

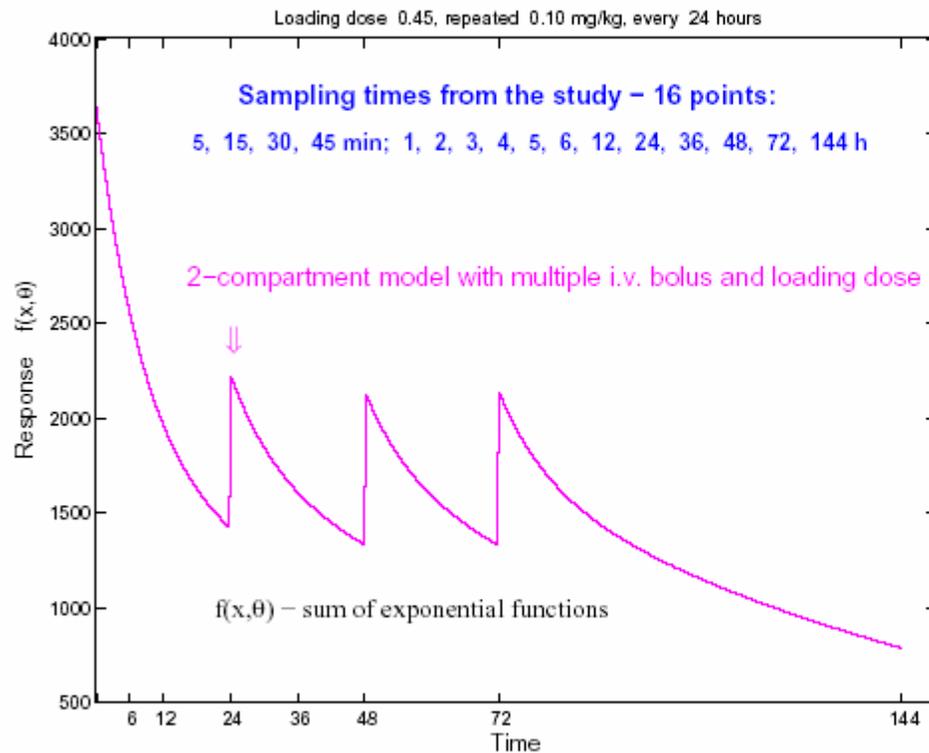
# Estimation of Population PK Measures: Selection of Sampling Grids

Valerii Fedorov, Sergei Leonov  
Research Statistics Unit, GlaxoSmithKline

# Outline

- Motivation: earlier study, model-based optimal population designs
- Model-based vs empirical (non-compartmental) approaches
- Sampling grids
- Splitting sampling grids
- AUC estimation: mean squared error for empirical approach
- Cost-based designs

# Earlier study: Gagnon, Leonov (2005)



## Questions

1. How many samples to take?
2. At which times?

“Better” sampling scheme  $\Leftrightarrow$  better precision of parameter estimates

# Information matrix, alternative normalizations

$\mu(\mathbf{x}, \boldsymbol{\vartheta})$  - information matrix for observations  $\mathbf{Y}$  at sequence  $\mathbf{x}$ ,

$\mathbf{x} = (t_1, t_2, \dots, t_k)$  - sampling times,  $\mathbf{Y} = [y(t_1), \dots, y(t_k)]^T$

If  $n_i$  patients on sequence  $\mathbf{x}_i$ ,  $\sum_i n_i = N \implies \mathbf{M}_N(\boldsymbol{\vartheta}) = \sum_i n_i \boldsymbol{\mu}(\mathbf{x}_i, \boldsymbol{\vartheta})$ .

1. Standard normalization:  $N$  - available resource,

$$\mathbf{M}(\xi, \boldsymbol{\vartheta}) = \sum_{i=1}^n p_i \boldsymbol{\mu}(\mathbf{x}_i, \boldsymbol{\vartheta}), \quad \xi = \{(\mathbf{x}_i, p_i), p_i = \frac{n_i}{N}, \mathbf{x}_i \in \mathcal{X}\}$$

$\xi$  - normalized (continuous) design,  $\mathcal{X}$  - design region

Key: derive (approximate)  $\boldsymbol{\mu}(\mathbf{x}, \boldsymbol{\vartheta})$  for population compartmental models

*Fedorov, Gagnon, Leonov (2002), Gagnon, Leonov (2005), Retout, Mentré (2003)*

# Information matrix, cost-based designs

2. Measurements at  $\mathbf{x}_i$  associated with cost  $c(\mathbf{x}_i)$ ,

$$\sum_i n_i c(\mathbf{x}_i) \leq \mathcal{C} \implies \mathbf{M}_{\mathcal{C}}(\boldsymbol{\vartheta}) = \sum_{i=1}^n \frac{n_i}{\mathcal{C}} \boldsymbol{\mu}(\mathbf{x}_i, \boldsymbol{\vartheta}) = \sum_i \tilde{p}_i \tilde{\boldsymbol{\mu}}(\mathbf{x}_i, \boldsymbol{\vartheta}),$$

Information matrix normalized by total cost  $\mathcal{C}$ ,

$$\tilde{p}_i = n_i c(\mathbf{x}_i) / \mathcal{C}; \quad \tilde{\boldsymbol{\mu}}(\mathbf{x}_i, \boldsymbol{\vartheta}) = \boldsymbol{\mu}(\mathbf{x}_i, \boldsymbol{\vartheta}) / c(\mathbf{x}_i) \implies \text{same framework,}$$

standard numerical algorithms

Costs in design problems: Elfving (1952), Cook, Fedorov (1995),

Mentré, Mallet, Baccar (1997), Fedorov, Gagnon, Leonov (2002)

