Bayesian hierarchical model of oscillatory cortisol response during drug intervention

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Background and motivation

Oscillating biomarker response-time courses challenge modelling of drug intervention. A periodically recurring pattern is typically seen for the stress hormone cortisol. This pattern can be captured by mechanism-based turnover models. Bayesian hierarchical modelling allows for full quantification of parameter uncertainty while also capturing the population aspects typical to nonlinear mixed effects modelling. Inter-occasion variability (IOV) is incorporated in addition to inter-individual variability (IIV). Finally, the adjusted model is used to predict specificity of a clinical test.

Key findings

- New techniques were developed for graphical analysis of the oscillatory cortisol response
- A predictive hierarchical model was successfully constructed and applied to equine cortisol data after dexamethasone intervention
- Oscillatory behaviour and level of variability had great impact on the sparse-sample DST-design

Dexamethasone exposure and cortisol response

- a) Two compartment model with bolus dose and 3h constant-rate infusion Data were collected for four different dosing regimens (bolus + total infusion amount) *Control (saline solution)*, $0.1 + 0.07 \mu g / kg$, $1.0 + 0.7 \mu g / kg$, $10 + 7 \mu g / kg$
- **b)** Turnover model with oscillating turnover rate and drug-induced suppression



Bayesian hierarchical model

- Incorporation of IIV and IOV
- Conceptually similar to nonlinear mixed effects modelling
- Inclusion of prior knowledge allows for regularisation of the estimation



Analytic Solution

For a fixed drug concentration C_p $R(t, C_p) = A + B \cos\left(\frac{2\pi}{24}(t - C)\right)$

where



Used to

- Calculate initial values
- Establish drug-response equilibrium curves

Parameter estimates, uncertainty and model predictions

Parameter estimates

Parameters were estimated in a Bayesian framework. Samples from the joint probability model

Parameter Estimated range including IIV/IOV (quantiles)

- were simulated with the Hamiltonian Monte Carlo algorithm implemented in Stan [2].
- Priors for hyperparameters were chosen by a meta-analysis of a previous study [1].
- Estimated ranges including IIV and IOV for parameters of the cortisol response model are shown
- Bayesian estimation allows estimation of three sources of variability and uncertainty
 - Uncertainty in typical values
 - Uncertainty in estimated variance components
 - Model uncertainty/Residual variance
- Variance components were hard to identify (data from N = 6 horses), regularisation with priors aided the parameter estimation

Model predictions

- 95% credible intervals for the predicted time-courses are shown
- Oscillation and suppression are being captured
- Reduction of variability for increasing drug doses is visible.



	2.5%	25%	50%	75%	97.5%
$k_{ m avg}$	6.44	9.22	12.7	17.2	23.5
α	1.38	3.00	5.40	9.38	17.9
t_0	-7.54	-5.44	-3.71	-2.17	0.494
$k_{ m out}$	0.221	0.272	0.315	0.378	0.493
I _{max}	0.874	0.900	0.923	0.944	0.965
IC_{50}	0.004 90	0.0136	0.0298	0.0628	0.155
n	1.03	1.26	1.57	2.00	2.61



Variability of oscillation parameters

- Through Monte Carlo simulations, the average baseline *A* and amplitude *B*, as described above, were simulated.
- Average baseline is subject to both IIV and IOV resulting in higher variability
- Both parameters are suppressed in magnitude and variability for increasing drug concentration

Predicted specificity of a dexamethasone suppression test (DST)

- Two previously published protocols were evaluated . Both stated specificity.
 - Protocol 1 in [3]: 100% specificity
 - Protocol 2 in [4]: 76% specificity







- Intravenous administration of 40 μg / kg of dexamethasone at 9.00 (protocol 2) or 17.00
 o'clock (protocol 1)
- Cortisol sample *R*_{after} taken after 19 hours
 (protocol 1) or 24 hours (protocol 2)
- DST indicates healthy subjects for $R_{after} < 10 \ \mu g / L$
- Clear dependence on "administration time" and "hours after administration"







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References

[1] C. Ekstrand et al., J. Vet. Pharmacol. Ther. 39, 255–263 (2016).
[2] B. Carpenter et al., J. Stat. Softw. 76 (2017), doi:10.18637/jss.v076.i01.
[3] N. O. Dybdal et al., J. Am. Vet. Med. Assoc. 204, 627–632 (1994).
[4] N. Frank et al., J. Vet. Intern. Med. 20, 987–93 (2006).

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