

Maximum likelihood estimation in nonlinear mixed effect models: adaptive Gaussian quadrature by sparse grid sampling

PAGE 2009

St. Petersburg 22-26 June

Wan Hui O. Clausen¹, Birgitte B. Rønn¹,
Ib M. Skovgaard²

1: Biometrics, Genmab a/s. 2: Department of Basic Sciences and Environment, University of Copenhagen



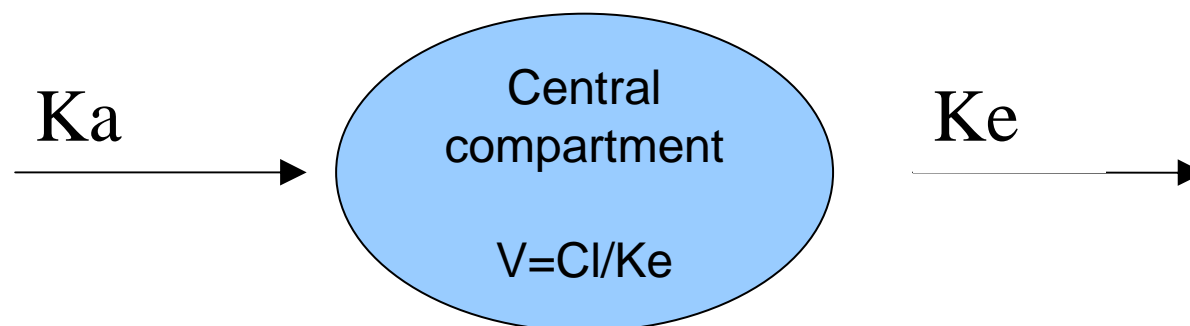


- Pinheiro and Bates (1995):

Comparison of estimation algorithms, NLME, Laplacian, AGQ and importance sampling

Conclusion: AGQ precise, but less efficient

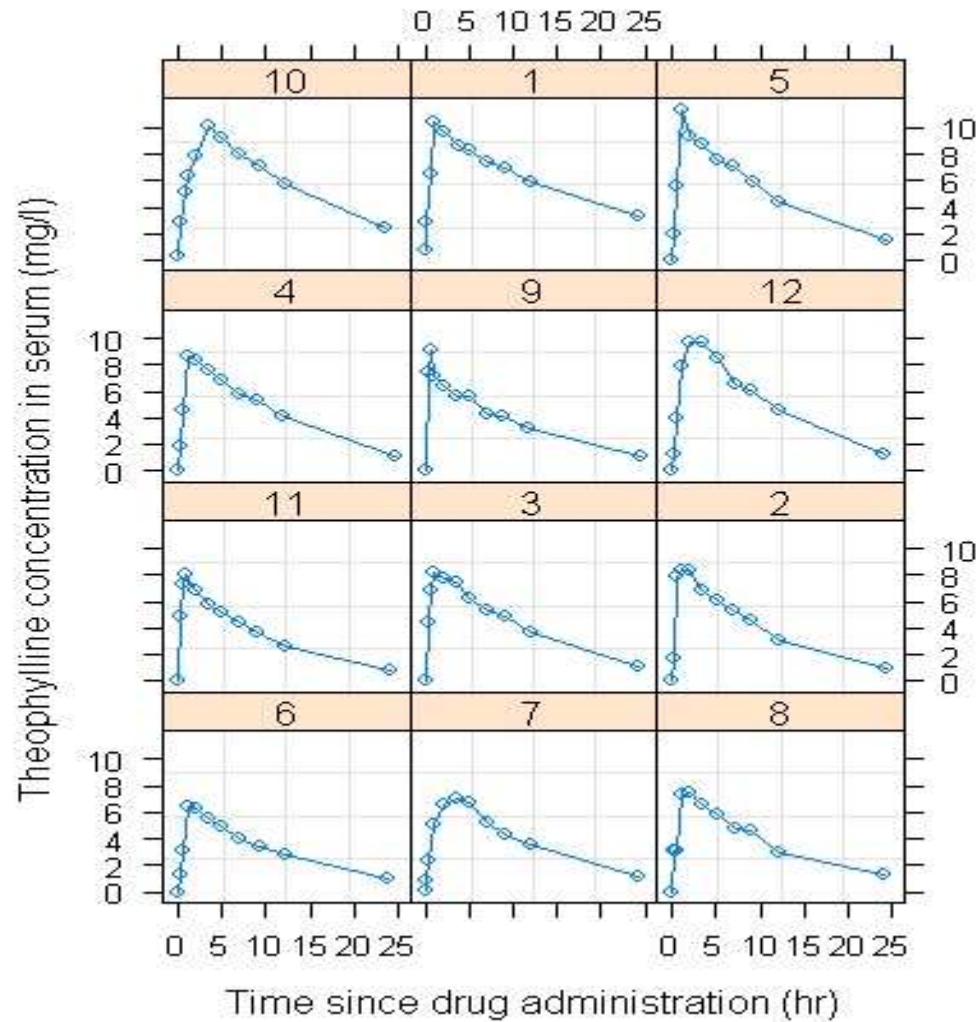
Compartment model for Theophylline data



$$c_t = \frac{DK_eK_a}{Cl(K_a - K_e)} (e^{-K_e t} - e^{-K_a t})$$

- D : Dose
 K_a : Absorption rate
 K_e : Elimination rate
 Cl : Clearance

Theophylline serum concentrations Boeckmann et al (1994)





