

Flexible joint modelling of longitudinal and survival data: The `stjm` command

17th Stata UK Users' Group Meeting

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Outline

- ▶ Introduction to joint modelling
- ▶ A new joint model
- ▶ `stjm`
- ▶ Example application - Primary Biliary Cirrhosis (PBC)
- ▶ Future work

Background

- ▶ Longitudinal response data affected by informative dropout
- ▶ Inclusion of time-varying covariates in survival analyses

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Approaches:

- ▶ Latent class approach (Proust-Lima and Taylor, 2009)
- ▶ Shared parameter models - dependence through shared random effects (Wulfsohn and Tsiatis, 1997)

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- ▶ Longitudinal response data affected by informative dropout
- ▶ Inclusion of time-varying covariates in survival analyses

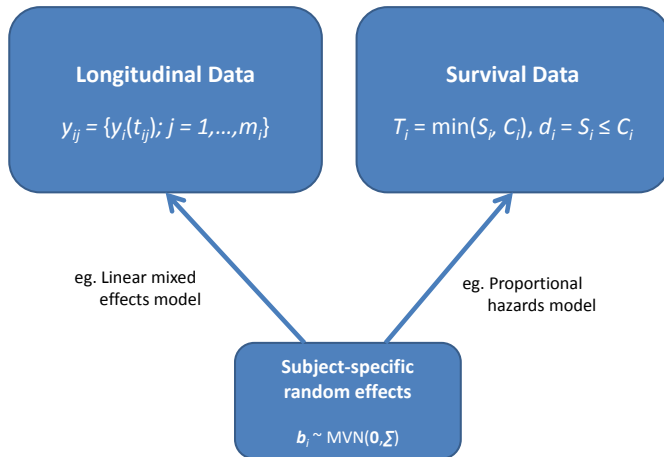
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Example dataset

- ▶ Primary Biliary Cirrhosis (PBC) dataset - 312 patients with 1945 repeated measurements of serum bilirubin (Murtagh et al., 1994).
- ▶ 158 randomised to receive D-penicillamine and 154 to placebo
- ▶ Interested in the treatment effect after adjusting for the longitudinal biomarker

Data structure

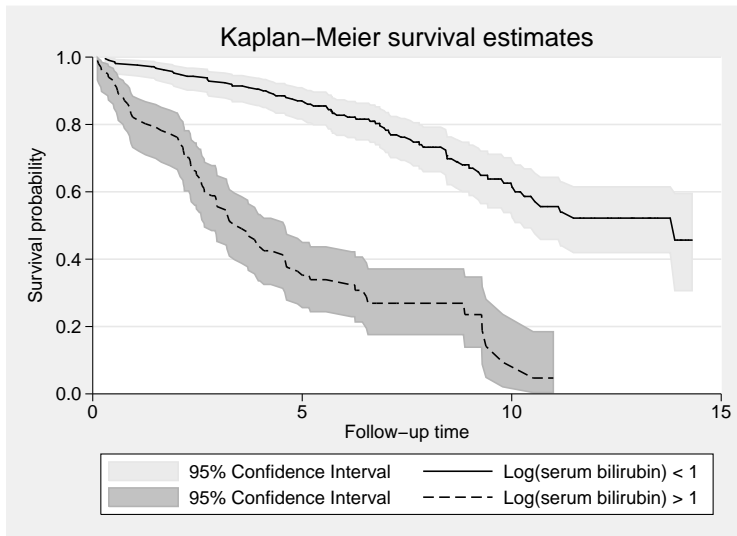


Data structure

```
. list id logb drug _t0 _t _d if id==3 | id==20, noobs sepby(id)
```

id	logb	drug	_t0	_t	_d
3	.3364722	D-penicil	0	.48187494	0
3	.0953102	D-penicil	.48187494	.99660498	0
3	.4054651	D-penicil	.99660498	2.0342789	0
3	.5877866	D-penicil	2.0342789	2.7707808	1
20	1.629241	placebo	0	.49556455	0
20	2.727853	placebo	.49556455	.91446722	0
20	2.406945	placebo	.91446722	3.6797721	0
20	3.465736	placebo	3.6797721	3.7126274	1

