A Bayesian Joint Dispersion Model With Flexible Links

Rui Martins



Egas Moniz Health School Egas Moniz Interdisciplinary Research Center, Portugal

Summary

Background

- Longitudinal studies
- Outline
- HIV/AIDS Application
 - Data
 - Exploratory analysis
 - Joint Model



Questions of interest

• Biomarker, Y₁

• e.g. CD4 counts, collected repeatedly over time (longitudinal data)

time to an event of interest, Y₂

• e.g. death from any cause (survival data)

Separate Analysis

- does treatment affect survival?
- are the average longitudinal evolutions different between males and females?

Joint Analysis

- what is the effect of the missing information due to drop-out in assessing the trends of the repeated measures?
- what is the effect of the longitudinal evolution of CD4 cell count in the hazard rate for death?

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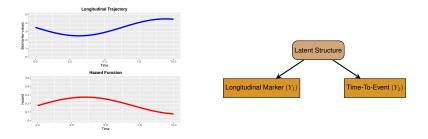
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Background HIV/AIDS Application

Results

Longitudinal studi Outline

Correlated data in longitudinal studies



If the two processes are associated \Rightarrow define a model for their joint probability distribution: $f(y_1, y_2)$

ata xploratory analysis oint Model

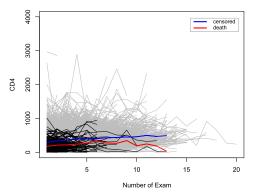
Analysing HIV/AIDS data through A Bayesian Joint Dispersion Model with Flexible Links

- network of 88 laboratories located in every state in Brazil during Jan 2002 – Dec 2006;
- **Sample**: n = 500 individuals; 2757 repeated measurements;
- **Outcomes**: CD4⁺T lymphocyte counts, *Y*, and time-to-death, *T*;
- Covariates: age (<50=0, ≥50=1); sex (Female=0, Male=1); PrevOl (previous opportunistic infection at study entry=1, no previous infection=0); measurement times; date of diagnosis; date of death; failure indicator, δ;
- Patients: 34 deaths. 88% between 15 and 49 years old; 60% males. 61% no previous infection. Initial CD4 median: 269 cells/mm³ (men 250 cells/mm³; women 295 cells/mm³).

Data E**xploratory analysis** loint Model

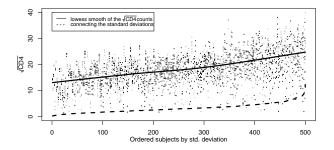
Longitudinal outcome





Data E**xploratory analysis** Ioint Model

Intra-individual variance (dispersion)



Individuals values of the $\sqrt{\text{CD4}}$ vs Std. Deviation (ordered) suggests considerable within-subject variance heterogeneity. Individuals with higher $\sqrt{\text{CD4}}$ values are associated with a higher variability.

Data Exploratory analysis loint Model

Longitudinal specification

Mixed-effects dispersion model (McLain et al. 2012)

$$y_{ij}|\boldsymbol{b}_i, \sigma_i^2 \sim \mathcal{N}(m_i(t_{ij}), \sigma_i^2), \quad j = 1, \dots, n_i$$
 (1)

$$m_i(t_{ij}) = \boldsymbol{\beta}_1^\top \mathbf{x}_{1i}(t_{ij}) + \boldsymbol{b}_{1i}^\top \mathbf{w}_{1i}(t_{ij}),$$
(2)

$$\sigma_i^2 = \sigma_0^2 \exp\{\beta_2^\top \mathbf{x}_{2i}(t_{ij}) + \boldsymbol{b}_{2i}^\top \mathbf{w}_{2i}(t_{ij})\},\tag{3}$$

- y_i = (y_{i1},..., y_{ini}) → n_i observed repeated measures, √CD4
 t_i = (t_{i1},..., t_{ini}) → visiting times
- $\mathbf{x}_{1i}, \mathbf{x}_{2i}, \mathbf{w}_{1i}$ and $\mathbf{w}_{2i} \rightarrow \text{individual covariates (time-dependent?)}$
- eta_1 and $eta_2
 ightarrow$ population parameters
- $(\boldsymbol{b}_{1i}^{\top}, \boldsymbol{b}_{2i}^{\top}) = \boldsymbol{b}_i | \Sigma \sim \mathcal{N}_p(\boldsymbol{0}, \Sigma) \rightarrow \text{time-independent random-effects}$