Maximum likelihood estimation

Maximum likelihood estimation in non-linear mixed effects models



- Non-linear mixed effect model:

$$\underline{Y} = h(\underline{\beta}, \underline{b}) + \underline{\varepsilon}$$

where \underline{Y} is the observation vector, h is the mean function, possible nonlinear in the fixed parameter vector, $\underline{\beta}$, and the random effect vector, \underline{b} .

The random effects are assumed to follow a multivariate normal distribution, $\underline{b} \sim N(\underline{0}, \underline{\Omega})$, independent of the residual error, $\underline{\varepsilon}$, also assumed to follow a multivariate normal distribution, $\underline{\varepsilon} \sim N(\underline{0}, \underline{\Sigma})$

Maximum likelihood estimation in non-linear mixed effects models



- Likelihood function:

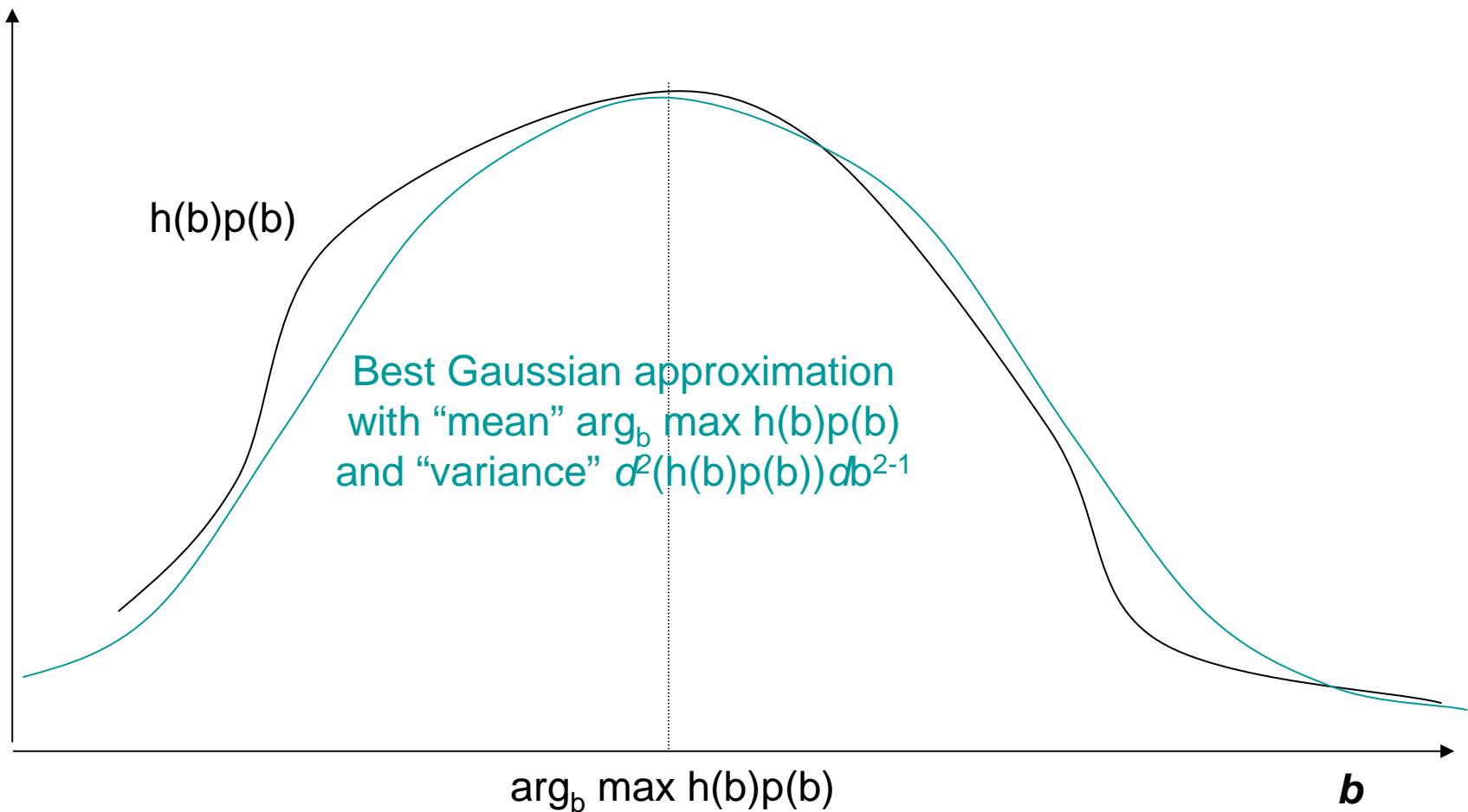
$$\begin{aligned} L(\underline{Y}, \underline{\beta}, \Omega, \Sigma) &= \int p(\underline{Y}, \underline{\beta}, \underline{b}, \Omega, \Sigma) d\underline{b} \\ &= \int p(\underline{Y}, \underline{\beta}, \Sigma | \underline{b}) p(\underline{b}, \Omega) d\underline{b} \end{aligned}$$

where p is the density function for the relevant normal distributions

- MLE: parameter values of $\underline{\beta}$, Ω , Σ that maximize the likelihood function

The final integral cannot be solved explicitly, hence approximations is needed, e.g. first order approximation, Laplace or AGQ.