Data structure



```
. stjmgraph logb, panel(id)
```

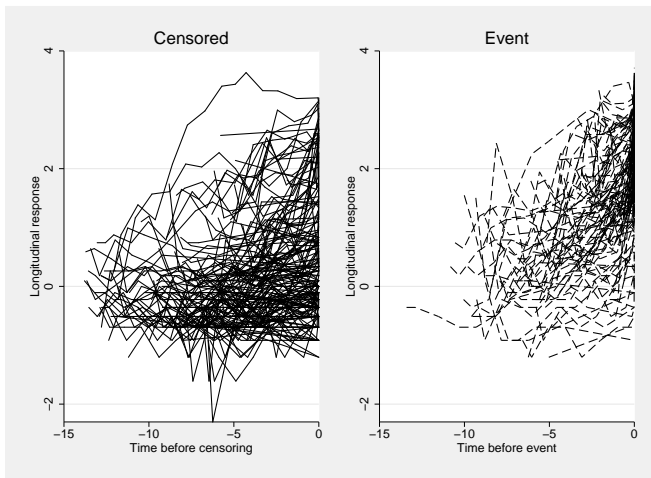


Figure: Longitudinal trajectories. Adjusted timescale.

Longitudinal submodel

- ▶ Linear mixed effects model (Laird and Ware, 1982):

$$y_i(t_{ij}) = W_i(t_{ij}) + e_{ij}, \quad e_{ij} \sim N(0, \sigma_e^2)$$

$$W_i(t_{ij}) = x_i'(t_{ij})\beta + z_i'(t_{ij})b_i + u_i\delta$$

```
. xtmixed logb time drug || id: time, cov(unstr)
```

- ▶ Increase flexibility through the use of fixed/random fractional polynomials of time (Royston and Altman, 1994).

Survival submodel

- ▶ Many choices proposed including standard parametric and, of course, Cox proportional hazards models

$$h_i(T_i) = h_0(T_i)\exp(\alpha W_i(T_i) + \phi v_i)$$

where v_i is a set of baseline covariates and, for example;

$$W_i(T_i) = \beta_{0i} + \beta_{1i}T_i + \delta u_i$$

- ▶ α is termed the association parameter; in this case we assume the association is based on the “current value” of the biomarker

We can now write down the full joint likelihood:

$$\prod_{i=1}^n \left[\int_{-\infty}^{\infty} \left(\prod_{j=1}^{m_i} f(y_i(t_{ij})|b_i, \theta) \right) f(b_i|\theta) f(T_i, d_i|b_i, \theta) db_i \right]$$

where

$$f(y_i(t_{ij})|b_i, \theta) = (2\pi\sigma_e^2)^{-1/2} \exp \left\{ -\frac{y_i(t_{ij}) - W_i(t_{ij})}{2\sigma_e^2} \right\},$$

$$f(b_i|\theta) = (2\pi|V|)^{-1/2} \exp \left\{ -\frac{b_i' V^{-1} b_i}{2} \right\},$$

and

$$f(T_i, d_i|b_i, \theta) = [h_0(T_i) \exp(\alpha W_i(t) + \phi v_i)]^{d_i} \exp \left\{ -\int_0^{T_i} h_0(u) \exp(\alpha W_i(u) + \phi v_i) du \right\}$$

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Gauss-Hermite quadrature

- ▶ Numerical method to approximate analytically intractable integrals (Pinheiro and Bates, 1995)

$$\int_{-\infty}^{\infty} e^{-x^2} f(x) dx \approx \sum_{q=1}^m w_q f(x_q)$$

- ▶ Can be extended to multivariate integrals i.e. multiple random effects

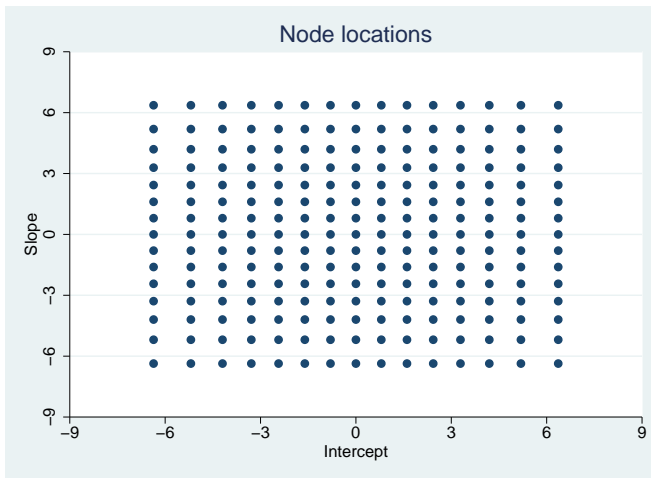


Figure: 2-dimensional 15 point node locations.