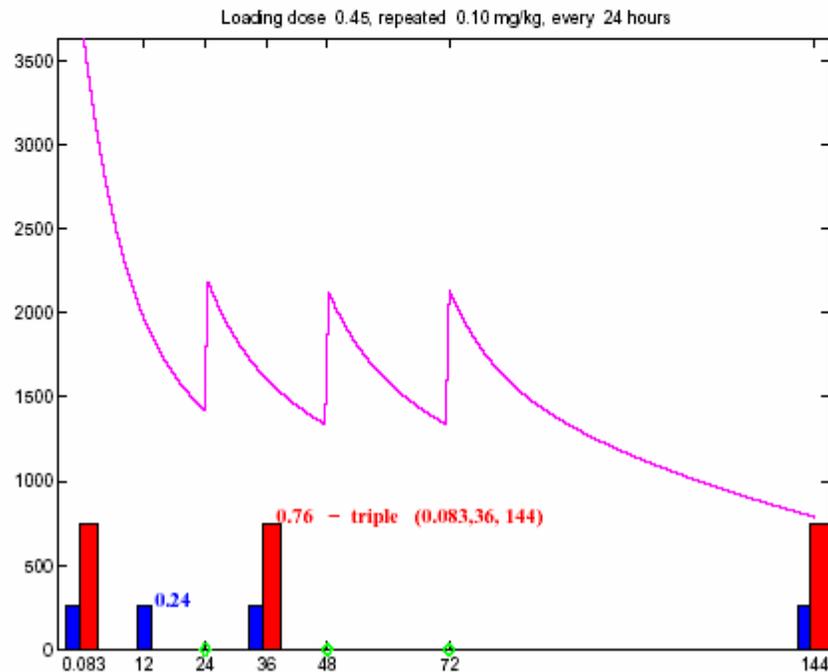
# Sampling schemes, earlier results

- Constructed locally D-optimal designs
- No costs: the more samples, the better
  - number of samples may be reduced without significant loss of precision
- Costs introduced (cost of analyzing sample  $c_s$  / cost of enrolling patient  $c_p$ ):
  - sequences with smaller number of samples may become optimal
  - optimal: combination of sequences (different schemes for different cohorts)
- Software developed: (1) Matlab: stand-alone, GUI-based  
(2) SAS (*Fedorov et al. (2006)*)

## Earlier study: cost-based design (compartmental model)

Allowed: 3-,4- and 5-sample sequences (candidate times - from original study)

Optimal population design: two sequences (3-sample, 76% of patients; 4-sample, 24%)



# Practical issues

- Often interested in certain PK measures (not parameters):  
area under the curve ( $AUC$ ), maximal concentration ( $C_{max}$ ),  
time to maximal concentration ( $T_{max}$ )  
Optimal design for PK measures: *Atkinson et al. (1993)*
- Regulatory agencies require non-compartmental analysis



We compare two approaches:

- model-based (compartmental) as a benchmark
- empirical (non-compartmental or nonparametric)

# General model

$$y_{ji} = f(x_{ji}, \theta_j) + \varepsilon_{ji}, \quad i = 1, \dots, n_j, \quad j = 1, \dots, N,$$

$x_{ji}$ :  $i$ -th sampling time for patient  $j$ ,  $x_{ji} \in [a, b]$ ,

$y_{ji}$ : measurement at time  $x_{ji}$  for patient  $j$ ;

$f(x, \theta)$ : response function which depends on time  $x$  and parameters  $\theta$ ,

$\theta_j$ : parameters of patient  $j$ ,  $\theta_j \sim \mathcal{N}(\theta^0, \mathbf{U})$  (population distribution)

$N = \#\{\text{enrolled patients}\}$ ,  $n_j = \#\{\text{sampling times for patient } j\}$ ,

$\varepsilon_{ji}$ : measurement errors  $\sim \mathcal{N}(0, \sigma^2)$ .

Simplest case: same sampling times for all patients:  $x_{ji} \equiv x_i$ ,  $n_j \equiv 2n$ .

## One-compartment model (simulations)

$$f(x, \boldsymbol{\theta}) = \frac{K_a}{V(K_a - K_{el})} (e^{-K_{el}x} - e^{-K_a x}), \quad \boldsymbol{\theta} = (K_a, K_{el}, V)^T,$$

$K_a, K_{el}$  - absorption and elimination rate constants;

$V$  - volume of distribution;  $x \in [0, 1]$  (normalized time scale),

$$AUC = \int_0^1 f(x, \boldsymbol{\theta}^0) dx, \quad T_{max} = \frac{\ln(K_a/K_{el})}{K_a - K_{el}}, \quad C_{max} = \frac{1}{V} \left( \frac{K_a}{K_{el}} \right)^{-K_{el}/(K_a - K_{el})}$$

Mean vector  $\boldsymbol{\theta}^0 = (46, 6, 0.1)$  (mimics data from an earlier clinical study)

Variance parameters:  $\sigma = 0.5$ ,  $\mathbf{U} = Var(\boldsymbol{\theta}) = \text{diag}(s_i^2)$  with  $s_i = 0.15 \theta_i$ .