Laplace approximation to $\int h(b)p(b)db$



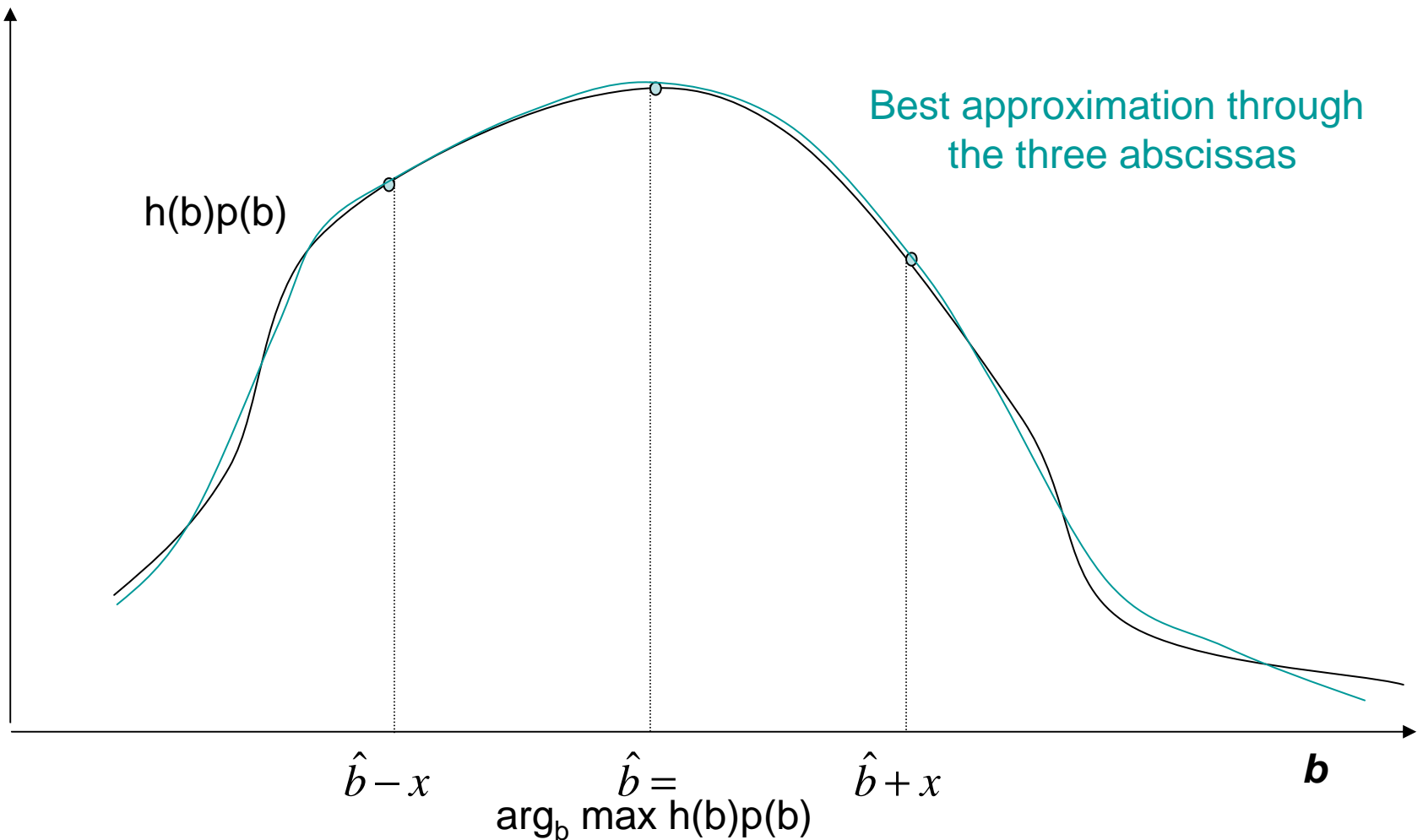
Laplace approximation to $\int h(b) p(b) db$



- The integral is approximated by the exact integral of the approximation
- The approximation is exact when the random effects occur linearly in the mean function
- The approximation works well if $h(b)p(b)$ is approximately quadratic in b

