



Correlated random effects in survival analysis

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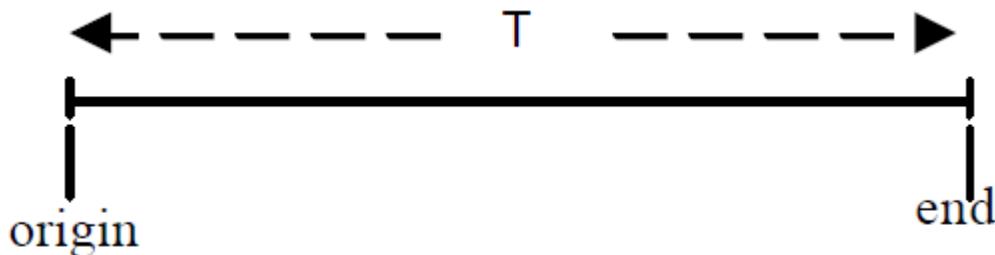
Session: S.30 Free communications: animal breeding methodology

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Survival Analysis

- To analyze the time until an event occurs
- Analysis of response time



- Can deal with censored observations and time dependent covariates

Survival Analysis

- General equation:

$$\lambda(t) = \lambda_0 * \exp(X(t)_i' \beta_i)$$

- $\lambda(t)$ – hazard for an individual
- λ_0 – baseline hazard
- $X(t)_i$ – set of (possibly time dependent) fixed explanatory variables
- β_i – vector of estimates

Survival Analysis – random effect

- Could be extended to incorporate (possibly time dependent) random effects

$$\lambda(t) = \lambda_0 * \exp(X(t)_i'\beta_i + Z(t)_i's_i)$$

- Resulting into: $u = (0, \sigma^2)$
- Widely used in genetic analysis for sire or animal models

Survival Analysis– 2 random effects

- Simultaneous estimation of variances for 2 random effects is also possible

$$\lambda(t) = \lambda_0 * \exp(X(t)_i' \beta_i + Z_1(t)_i' s_{1i} + Z_2(t)_i' s_{2i})$$

- $u = (0, \sigma_1^2)$
- $v = (0, \sigma_2^2)$
- *E.g. herd×year and sire effect*

Correlated random effects

- Until now the estimates for the random effects assumed to be independent from each other...
- ... although it might not be always the case
- E.g. culling during early vs. late lactations

Correlated random effects

- An extension of the *Survival Kit* was made to incorporate this possibility

$$\lambda(t) = \lambda_0 * \exp(X(t)_i' \beta_i + Z_1(t)_i' s_{1i} + Z_2(t)_i' s_{2i})$$

$$\begin{pmatrix} u \\ v \end{pmatrix} = \begin{pmatrix} 0 \\ 0 \end{pmatrix} \begin{pmatrix} \sigma_1^2 & \rho\sigma_1\sigma_2 \\ \rho\sigma_1\sigma_2 & \sigma_2^2 \end{pmatrix}$$

Simulation study

- 50 and 100 groups (sires) with 100 individuals (daughters) in each
- Weibull distribution with $\rho=3$
intercept=0.02
- One fixed effect with 2 levels
- 200 replicates for each alternative

Simulation results

	σ_1^2 (true) = 0.3	σ_2^2 (true) = 0.3	ρ (true) = -0.2		
	without ρ	with ρ	without ρ	with ρ	with ρ
50 sires 100 daughters each	\bar{x}	0,285	0,285	0,275	0,275
	s	0,061	0,060	0,060	0,150
100 sires 100 daugh. each	\bar{x}	0,279	0,282	0,274	0,277
	s	0,040	0,041	0,044	0,107

- \bar{x} and s are the means and standard deviations from the 200 test runs

Simulation results

	σ_1^2 (true) = 0.3	σ_2^2 (true) = 0.3	ρ (true) = -0.6		
	without ρ	with ρ	without ρ	with ρ	with ρ
50 sires 100 daughters each	\bar{x}	0,268	0,284	0,257	0,274
	s	0,058	0,060	0,060	0,062
100 sires 100 daugh. each	\bar{x}	0,262	0,282	0,256	0,277
	s	0,039	0,041	0,042	0,044