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Background Data HIV/AIDS Application Results Joint M

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Longitudinal outcome

$$\sqrt{\mathsf{CD4}}_{ij} | \boldsymbol{b}_i, \sigma_i^2 \sim \mathcal{N}(m_i(t_{ij}), \sigma_i^2)$$

Longitudinal mean

 $m_i(t_{ij}) = \beta_{10} + \beta_{11} \mathbf{sex}_i + \beta_{12} \mathbf{age}_i + \beta_{13} \mathsf{PrevOl}_i + \beta_{14} t_{ij} + b_{1i,1} + b_{1i,2} t_{ij}$ (4)

• Dispersion model (3) may assume:

$$\sigma_i^2 = \sigma_0^2 \exp\{\beta_{21} \mathbf{sex} + \beta_{22} \mathbf{age} + \beta_{23} \mathsf{PrevOI} + b_{2i}\},\tag{5}$$

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$$\sigma_i^2 = \sigma_0^2. \tag{8}$$

Priors

- $\beta_{1p} \sim \mathcal{N}(0, 100); p = 0, \dots, 4 \text{ and } \beta_{2q} \sim \mathcal{N}(0, 100); q = 1, \dots, 3$
- $b_i | \Sigma \sim \mathcal{N}_p(\mathbf{0}, \Sigma); \quad \Sigma^{-1} \sim \mathcal{W}ish(R, \xi)$
- $\log(\sigma_0) \sim \mathcal{U}(-100, 100)$; or $\log(\sigma_i) \sim \mathcal{U}(-100, 100)$
- Other options: $1/\sigma_0^2 \sim \mathcal{G}(\epsilon, \epsilon)$ and $\sigma_0 | \varpi \sim h-\mathcal{C}(\varpi), \, \varpi \sim \mathcal{U}(0, 100).$

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• Time-dependent coefficients (Penalized cubic B-Splines)

 $h_{i}(t|\boldsymbol{b}_{i},\sigma_{i}) = h_{0}(t) \exp\{\boldsymbol{\beta}_{3}^{\top} \mathbf{x}_{3i} + C_{i}\{\boldsymbol{b}_{i},\sigma_{i};\boldsymbol{g}(t)\}\} = h_{0}(t) \exp\{\varrho_{i}(t)\}$ (9)

- $C_i\{.\} \rightarrow$ specifies which components of the longitudinal process are related to $h_i(.)$
- Link \rightarrow Shared parameters
 - $\blacktriangleright b_i, \sigma_i$
- $\mathbf{x}_{3i}
 ightarrow$ baseline covariates
- $\beta_3 \rightarrow$ population parameters
- $h_0(t) \rightarrow \text{parametric}$ (*e.g.* Weibull); P-Splines; Piecewise constant function.
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Time-to-death

$$h_i(t|\boldsymbol{b}_i, \sigma_i) = h_0(t) \exp\{\boldsymbol{\beta}_3^\top \mathbf{x}_{3i} + \mathcal{C}_i\{\boldsymbol{b}_i, \sigma_i; \boldsymbol{g}(t)\}\} = h_0(t) \exp\{\varrho_i(t)\}$$
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• all models

$$\beta_3^{\top} \mathbf{x}_{3i} = \beta_{31} \mathbf{sex}_i + \beta_{32} \mathbf{age}_i + \beta_{33} \mathsf{PrevOI}_i$$
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• $C_i(.)$ may assume:

$$C_i(.) = g_1(t)b_{1i,1} + g_2(t)b_{1i,2} + g_3(t)b_{2i}$$
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• $g_1(t), g_2(t), g_3(t) \rightarrow$ **Penalized Splines** with 19 internal knots.

