

Introduction to `rstpm2`

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1 Cure models

For cure, we use the melanoma dataset used by Andersson and colleagues for cure models with Stata's `stpm2` (see <http://www.pauldickman.com/survival/>).

Initially, we merge the patient data with the all cause mortality rates.

```
> require(rstpm2)
> data(popmort)
> data(colon)
> popmort2 <- transform(popmort, exitage=age, exityear=year, age=NULL, year=NULL)
> colon2 <- within(colon, {
+   status <- ifelse(surv_mm>120.5, 1, status)
+   tm <- pmin(surv_mm, 120.5)/12
+   exit <- dx+tm*365.25
+   sex <- as.numeric(sex)
+   exitage <- pmin(floor(age+tm), 99)
+   exityear <- floor(yydx+tm)
+   ##year8594 <- (year8594=="Diagnosed 85-94")
+ })
> colon2 <- merge(colon2, popmort2)
```

For comparisons, we fit the relative survival model without and with cure.

```
> fit0 <- stpm2(Surv(tm, status %in% 2:3)~I(year8594=="Diagnosed 85-94"),
+               data=colon2,
+               bhazard=colon2$rate, df=5)

> summary(fit <- stpm2(Surv(tm, status %in% 2:3)~I(year8594=="Diagnosed 85-94"),
+                      data=colon2,
+                      bhazard=colon2$rate,
+                      df=5, cure=TRUE))
```

Maximum likelihood estimation

Call:

```
mle2(minuslogl = negll, start = coef, eval.only = TRUE, vecpar = TRUE,
     gr = function (beta)
     {
       eta <- as.vector(X %*% beta)
       etaD <- as.vector(XD %*% beta)
```

```

h <- etaD * exp(eta) + bhazard
g <- colSums(exp(eta) * wt * (-X + ifelse(event, 1/h,
0) * (XD + X * etaD)))
if (delayed) {
eta0 <- as.vector(X0 %*% beta)
g <- g + colSums(exp(eta0) * wt0 * X0)
}
return(-g)
}, control = list(parscale = c(0.1, 0.1, 0.1, 0.1, 0.1, 0.1,
0.1), maxit = 300), lower = -Inf, upper = Inf)

```

Coefficients:

	Estimate	Std. Error	z value	Pr(z)
(Intercept)	-3.977323	0.054778	-72.6087	< 2.2e-16
I(year8594 == "Diagnosed 85-94")TRUE	-0.155612	0.025088	-6.2027	5.552e-10
nsx(log(tm), df = 5, cure = TRUE)1	3.323191	0.053165	62.5071	< 2.2e-16
nsx(log(tm), df = 5, cure = TRUE)2	3.628630	0.053159	68.2599	< 2.2e-16
nsx(log(tm), df = 5, cure = TRUE)3	1.634847	0.022465	72.7746	< 2.2e-16
nsx(log(tm), df = 5, cure = TRUE)4	6.592021	0.111503	59.1198	< 2.2e-16
nsx(log(tm), df = 5, cure = TRUE)5	3.371809	0.042788	78.8032	< 2.2e-16

```

(Intercept) ***
I(year8594 == "Diagnosed 85-94")TRUE ***
nsx(log(tm), df = 5, cure = TRUE)1 ***
nsx(log(tm), df = 5, cure = TRUE)2 ***
nsx(log(tm), df = 5, cure = TRUE)3 ***
nsx(log(tm), df = 5, cure = TRUE)4 ***
nsx(log(tm), df = 5, cure = TRUE)5 ***
---

```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

-2 log L: 42190.77

```
> predict(fit, head(colon2), se.fit=TRUE)
```

	Estimate	lower	upper
1	0.8610828	0.8542898	0.8675842
2	0.7934651	0.7850103	0.8016309
3	0.6967400	0.6863191	0.7068926
4	0.8610828	0.8542898	0.8675842
5	0.8221243	0.8143226	0.8296334
6	0.8610828	0.8542898	0.8675842

The estimate for the year parameter from the model without cure is within three significant figures with that in Stata. For the predictions, the Stata model gives:

```

+-----+
|      surv      surv_lci      surv_uci |
+-----+
1. | .86108264      .8542898      .8675839 |
2. | .79346526      .7850106      .8016309 |