# Model-based (compartmental) approach

**Method 1:** start with individual estimates of PK measures

- For each patient, parameters  $\bar{\theta}_j$  are estimated (MLE, NLS), then

$$AUC_j = \int_a^b f(x, \bar{\theta}_j) dx, \quad C_{max,j} = \max_x f(x, \bar{\theta}_j), \quad T_{max,j} = \arg \max_x f(x, \bar{\theta}_j).$$

- Individual estimates are averaged across population:

$$AUC_{M1} = \frac{1}{N} \sum_{j=1}^N AUC_j, \quad \text{same for } T_{max,M1} \text{ and } C_{max,M1}.$$

**Method 2:** average individual parameter estimates  $\hat{\theta} = \sum_j \bar{\theta}_j / N$ ,

- Use  $\hat{\theta}$  to obtain population estimates

$$AUC_{M2} = \int_a^b f(x, \hat{\theta}) dx, \quad C_{max,M2} = \max_x f(x, \hat{\theta}), \quad T_{max,M2} = \arg \max_x f(x, \hat{\theta}).$$

# Empirical (non-compartmental) approach

**Method 1:** for each patient, get individual  $T_{max,j}$ ,  $C_{max,j}$ ,  $AUC_j$

- Average individual estimates to obtain population estimates

$$T_{max,E1} = \frac{1}{N} \sum_{j=1}^N T_{max,j}, \quad \text{same for } C_{max,E1} \text{ and } AUC_{E1}$$

**Sparse sampling:** method 1 cannot be used

**Method 2:** responses at each time point are averaged across patients,

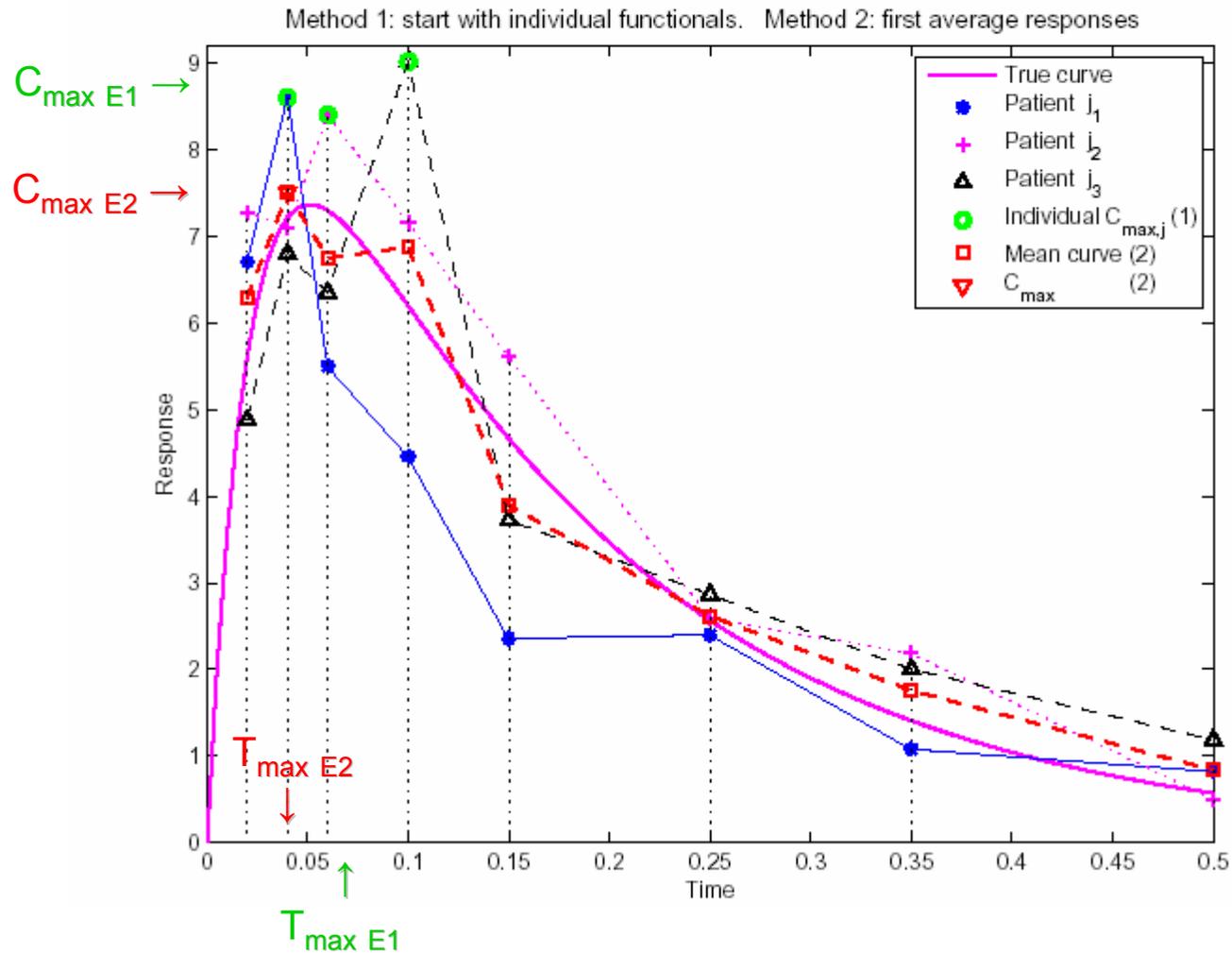
$$\hat{f}_i = \frac{1}{N} \sum_{j=1}^N y_{ij}, \quad i = 0, \dots, n.$$

- Get estimates  $T_{max,E2}$ ,  $C_{max,E2}$  for 'population curve'  $\{\hat{f}_i\}$ ,

use numerical integration to estimate  $AUC_{E2}$ :

$$AUC_{E2} = \sum_{i=1}^{2n} \int_{x_{i-1}}^{x_i} g(x, \mathbf{a}_i) dx \quad (g - \text{interpolant passing through } \hat{f}_{i-1} \text{ and } \hat{f}_i)$$

# Averaging methods, population PK measures



# Numerical integration

(1) Trapezoidal rule :  $I_i = \int_{x_{i-1}}^{x_i} g(x, \mathbf{a}_i) dx = \Delta x_i \frac{\hat{f}_{i-1} + \hat{f}_i}{2}$ ,  $\Delta x_i = x_i - x_{i-1}$