Adaptive Gaussian Quadrature of

$$\int h(b)p(b)db$$



Adaptive Gaussian Quadrature of

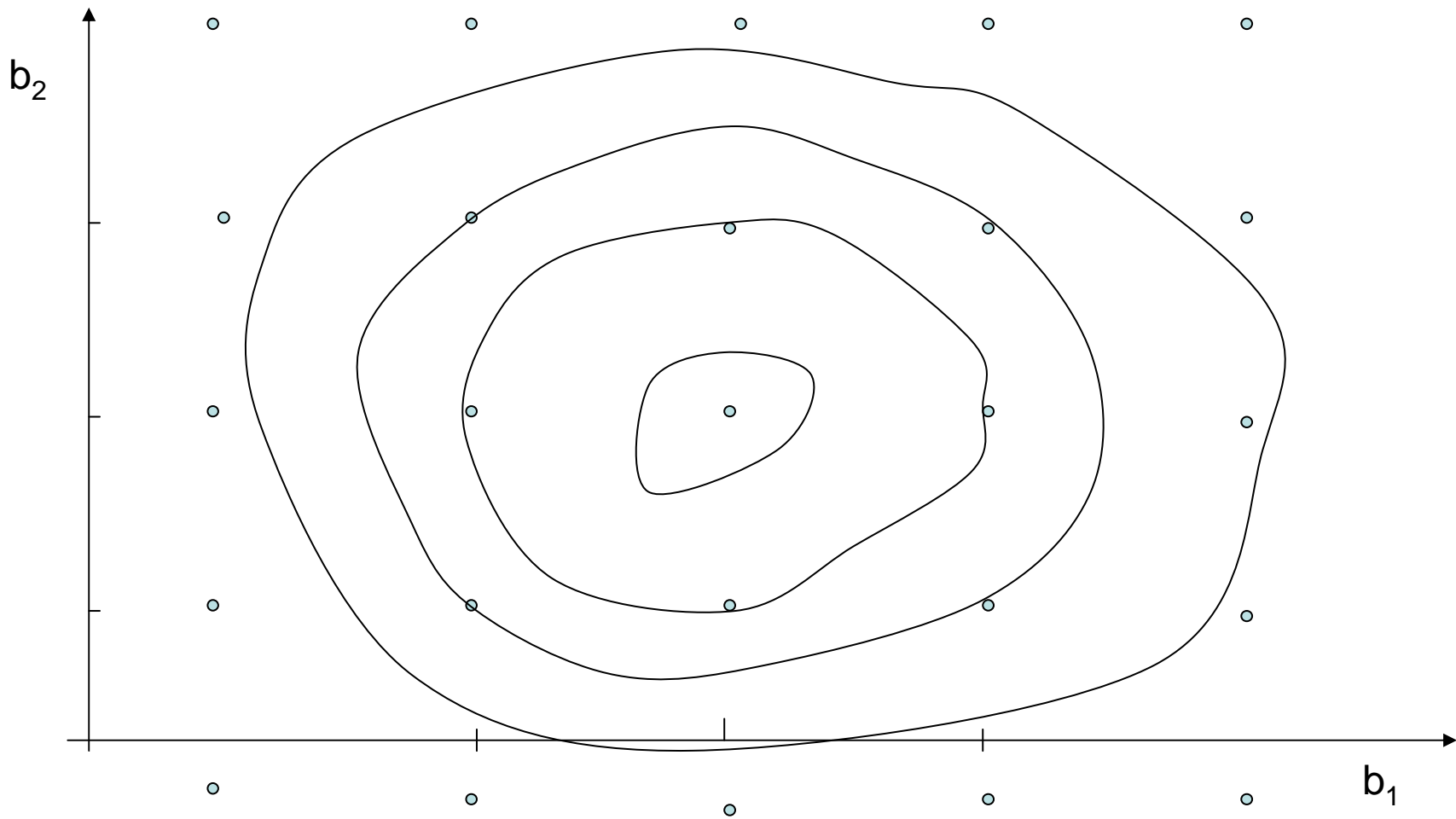
$$\int h(b)p(b)db$$


- The integral is approximated by a weighted sum:

$$\int h(b)p(b)db = \sum_{i=1}^n h(x_i)p(x_i)w_i$$

- Where the x_i , $i=1, \dots, n$ are the abscissas and w_i the weight functions. Adaptive Gauss Hermite Quadrature have abscissas equal to roots of Hermite polynomials
- The approximation is exact when $h(b)p(b)$ is a polynomial of degree $2n-1$ (or less)

Adaptive Gaussian Quadrature, with 2-dim b
and 5 abscissas, of $\int h(b)p(b)db$ (product rule)



AGQ for multivariate random effect



- The number of function evaluations grow exponentially with dimension d of b :

	2	3	4	5	10
3	9	27	81	243	59049
7	49	343	2401	16807	$0.2 \cdot 10^9$
13	169	2197	28561	371293	$138 \cdot 10^9$

- AGQ becomes heavy computationally
- However, not all evaluation points are important for precision

Smolyak's rule



- Old news: Smolyak (1963)
- We follow the tensor product construction by Gerstner and Griebel (2003)

- Example:

Smolyak's level 2 rule for d-dimensions:

$$\int h(b) e^{-1/2 b^2} db \approx \sum_{i=1}^d \left\{ h(-\sqrt{3}e_i) + h(\sqrt{3}e_i) \right\} + \left(1 - \frac{d}{3}\right) h(0)$$

- Weights equals 1/6 for the 2d axial points and 1-1/3 for center
- Exact for polynomials of degree 3 or less

Function evaluation with multivariate parameter



- Number of function evaluations reduced significantly:

	2	3	4	5	10
3	9 5	27 7	81 9	243 11	59049 21
7	49 7	343 31	2401 49	16807 71	0.2*10 ⁹ 241
13	169 45	2197 105	28561 201	371293 341	138*10 ⁹ 1981



Examples

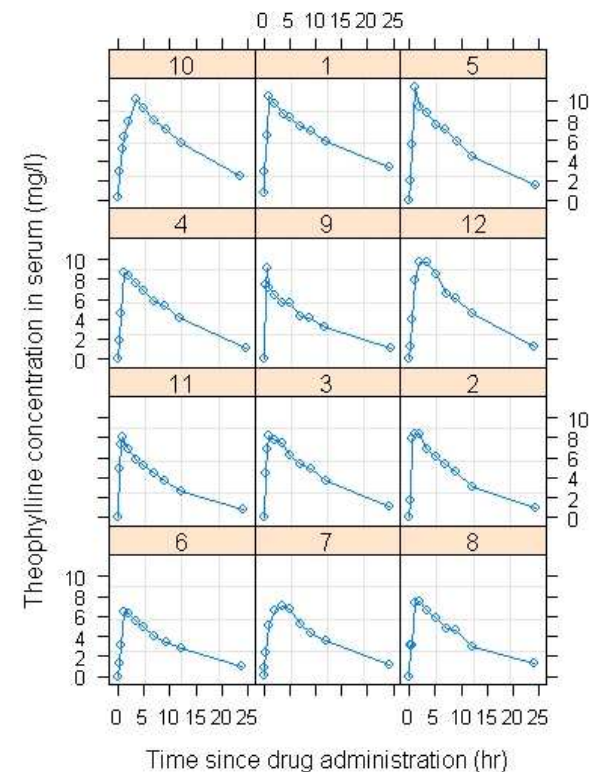
Theophylline serum concentrations



- Model:

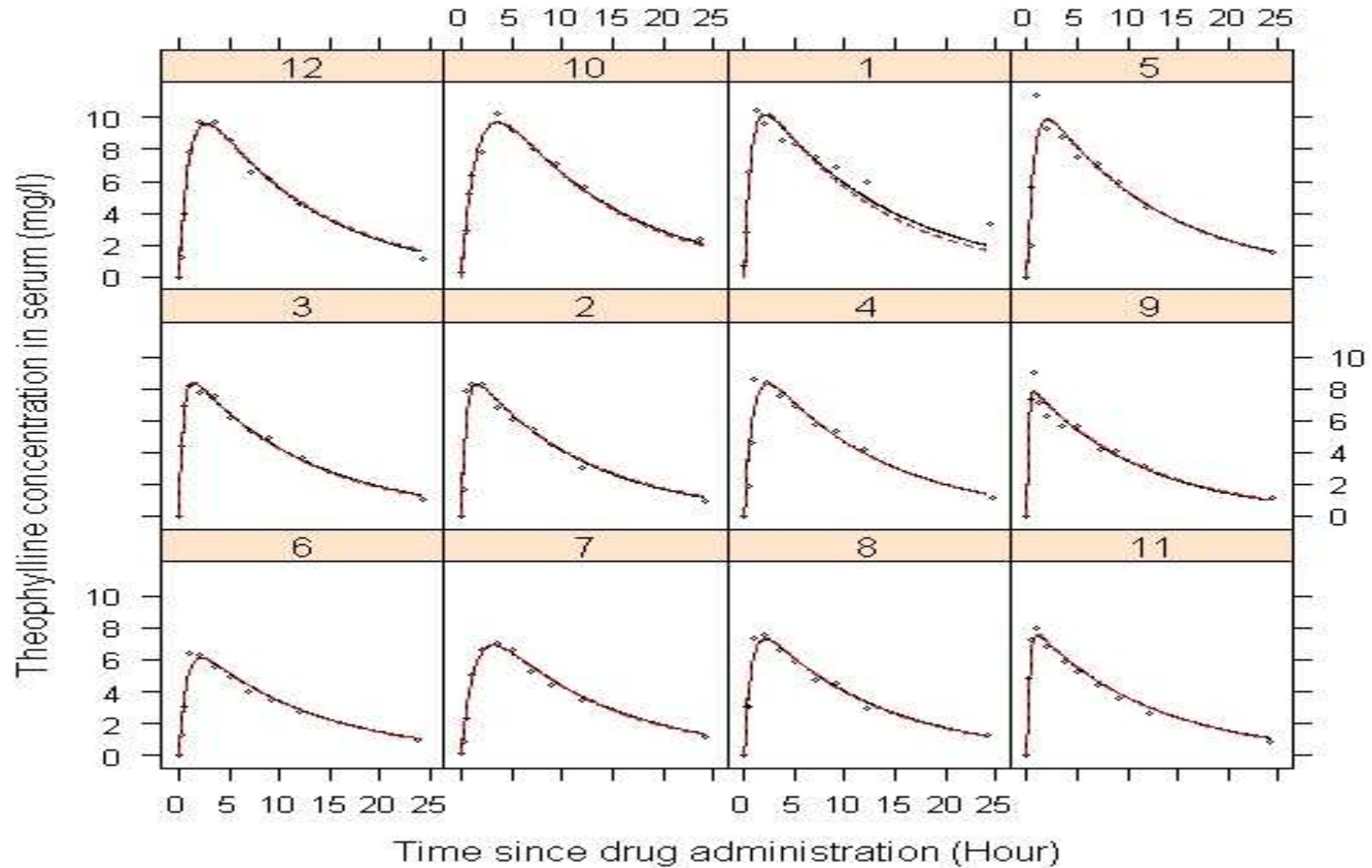
$$c_t = \frac{DK_eK_a}{Cl(K_a - K_e)}(e^{-K_e t} - e^{-K_a t})$$