```

3.		.69674037	.6863196	.7068927	
4.		.86108264	.8542898	.8675839	
5.		.82212425	.8143227	.8296332	

6.		.86108264	.8542898	.8675839	
	+	-----			+

We can estimate the proportion of failures at the end of follow-up using:

```
> newdata.eof <- data.frame(year8594 = unique(colon2$year8594),
+                             tm=max(colon2$tm))
> 1-predict(fit0, newdata.eof, type="surv", se.fit=TRUE)
```

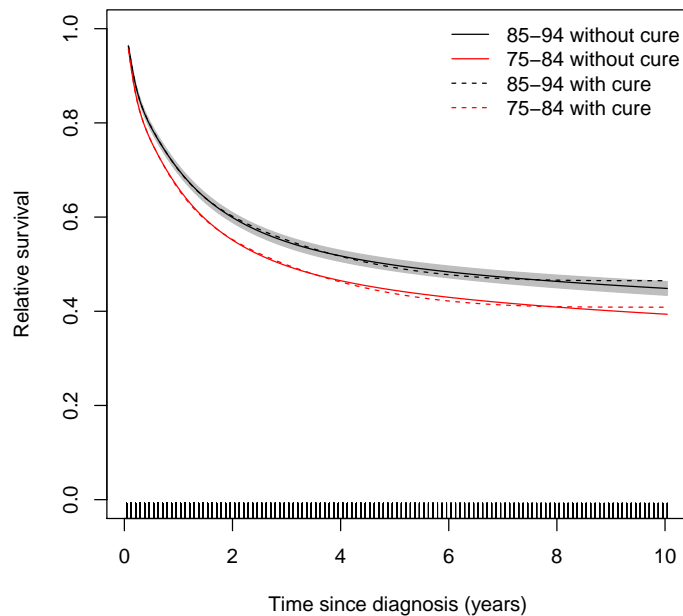
	Estimate	lower	upper
1	0.6063703	0.6211752	0.5916057
2	0.5515140	0.5661328	0.5370119

```
> 1-predict(fit, newdata.eof, type="surv", se.fit=TRUE)
```

	Estimate	lower	upper
1	0.5913317	0.6055025	0.5772183
2	0.5350825	0.5485384	0.5217445

We can plot the predicted survival estimates:

```
> plot(fit0,newdata=data.frame(year8594 = "Diagnosed 85-94"), ylim=0:1,
+       xlab="Time since diagnosis (years)", ylab="Relative survival")
> plot(fit0,newdata=data.frame(year8594 = "Diagnosed 75-84"),
+       add=TRUE,line.col="red",rug=FALSE)
> plot(fit,newdata=data.frame(year8594 = "Diagnosed 85-94"),
+       add=TRUE,ci=FALSE,lty=2,rug=FALSE)
> plot(fit,newdata=data.frame(year8594="Diagnosed 75-84"),
+       add=TRUE,rug=FALSE,line.col="red",ci=FALSE,lty=2)
> legend("topright",c("85-94 without cure","75-84 without cure",
+                     "85-94 with cure","75-84 with cure"),
+       col=c(1,2,1,2), lty=c(1,1,2,2), bty="n")
```



And the hazard curves:

```
> plot(fit0,newdata=data.frame(year8594 = "Diagnosed 85-94"),
+       ylim=c(0,0.5), type="hazard",
+       xlab="Time since diagnosis (years)",ylab="Excess hazard")
> plot(fit0,newdata=data.frame(year8594 = "Diagnosed 75-84"),
+       type="hazard",
+       add=TRUE,line.col="red",rug=FALSE)
> plot(fit,newdata=data.frame(year8594 = "Diagnosed 85-94"),
+       type="hazard",
+       add=TRUE,ci=FALSE,lty=2,rug=FALSE)
> plot(fit,newdata=data.frame(year8594="Diagnosed 75-84"),
+       type="hazard",
+       add=TRUE,rug=FALSE,line.col="red",ci=FALSE,lty=2)
> legend("topright",c("85-94 without cure","75-84 without cure",
+                     "85-94 with cure","75-84 with cure"),
+       col=c(1,2,1,2), lty=c(1,1,2,2), bty="n")
```