(2) Log-trapezoidal rule :  $I_i = \Delta x_i \frac{\hat{f}_i - \hat{f}_{i-1}}{\log(\hat{f}_i / \hat{f}_{i-1})}$  (exact for exponential)

(3) Hybrid method: use (1) before  $T_{max}$  and (2) - after  $T_{max}$  (descending portion)

(4) Cubic splines: piecewise cubic polynomial (join in the knots  $\{x_i\}$ , obeying continuity conditions for  $f$  and its first two derivatives)

# Sampling schemes

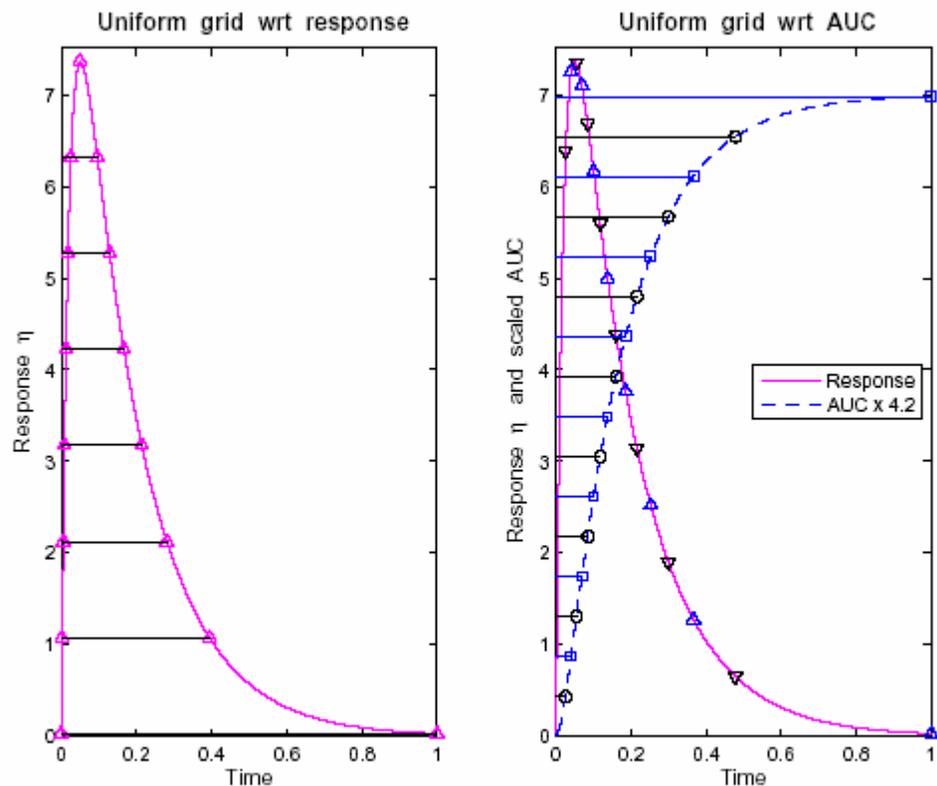
PK studies: more samples at the left end (immediately after administering the drug), then more sparse sampling (after 'anticipated'  $T_{max}$ )

## Alternative sampling schemes

- Take a uniform grid on the Y-axis with respect to values of response and project points on the response curve to the X-axis (next slide, left panel)
- Take a uniform grid on the Y-axis with respect to values of  $AUC$  (next slide, right panel)

Simulations: 16 sampling times,  $N=20$  (patients)

# Sampling schemes (cont.)

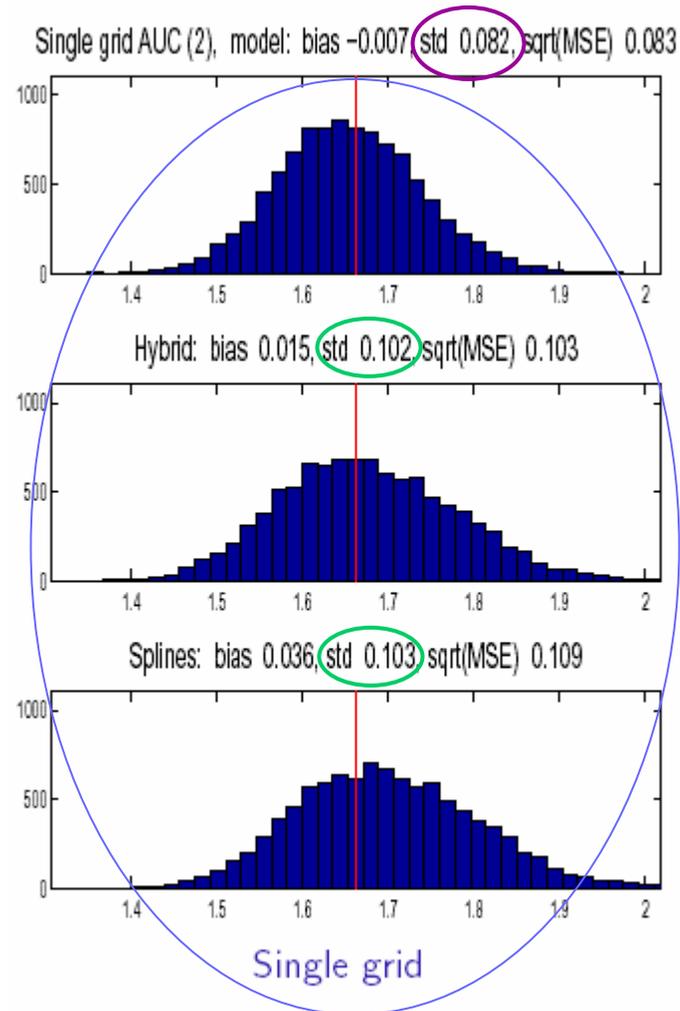


Uniform grid with respect to values of response (left panel) and AUC(right panel).