•
$$g_l(t) = \sum_{q=1}^{19} \gamma_{lq} B_{lq}(t), \quad l = 1, 2, 3$$

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$$\gamma_{l1} \sim \mathcal{N}(0, 1000), \ \gamma_{lq} | \tau_l^2 \sim \mathcal{N}(\gamma_{l,q-1}, \tau_l^2), \ q = 2, \dots, 19$$

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Joint likelihood

We consider:

• $\mathbf{y}_i | \mathbf{b}_i \perp T_i | \mathbf{b}_i; \quad y_{ij} | \mathbf{b}_i \perp y_{il} | \mathbf{b}_i, j \neq l$

non-informative right censoring

$$L(\boldsymbol{\theta}, \mathbf{b}, \boldsymbol{\sigma} \mid \mathcal{D}) = \prod_{i=1}^{N} \left(\prod_{j=1}^{n_i} p(y_i(t_{ij}) | \boldsymbol{\theta}, \boldsymbol{b}_i, \sigma_i^2) \right) p(T_i, \delta_i | \boldsymbol{\theta}, \boldsymbol{b}_i, \sigma_i)$$

where

- $\mathcal{D} = {\mathcal{D}_i}_{i=1}^N = {(\mathbf{y}_i, \mathbf{t}_i, T_i, \delta_i)}_{i=1}^N \rightarrow \text{observed data for the } N$ independent individuals
- $\theta \rightarrow$ other parameters;
- $p(.) \rightarrow$ suitable density function

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where

$$p(y_i(t_{ij}) \mid \boldsymbol{\theta}, \boldsymbol{b}_i, \sigma_i^2) = \frac{1}{\sqrt{2\pi\sigma_i^2}} \exp\left\{-\frac{[y_i(t_{ij}) - m_i(t_{ij})]^2}{2\sigma_i^2}\right\}$$

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where

$$p(T_i, \delta_i \mid \boldsymbol{\theta}, \boldsymbol{b}_i, \sigma_i) = h(T_i \mid \boldsymbol{\theta}, \boldsymbol{b}_i, \sigma_i)^{\delta_i} \times S(T_i \mid \boldsymbol{\theta}, \boldsymbol{b}_i, \sigma_i)$$

= $[h_0(T_i) \exp\{\boldsymbol{\beta}_3^\top \mathbf{x}_{3i} + \mathcal{C}_i\{\boldsymbol{b}_i, \sigma_i; \boldsymbol{g}(t)\}\}]^{\delta_i} \times$
= $\exp\left\{-\int_0^{T_i} h_0(u) \exp\{\boldsymbol{\beta}_3^\top \mathbf{x}_{3i} + \mathcal{C}_i\{\boldsymbol{b}_i, \sigma_i; \boldsymbol{g}(t)\}\}du\right\}$

MCMC simulation within WinBUGS.

Longitudinal model		Survival model			
m_i	σ_i^2	$\varrho_i(t)$		h_0	
	-		Weibull	P-Spline	Piecewise
(4)	(5)	(11) + (12)	14671	12573	14317
(4)	(6)		14700	12848	14483
(4)	(5)	(11) + (13)	14307	12605	13365
(4)	(6)		14452	12917	13571
(4)	(7)		13134	12104 🌲	12921
(4)	(8)		13956	12887	13533
(4)	(5)	(11) + (14)	14811	13334	14463
(4)	(6)		14923	13688	14599
(4)	(7)		14314	13144	13968
(4)	(8)		14627	13553	14355
(4)	(8)	$(11)+g_1b_{1i,1}+g_2b_{1i,2}$	16984	15779	16383

Tabela: WAIC values for the 33 joint models.

Best fit \Rightarrow share the individual random-effects and the individual std-deviation considered as a covariate for the hazard model (Model **4**). The heteroscedasticity is related to the survival time.

Posterior estimates for the time-dependent coefficients

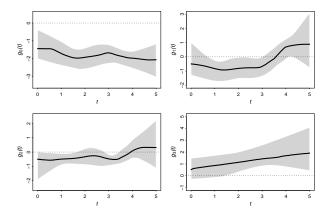


Figure 1: Posterior mean estimates, together with the corresponding 95% Credible Bands (CB), for the selected model **4**. The top left panel shows $g_0 = \log(h_0)$ and the subsequent panels have the time-varying regression coefficients as a function of time in years, *t*.

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Thank you!