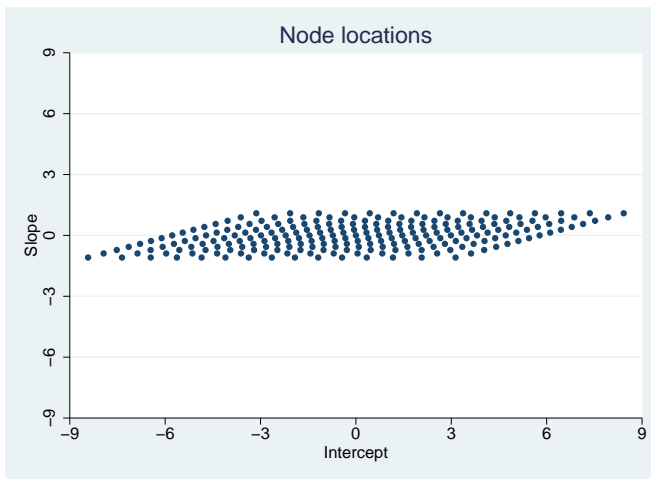


Figure: Adjusted 2-dimensional 15 point node locations.

Survival submodel

- ▶ Flexible parametric survival model (Royston and Parmar, 2002; Lambert and Royston, 2009)
- ▶ Modelled on the log cumulative hazard scale using restricted cubic splines (Durrleman and Simon, 1989)

$$\log\{H_0(t)\} = s\{\log(t)|\gamma, \mathbf{k}_0\}$$

- ▶ Can evaluate the likelihood directly

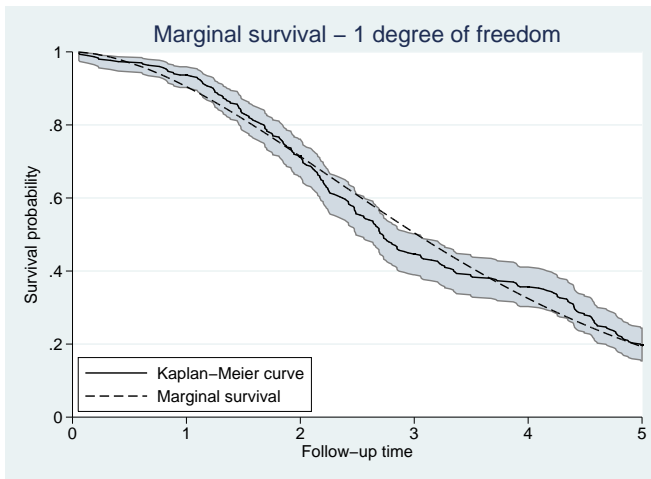


Figure: Predicted marginal survival function from joint model with 1 degree of freedom, overlaid on the Kaplan-Meier survival curve.

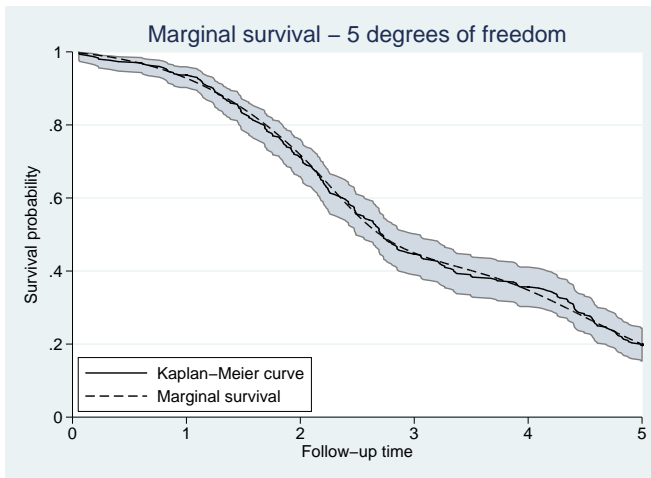


Figure: Predicted marginal survival function from joint model with 5 degrees of freedom, overlaid on the Kaplan-Meier survival curve.