Black inverted triangles: odd samples on mean response curve; black circles: odd on AUC curve.

Blue triangles: even samples on mean response curve; blue squares: even on AUC curve.

Method 2,  $AUC$ :  $AUC_{true}=1.662$

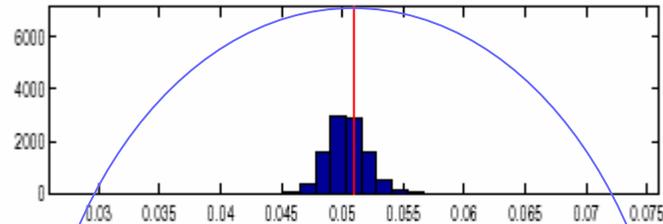


Method 2: first average responses at each  $x_i$

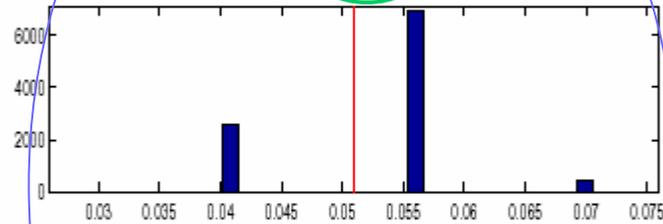
Upper - model-based, middle-hybrid, lower-splines

# Method 2, $T_{max}$ : true $T_{max}=0.051$

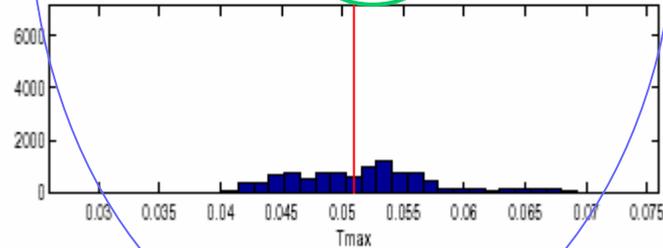
Single grid  $T_{max}^{(2)}$ , model: bias  $-0.0006$ , std  $0.0016$ , sqrt(MSE)  $0.0017$



Hybrid: bias  $0.0015$ , std  $0.0072$ , sqrt(MSE)  $0.0074$



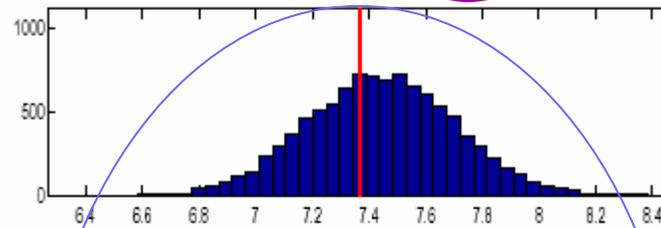
Splines: bias  $0.0008$ , std  $0.0058$ , sqrt(MSE)  $0.0059$



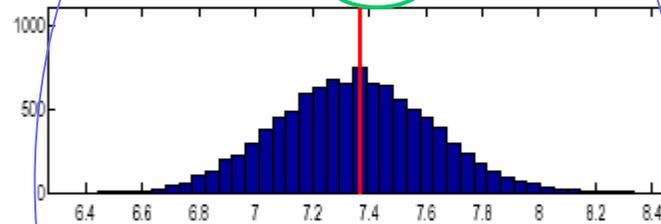
Single grid

# Method 2, $C_{max}$ : true $C_{max}=7.367$

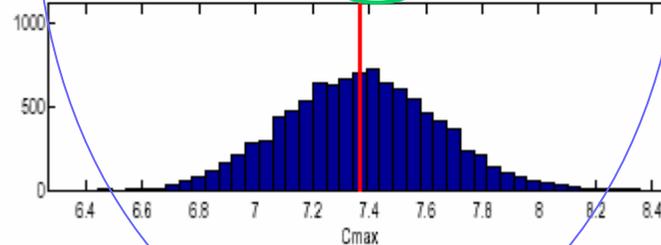
Single grid  $C_{max}$  (2), model: bias 0.076, std 0.259, sqrt(MSE) 0.270