- Absorption rate, elimination rate and clearance are random
- Smolyak algorithm converged with non-singular covariance matrix of parameter estimates
- Smaller (slightly) residual variance compared to Laplace



Theophylline data

- observed and predicted profiles



Indomethacin data

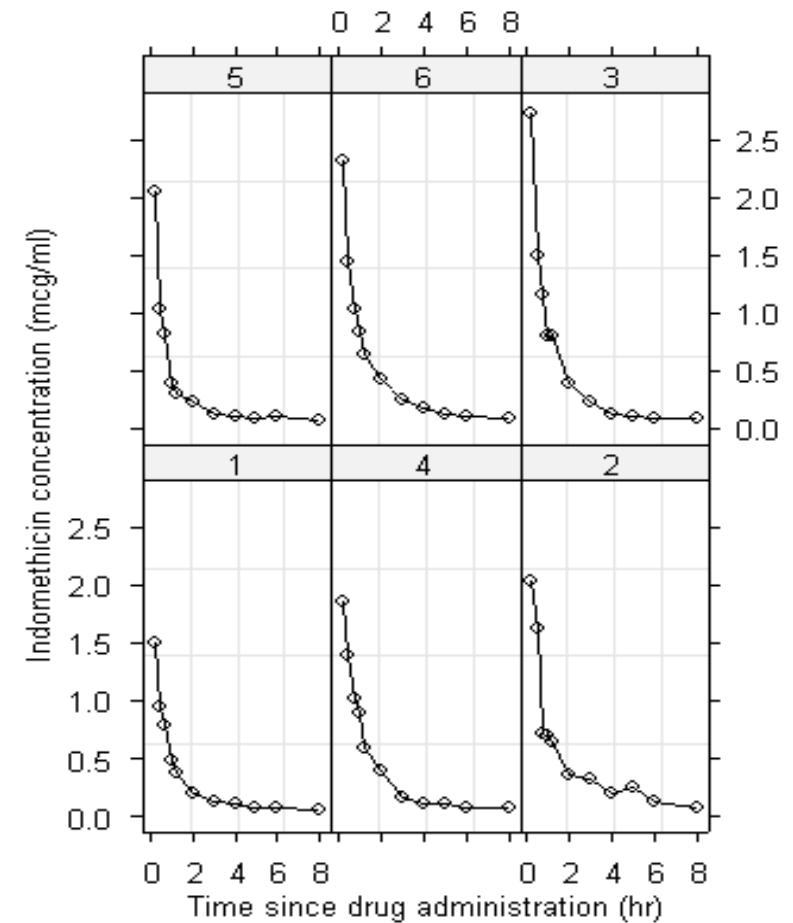
- observed and predicted profiles



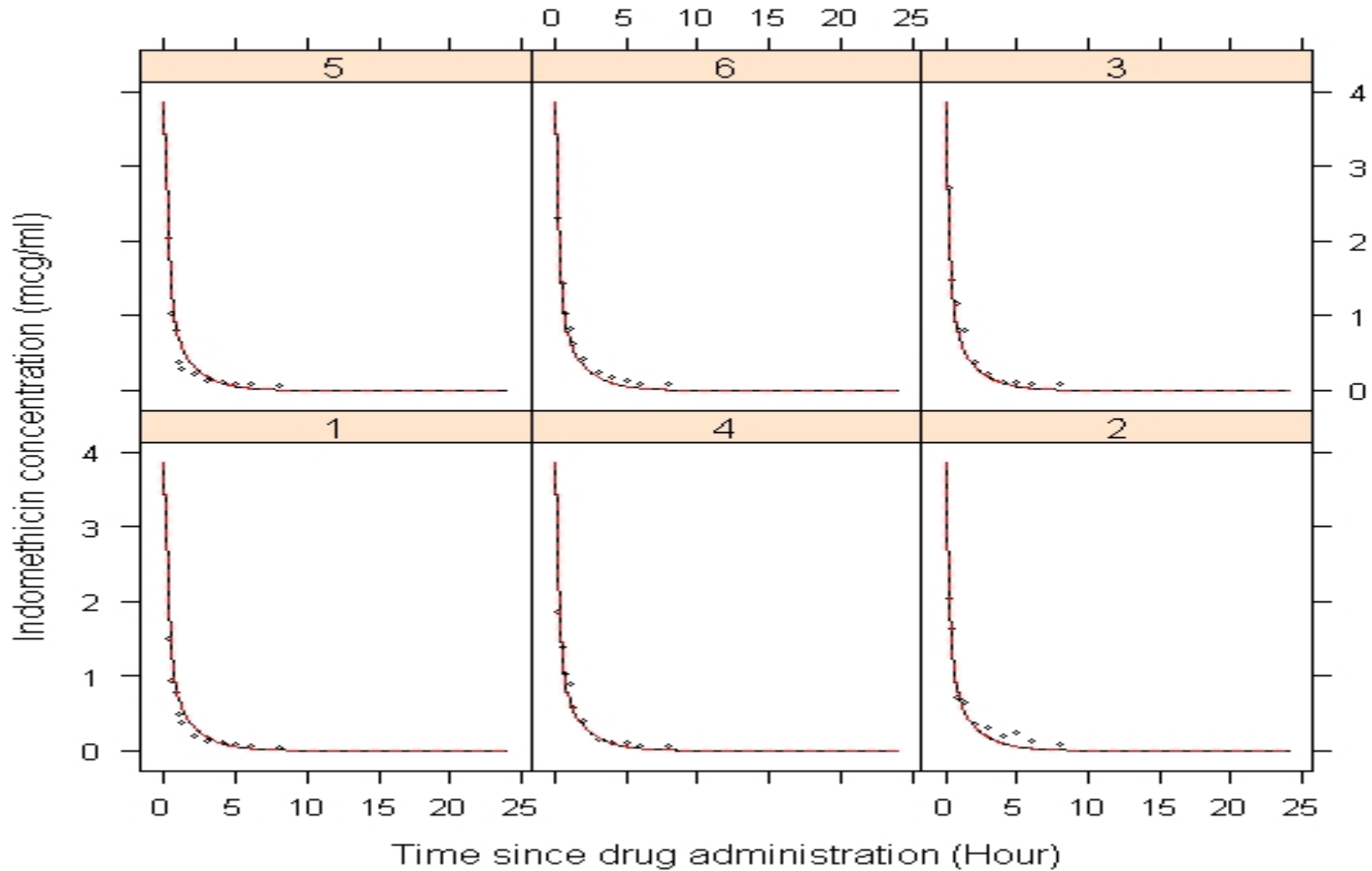
- Model:

$$c_t = A_1 \exp(-rc_1 \cdot time) + B_1 \exp(-rc_2 \cdot time)$$

- A_1 , $\log(rc_1)$ and B_1 are random
- Smolyak algorithm converged with nonsingular covariance matrix



Indomethacin data





Simulations

Simulation: First-order open compartment model (Theophylline data)



- 500 simulations
- 12 subjects
- 10 concentrations at
 $t=0, 0.25, 0.5, 1, 2, 3.5, 7, 9, 12, 24\text{h}$
- Dose=4.5mg
- $IKa = 0.5, ICl=-3, IKe = -2.5$
- IKa and ICl are allowed to vary randomly, $b_i \sim N(0, \psi)$, where ψ is diagonal, 0.36 and 0.04 respectively