Survival model linear predictor:

$$\log\{H(T_i|\mathbf{b}_i, v_i)\} = \eta_i = s\{\log(T_i)|\gamma, \mathbf{k}_0\} + \alpha W_i(T_i) + \phi v_i$$

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Transform to the hazard and survival scales:

$$h(T_i|\mathbf{b}_i, v_i) = \left\{ \frac{1}{T_i} \frac{ds\{\log(T_i)|\gamma, \mathbf{k}_0\}}{d \log(T_i)} + \alpha \frac{dW(T_i)}{dT_i} \right\} \exp(\eta_i)$$

$$S(T_i|\mathbf{b}_i, v_i) = \exp\{-\exp(\eta_i)\}$$

(Crowther et al., 2011)

Implementation in Stata

```
stjm longdepvar [varlist], panel(varname) df(#)  
    [nodes(#) ...]
```


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 - ▶ `ffracpoly(numlist)` - Fixed FP's of time
 - ▶ `rfracpoly(numlist)` - Random FP's of time
 - ▶ [*varlist*] - Baseline covariates

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 - ▶ `df(#)/knots(numlist)` - Baseline cum. hazard
 - ▶ `survcov(varlist)` - Baseline covariates
- ▶ Association:
 - ▶ `nocurrent` - Current value is the default
 - ▶ `derivassoc(1)` - 1st derivative
 - ▶ `sepintassoc/sepassoc(numlist)` - Random coefficient, e.g. random intercept

Predictions

```
predict newvarname, option
```

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predict *newvarname, option*

▶ Longitudinal:

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- ▶ *residuals* - Subject level residuals
- ▶ *rstandard* - Standardised residuals
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- ▶ Survival:
 - ▶ `hazard` - Hazard function
 - ▶ `survival` - Survival function
 - ▶ `cumhazard` - Cumulative hazard function
 - ▶ `martingale` - Martingale residuals
 - ▶ `stjmcondsurv` - Conditional survival

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Predictions can be evaluated at measurement/survival times, or user specified times.

- ▶ Random intercept with fixed slope, current value association, one degree of freedom:

```
. stjml logb drug, ffracp(1) nodes(15) df(1) survcov(drug)
```
- ▶ Random intercept and slope with fixed time powers 2 and 3, association based on 1st derivative, 3 degrees of freedom:

```
. stjml logb drug, rfracp(1) ffracp(2 3) survcov(drug) ///  
nodes(15) df(3) nocurrent derivassoc(1)
```


Application to PBC dataset

```
. stjml logb trt, panel(id) nodes(15) rfracp(1) df(1) survcov(trt)
-> gen double timevar_1 = X^(1)
(where X = _t0)
```

Obtaining initial values:

Fitting full model:

```
Joint model estimates                               Number of obs.   =    1945
Patient variable: id                               Number of patients =    312
Log-likelihood = -1952.7411
```

	Coef.	Std. Err.	z	P> z	[95% Conf. Interval]	
Longitud.:						
timevar_1	.1636943	.0042372	38.63	0.000	.1553895	.171999
trt	-.1705512	.0349558	-4.88	0.000	-.2390633	-.1020391
_cons	.682979	.0348529	19.60	0.000	.6146686	.7512894
Survival:						
trt	-.0209648	.177859	-0.12	0.906	-.369562	.3276325
_rcs1	.8489682	.0820932	10.34	0.000	.6880684	1.009868
_cons	-3.330624	.2450019	-13.59	0.000	-3.810819	-2.850429
Association:						
current	1.010613	.0836087	12.09	0.000	.8467429	1.174483