Hybrid: bias -0.018, std 0.270, sqrt(MSE) 0.271



Splines: bias 0.003, std 0.270, sqrt(MSE) 0.270



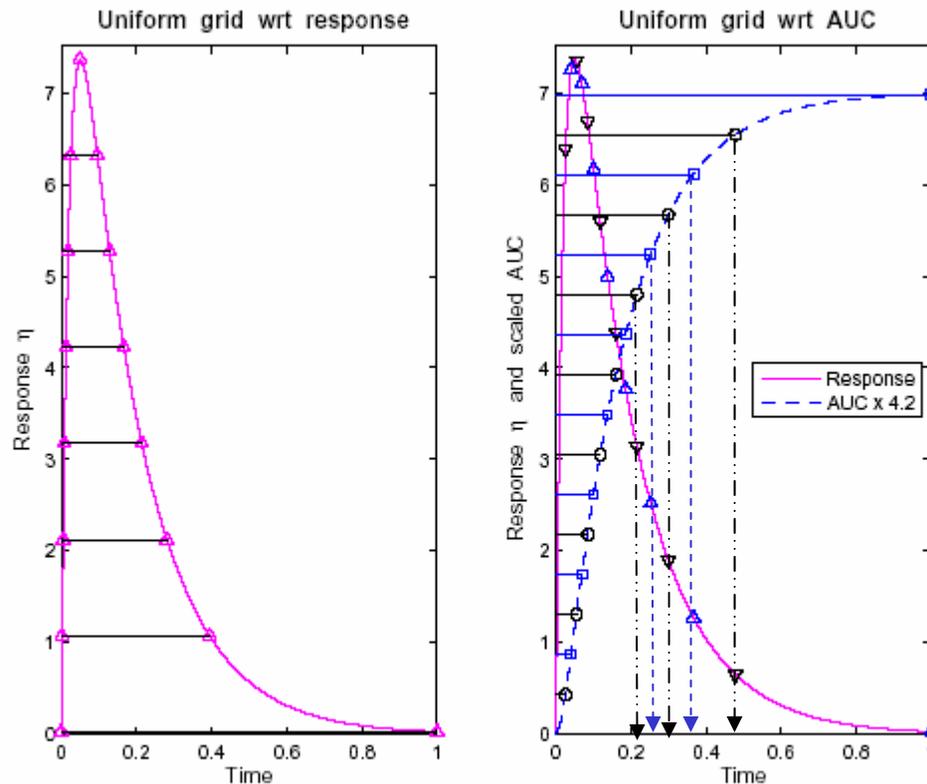
Single grid

## Splitting sampling grids (reducing sampling density)

- Let  $\{x_i, i = 1, \dots, 2n\}$  be a single grid with  $2n$  sampling points,
- Take samples at  $\{x_{2i-1}, i = 1, \dots, n\}$  for  $N/2$  subjects (black inverted triangles, p.16),
- Take samples at  $\{x_{2i}, i = 1, \dots, n\}$  for the rest half (blue triangles, p.16),
- Empirical estimate of  $AUC$ , method 2: average responses in two series (half-cohorts) separately, then combine two series and get  $AUC_{E2}$ .

Total number of samples is reduced by half - back to histograms

# Sampling schemes (cont.)

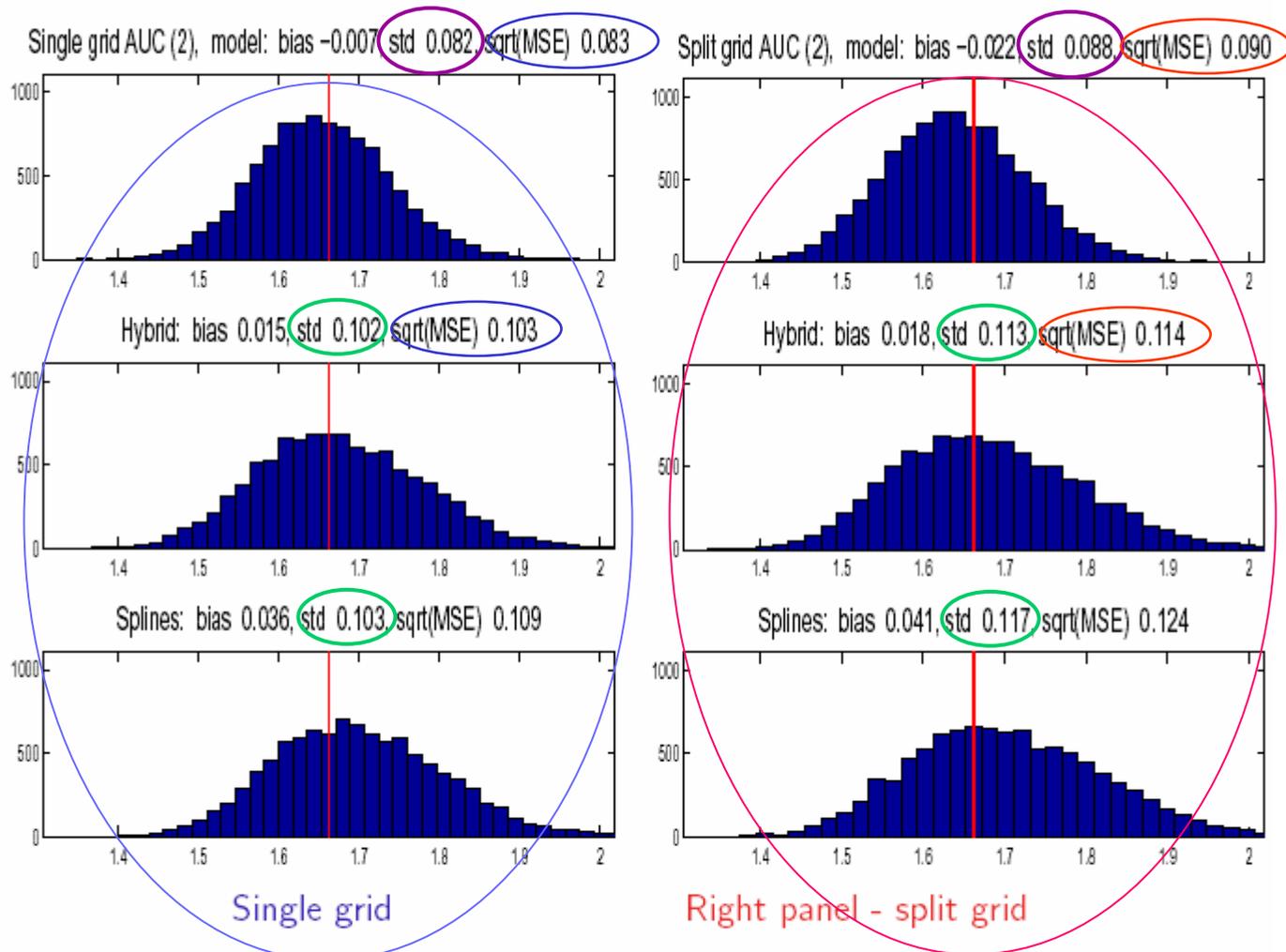


Uniform grid with respect to values of response (left panel) and AUC(right panel).

Black inverted triangles: odd samples on mean response curve; black circles: odd on AUC curve.