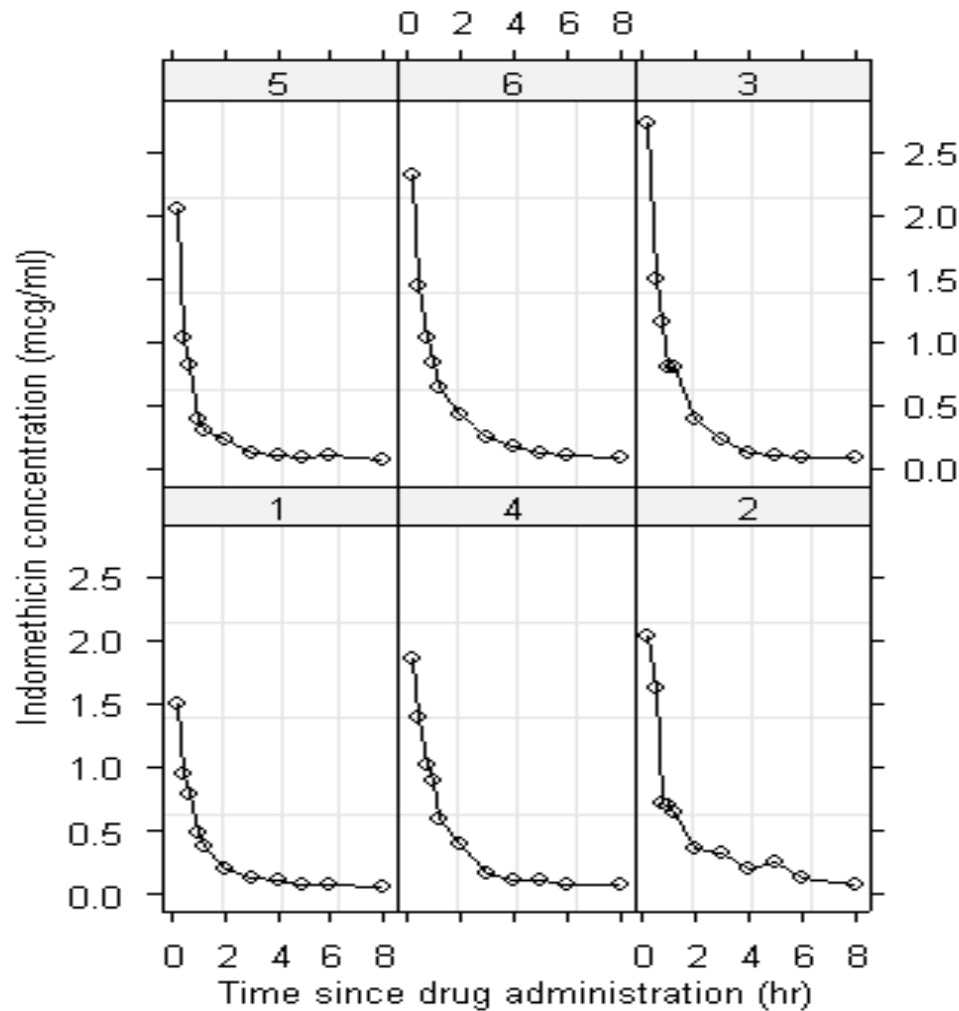
Simulation results (Theophylline data)



500 simulations based on Theophylline data

	IKe	IKa	ICl	psi.IKa	psi.ICl	sigma
True Value	-2.5	0.5	-3	0.6	0.2	0.7
NLME (starting values)	-2.4940	0.4792	-3.0040	0.5799	0.1928	0.6993
sd	0.0403	0.1174	0.0405	0.0853	0.0300	0.0296
Smolyak	-2.5010	0.5057	-3.0010	0.5716	0.1935	0.6929
sd	0.0407	0.1210	0.0410	0.1087	0.0313	0.0361
AGQ	-2.5010	0.5004	-3.0010	0.5893	0.1952	0.6984
sd	0.0404	0.1196	0.0406	0.0889	0.0304	0.0296

Serum Concentration of Indomethecin



Simulation: Biexponential model (Indomethacin data)



- 1000 simulations
- 6 subjects
- 11 concentrations at
 $t=0.25, 0.5, 0.75, 1, 1.25, 2, 3, 4, 5, 6, 8\text{h}$
- $\alpha = 2.8, \text{IKe}1 = 0.7, \beta = 0.4, \text{IKe}2 = -1.5$
- α and $\text{IKe}1$ are allowed to vary randomly, $b_i \sim N(0, \psi)$, where ψ is diagonal, 0.36 and 0.04 respectively

Simulation results (Indomethecin data)



1000 simulation based on Indomethecin data

	A1	Irc1	A2	Irc2	psiA1	psilrc1	sigma
True value	2.8	0.7	0.4	-1.5	0.6	0.2	0.09
Starting values (NLME)	2.806	0.6644	0.3637	-1.6967	0.4975	0.1636	0.08772
sd	0.2701	0.1242	0.0953	0.3856	0.1859	0.0700	0.0089
Smolyak	2.814	0.7122	0.4169	-1.5432	0.5151	0.1920	0.08661
sd	0.2690	0.1335	0.11547	0.35370	0.1712	0.06829	0.008654
AGQ	2.798	0.7039	0.4111	-1.5572	0.4738	0.1817	0.08758
sd	0.2701	0.1311	0.11434	0.35904	0.1828	0.06894	0.008803



Conclusion

Conclusion



- AGQ precise method for MLE in nonlinear mixed effects models
- For multivariate parameters AGQ becomes difficult
- Smolyaks rule reduces the number of function evaluations significant
- The method works well on the examples aswell as in the simulation study

Thank you!



- References:
 - Pinheiro, J.C. and Bates, D.M.: Approximations to the log-likelihood function in the nonlinear mixed-effects model. *Journal of Computational and Graphical Statistics*, Volume 4, Number 1, pages 12-35 (1995)
 - Boeckmann, A. J., Sheiner, L. B. and Beal, S. L. (1994), *NONMEM Users Guide: Part V*, NONMEM Project Group, University of California, San Francisco.
 - Smolyak, S.A.: Quadrature and interpolation formulas for tensor products of certain classes of functions, *Dokl.Akad.Nauk SSSR* 4 (1963) 240-243
 - Gerstner, T. and Griebel, M.: Dimension-Adaptive Tensor-Product Quadrature, *Computing* 71, 65-87 (2003)