Random effects table

Random effects Parameters	Estimate	Std. Err.	[95% Conf. Interval]	
id: Unstructured				
sd(timevar_1)	.1588024	.0055511	.1482869	.1700637
sd(intercept)	.8564879	.0173008	.8232413	.8910771
corr(timevar_1,intercept)	.5405518	.0208844	.4983468	.580201
sd(Residual)	.3687027	.0067102	.3557827	.3820918

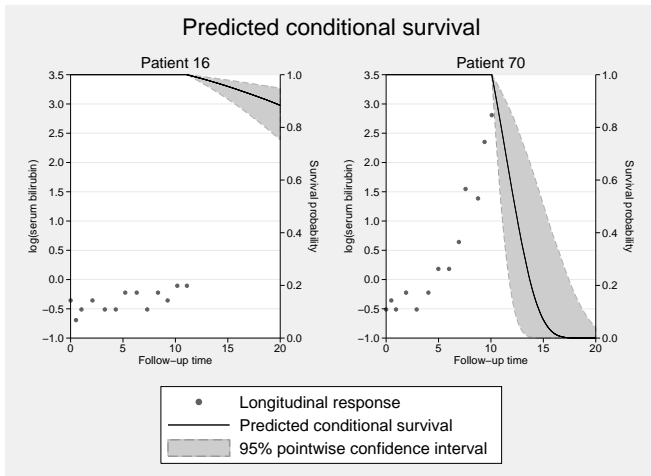
Longitudinal submodel: Linear mixed effects model

Survival submodel: Flexible parametric model with 1 degree of freedom

Integration method: Gauss-Hermite quadrature using 15 quadrature points

Individual level predictions

```
stjmcondsurv, panel(id) id(16) fu(20)
```



Future work

- ▶ Survival submodels:
 - ▶ Weibull PH model
 - ▶ Gompertz PH model
 - ▶ 2-component mixture Weibull PH model
 - ▶ Mixture Weibull-exponential PH model
- ▶ Extension to competing risks
- ▶ Extension to include a cure proportion
- ▶ Longitudinal categorical responses
- ▶ EM algorithm
- ▶ Adaptive GH quadrature

Command acknowledgments

- ▶ rcsген - Paul Lambert
- ▶ stpm2 - Paul Lambert
- ▶ ghquadm - Bill Sribney
- ▶ esttab - Ben Jann
- ▶ fracgen - Patrick Royston

References I

- M. J. Crowther, K. R. Abrams, and P. C Lambert. Flexible parametric joint modelling of longitudinal and survival data. *Submitted*, 2011.
- S. Durrleman and R. Simon. Flexible regression models with cubic splines. *Statistics in Medicine*, 8(5):551–561, 1989.
- N. M. Laird and J. H. Ware. Random-effects models for longitudinal data. *Biometrics*, 38(4):963–974, 1982.
- P. C Lambert and P. Royston. Further development of flexible parametric models for survival analysis. *The Stata Journal*, 9:265–290, 2009.
- P. Murtagh, E. Dickson, M. Van Dam, G. Malincho, and P. Grambsch. Primary biliary cirrhosis: Prediction of short-term survival based on repeated patient visits. *Hepatology*, 20:126–134, 1994.
- José C. Pinheiro and Douglas M. Bates. Approximations to the log-likelihood function in the nonlinear mixed-effects model. *Journal of Computational and Graphical Statistics*, 4(1):pp. 12–35, 1995. ISSN 10618600.
- C. Proust-Lima and J. M. G. Taylor. Development and validation of a dynamic prognostic tool for prostate cancer recurrence using repeated measures of posttreatment psa: a joint modeling approach. *Biostatistics*, 10(3): 535–549, 2009.
- P. Royston and D. G. Altman. Regression using fractional polynomials of continuous covariates: Parsimonious parametric modelling. *Journal of the Royal Statistical Society. Series C (Applied Statistics)*, 43(3):429–467, 1994.
- P. Royston and M. K. B. Parmar. Flexible parametric proportional-hazards and proportional-odds models for censored survival data, with application to prognostic modelling and estimation of treatment effects. *Stat Med*, 21(15):2175–2197, 2002.
- M. S. Wulfsohn and A. A. Tsiatis. A joint model for survival and longitudinal data measured with error. *Biometrics*, 53(1):330–339, 1997.