Blue triangles: even samples on mean response curve; blue squares: even on AUC curve.

Method 2,  $AUC$ :  $AUC_{true}=1.662$

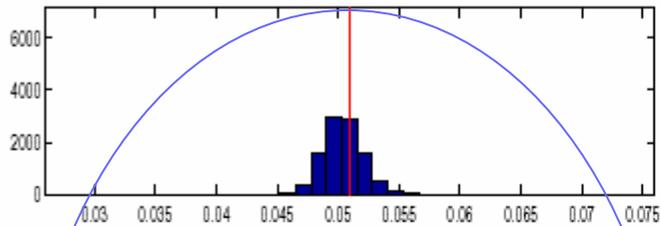


Method 2: first average responses at each  $x_i$

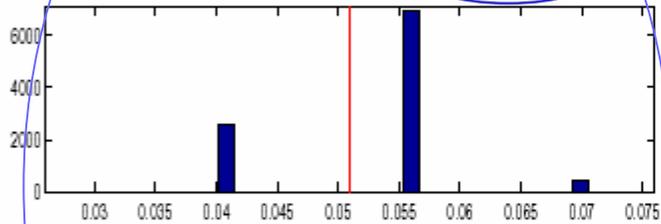
Upper - model-based, middle-hybrid, lower-splines

# Method 2, $T_{max}$ : true $T_{max}=0.051$

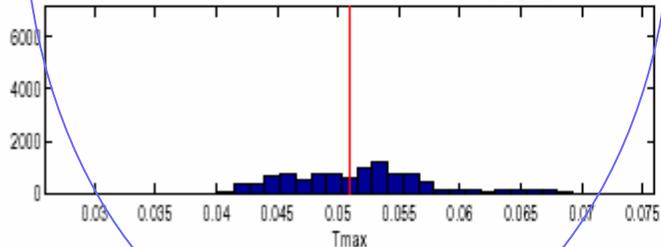
Single grid  $T_{max}$  (2), model: bias -0.0006, std 0.0016,  $\sqrt{\text{MSE}}$  0.0017



Hybrid: bias 0.0015, std 0.0072,  $\sqrt{\text{MSE}}$  0.0074

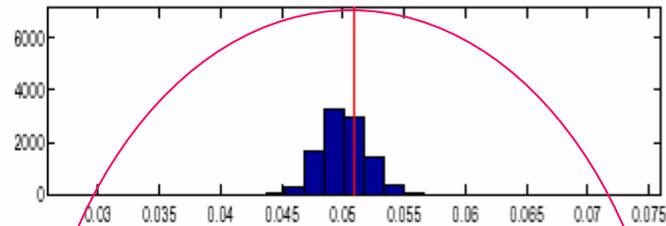


Splines: bias 0.0008, std 0.0058,  $\sqrt{\text{MSE}}$  0.0059

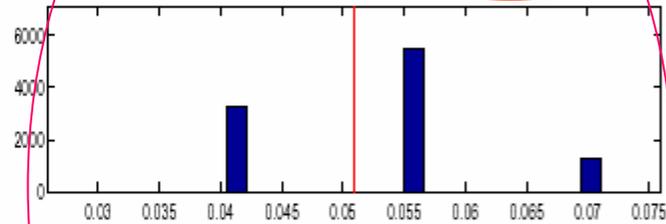


Single grid

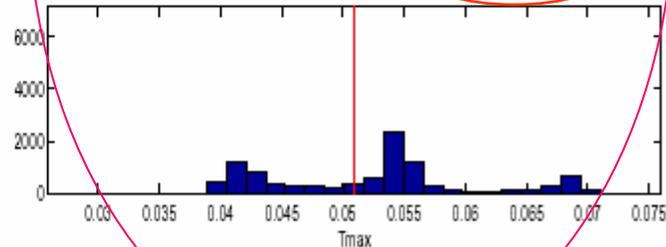
Split grid  $T_{max}$  (2), model: bias -0.0008, std 0.0018,  $\sqrt{\text{MSE}}$  0.0020



Hybrid: bias 0.0017, std 0.0092,  $\sqrt{\text{MSE}}$  0.0093



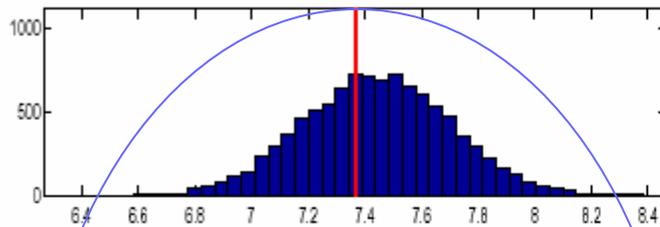
Splines: bias 0.0015, std 0.0085,  $\sqrt{\text{MSE}}$  0.0086



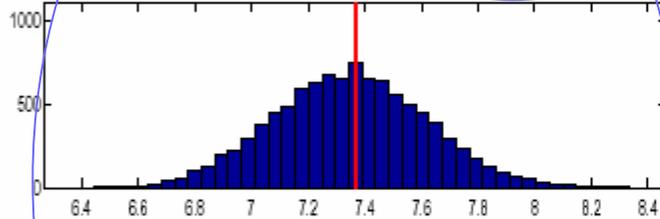
Right panel - split grid

# Method 2, $C_{max}$ : true $C_{max}=7.367$

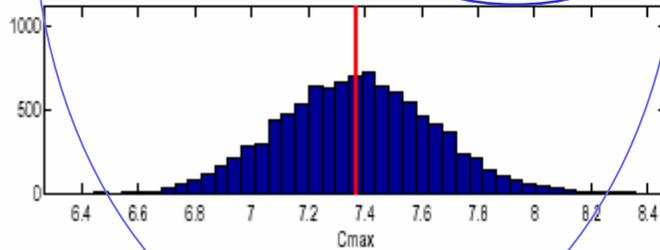
Single grid  $C_{max}^{(2)}$ , model: bias 0.076, std 0.259,  $\sqrt{\text{MSE}}$  0.270



