

Errata List for “Joint Models for Longitudinal and Time-to-Event Data, with Applications in R”

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Chapter 3

- pp. 45: The last on the equation on the page should read

$$p(t | \mathcal{Y}_i(t)) = h_i(t | \mathcal{Y}_i(t))\mathcal{S}_i(t | \mathcal{Y}_i(t))$$

- pp. 47: The expression for the partial likelihood should read

$$p\ell(\gamma) = \sum_{i=1}^n \int_0^{\infty} \left\{ R_i(t) \exp\{\gamma^\top w_i + \alpha y_i(t)\} - \log \left[\sum_j R_j(t) \exp\{\gamma^\top w_j + \alpha y_j(t)\} \right] \right\} dN_i(t)$$

Chapter 5

- Section 5.2, pp. 117–118: Using **JM** (version $\geq 1.0-1$) an error message appears that Patient 81 has longitudinal measurements after the event time. This happens because for the time-dependent covariate **spiders** that is included in the survival submodel that last two records are missing, and therefore the last available record for this patient is the one at 6.78458 years. The linear mixed-effects model did not have spiders as a covariate and thus, the last available measurement was at 6.9242142 years causing the error.

	id	serBilir	drug	year	years	status2	spiders	start	stop	event
639	81	2.0	D-penicil	0.0000000	6.954331	1	Yes	0.0000000	0.6023437	0
640	81	2.7	D-penicil	0.6023437	6.954331	1	Yes	0.6023437	1.0294601	0
641	81	1.3	D-penicil	1.0294601	6.954331	1	Yes	1.0294601	2.0068996	0
642	81	1.9	D-penicil	2.0068996	6.954331	1	Yes	2.0068996	3.1759939	0
643	81	4.3	D-penicil	3.1759939	6.954331	1	No	3.1759939	4.1890264	0
644	81	4.1	D-penicil	4.1890264	6.954331	1	No	4.1890264	5.0898040	0
645	81	5.5	D-penicil	5.0898040	6.954331	1	No	5.0898040	5.7578578	0
646	81	8.1	D-penicil	5.7578578	6.954331	1	No	5.7578578	6.7845800	0
647	81	8.1	D-penicil	6.7845800	6.954331	1	<NA>	6.7845800	6.9242142	0
648	81	10.2	D-penicil	6.9242142	6.954331	1	<NA>	6.9242142	6.9543314	1

To resolve this we need to refit `lmeFit.pbc` as

```
lmeFit.pbc <- lme(log(serBilir) ~ drug * (year + I(year^2)),
  random = ~ year + I(year^2) | id, data = pbc[!is.na(pbc$spiders), ])
```

which slightly changes the results in the book, namely

```
summary(jointFit8.pbc)
```

```

. . .
Event Process
                                Value Std.Err z-value p-value
drugD-penicil                   -0.2353  0.3155 -0.7458  0.4558
spidersYes                       0.4837  0.2756  1.7550  0.0793
drugD-penicil:spidersYes         0.2289  0.4030  0.5681  0.5700
Assoct                           1.2140  0.1092 11.1201 <0.0001
. . .

```

and

```

exp(confint(jointFit8.pbc, parm = "Event"))
                                2.5 %    est.    97.5 %
drugD-penicil                   0.4258737 0.790341 1.466723
spidersYes                       0.9450712 1.622060 2.784000
drugD-penicil:spidersYes         0.5706754 1.257258 2.769870
Assoct                           2.7184043 3.366996 4.170337

```

Appendix B

- pp. 232: The element of the score vector for parameter α should read

$$\begin{aligned}
S(\alpha) &= \sum_i \delta_i \{x_i^\top(T_i)\beta + z_i^\top(T_i)\tilde{b}_i\} \\
&\quad - \exp(\gamma^\top w_i) \int \int_0^{T_i} h_0(s) \{x_i^\top(s)\beta + z_i^\top(s)b_i\} \exp[\alpha \{x_i^\top(s)\beta + z_i^\top(s)b_i\}] \\
&\quad \times p(b_i | T_i, \delta_i, y_i; \theta) ds db_i
\end{aligned}$$

- pp. 232: The elements of the score vector for parameters θ_{h_0} should read

$$\begin{aligned}
S(\theta_{h_0}) &= \sum_i \delta_i \frac{\partial \log h_0(T_i; \theta_{h_0})}{\partial \theta_{h_0}^\top} \\
&\quad - \exp(\gamma^\top w_i) \int \int_0^{T_i} \frac{\partial h_0(s; \theta_{h_0})}{\partial \theta_{h_0}^\top} \exp[\alpha \{x_i^\top(s)\beta + z_i^\top(s)b_i\}] \\
&\quad \times p(b_i | T_i, \delta_i, y_i; \theta) ds db_i
\end{aligned}$$