- \bar{x} and s are the means and standard deviations from the 200 test runs

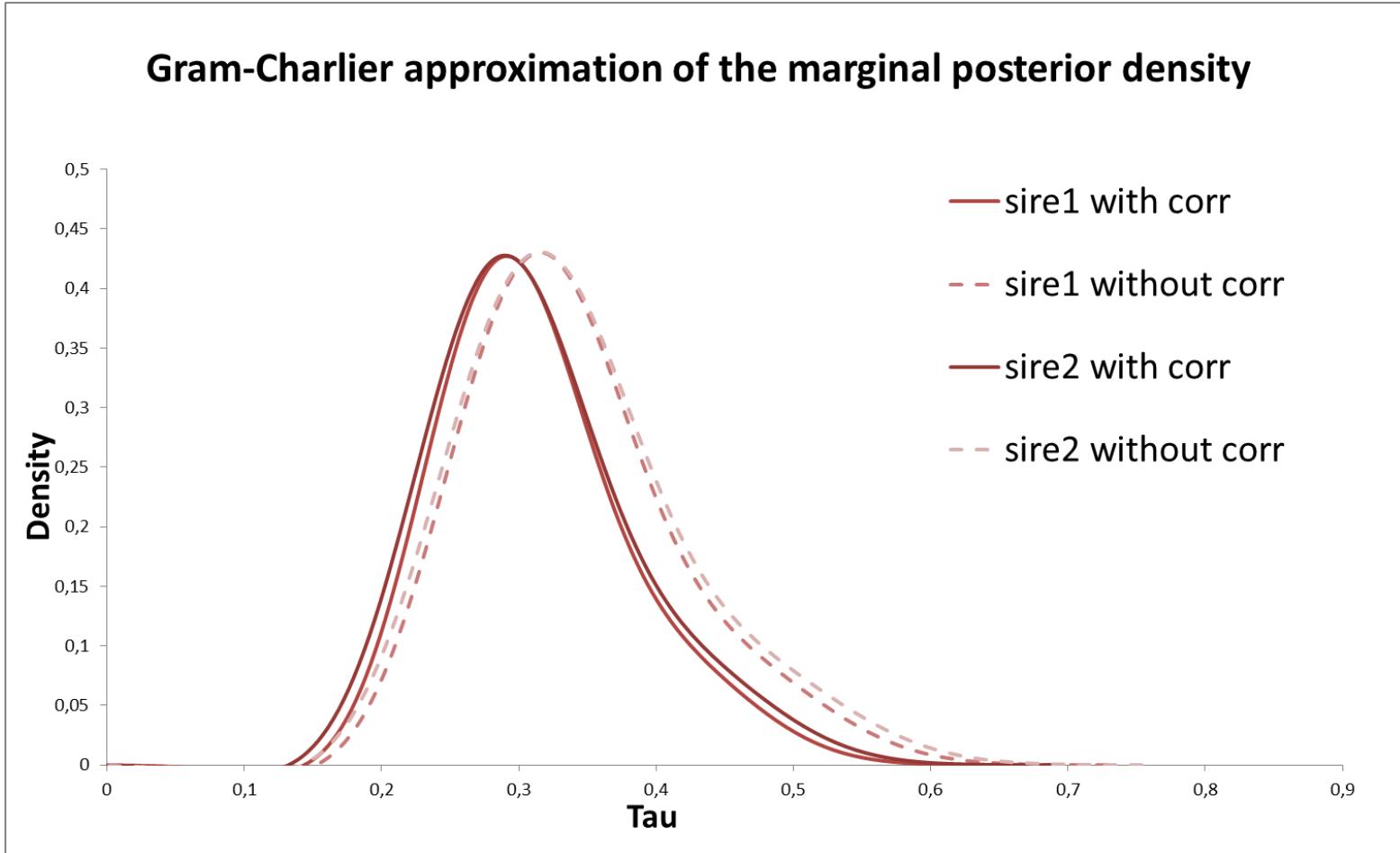
Simulation results

	σ_1^2 (true) = 0.3	σ_2^2 (true) = 0.3	ρ (true) = 0.6		
	without ρ	with ρ	without ρ	with ρ	with ρ
50 sires 100 daughters each	\bar{x}	0,313	0,285	0,313	0,284
	s	0,065	0,060	0,073	0,068
100 sires 100 daugh. each	\bar{x}	0,307	0,283	0,307	0,282
	s	0,043	0,041	0,052	0,049

