stset` to define the sample, `stpm2` and `constraints` to fit the models
- Importance of regularly updating models when new data becomes available
- These methods can also be used for non-proportional hazard models

# Selected References



dos Reis, F. J. C., Wishart, G. C., Dicks, E. M. et al. (2017)

An updated PREDICT breast cancer prognostication and treatment benefit prediction model with independent validation, *Breast Cancer Research*, 19. PREDICT Version 2.1 tool available from: [http://www.predict.nhs.uk/predict\\_v2.1/](http://www.predict.nhs.uk/predict_v2.1/)



Surveillance, Epidemiology, and End Results (SEER) Program ([www.seer.cancer.gov](http://www.seer.cancer.gov)) Research Data (1973-2015), National Cancer Institute, DCCPS, Surveillance Research Program, released April 2018, based on the November 2017 submission.



Royston, P. & Lambert, P. C. (2011)

Flexible Parametric Survival Analysis Using Stata: Beyond the Cox Model, *Stata Press*.



Hinchliffe, S. R. & Lambert, P. C. (2013)

Flexible parametric modelling of cause-specific hazards to estimate cumulative incidence functions, *BMC Medical Research Methodology*, Springer Nature, 13.



Brenner, H. & Gefeller, O (1996)

An alternative approach to monitoring cancer patient survival, *Cancer*, 78, 2004-2010.



Brenner, H. & Hakulinen, T. (2009)

Up-to-date cancer survival: Period analysis and beyond, *International Journal of Cancer*, 124, 1384-1390.