- \bar{x} and s are the means and standard deviations from the 200 test runs

Simulation results – corr=0.6

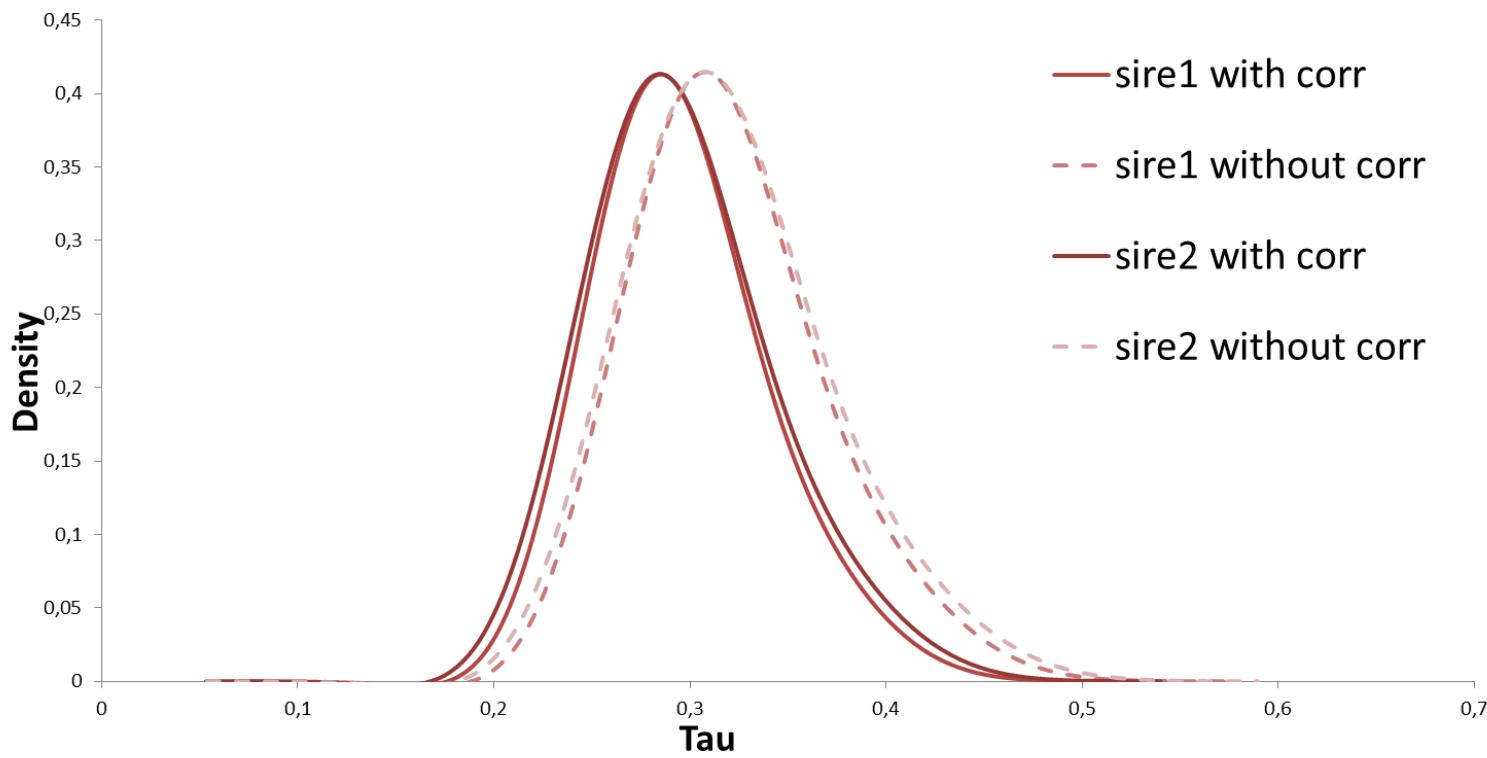
50 sires -100 daughters



Simulation results – corr=0.6

100 sires - 100 daughters

Gram-Charlier approximation of the marginal posterior density



Practical example

- Work in progress
- In cooperation with Birgit Fürst-Waltl
- Influence of the sire on mortality of female calves
- 2 periods:
 - Calf up to 180 days
 - Heifer from 181 days to first calving

Practical example

- “Time dependent sire” random effect along with other fixed effects
- Censoring >96%
- $\text{var}(\text{"early sire effect"}) = 0.045$
 - $h^2 = 0.007$ (cens. not considered: $h^2 = 0.17$)
- $\text{var}(\text{"late sire effect"}) = 0.023$
 - $h^2 = 0.004$ (cens. not considered: $h^2 = 0.09$)
- correlation = 0.75

Conclusions

- Work in progress
- Little difference in estimates of variances when correlation is small
- Correlations estimated well
- Interesting opportunities of application
 - Direct and maternal genetic effects
 - Time dependent genetic effects
 - ...



Thanks for your attention!

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