Hybrid: bias -0.018, std 0.270,  $\sqrt{\text{MSE}}$  0.271

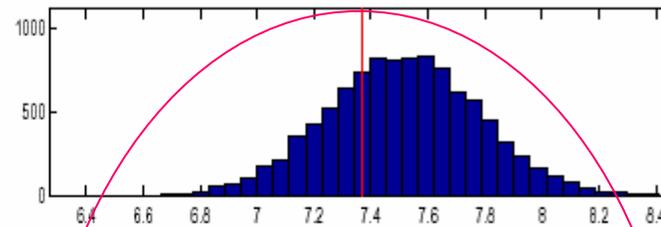


Splines: bias 0.003, std 0.270,  $\sqrt{\text{MSE}}$  0.270

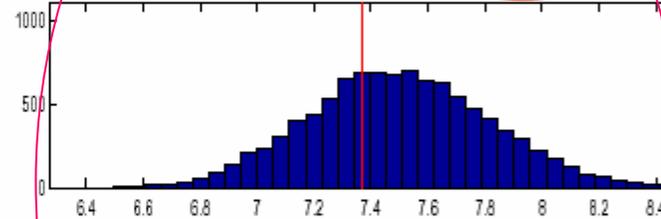


Single grid

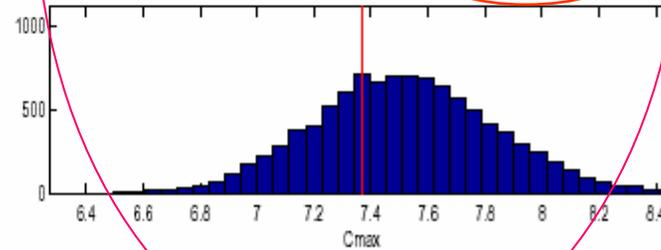
Split grid  $C_{max}^{(2)}$ , model: bias 0.144, std 0.266,  $\sqrt{\text{MSE}}$  0.302



Hybrid: bias 0.135, std 0.322,  $\sqrt{\text{MSE}}$  0.349



Splines: bias 0.152, std 0.320,  $\sqrt{\text{MSE}}$  0.354



Right panel - split grid

## $AUC_{E2}$ : mean squared error for single/split grids

Closed-form solution for a simplified case:

- Response approximated by a 2nd order polynomial:

$$f(x, \theta) = \theta_0 + \theta_1 x + \theta_2 x^2,$$

- Population variability: intercept only,  $Var(\theta_{0j}) = s^2$ ,
- Uniform sampling grid

## Formulae for $MSE$

Single grid:

$$MSE_{(1)} = \underbrace{Bias_{(1)}}_{\downarrow} \left[ \frac{f''_x(\tilde{x}, \theta)}{12} \frac{1}{4n^2} \right]^2 + \underbrace{Var_{(1)}}_{\downarrow} \left[ \frac{\sigma^2}{2Nn} + \frac{s^2}{N} \right]$$

Split grid:

$$MSE_{(2)} = \underbrace{Bias_{(2)}}_{\downarrow} \left( \text{no difference!} \right) \left[ \frac{f''_x(\tilde{x}, \theta)}{12} \frac{1}{4n^2} \right]^2 + \underbrace{Var_{(2)}}_{\downarrow} \left( \text{no loss in population term} \right) \left[ \frac{\sigma^2}{Nn} + \frac{s^2}{N} \right]$$

No costs: - **single grid** ( $2n$  samples/patient) will always be “better”

- how much “better”: depends on values of  $f''$ ,  $\sigma^2$  and  $s^2$

# Cost-based optimization

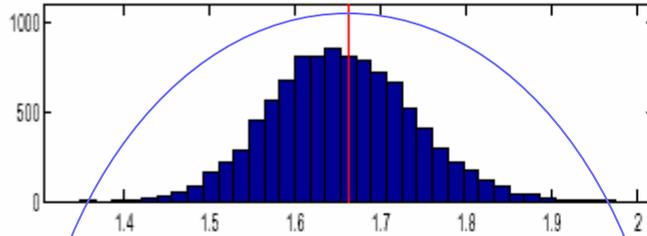
- $c_s$  - cost of analyzing a sample,  $c_p$  - cost of patient enrollment,
- $C_{total}$  - budget (resource)
- Overall cost, **single grid**:  $2n N c_s + N c_p \leq C_{total}$ , (C1)
- Overall cost, **split grid**:  $n N c_s + N c_p \leq C_{total}$ . (C2)

Thus, values of  $n$  and  $N$  are not independent! Given  $C_{total}$ ,

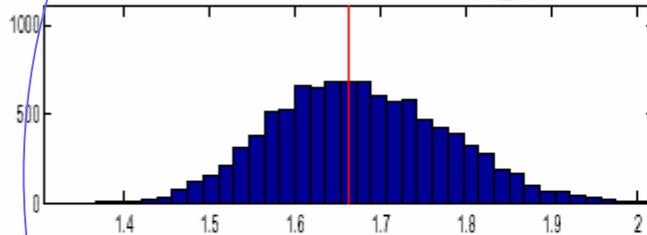
- for a given  $N$ , find maximal  $n = n(N, C_{total})$  satisfying (C1) or (C2),
- fix  $n$ , then find maximal  $N = N(n, C_{total})$  satisfying (C1) or (C2)

# Method 2, $AUC$ : $AUC_{true}=1.662$

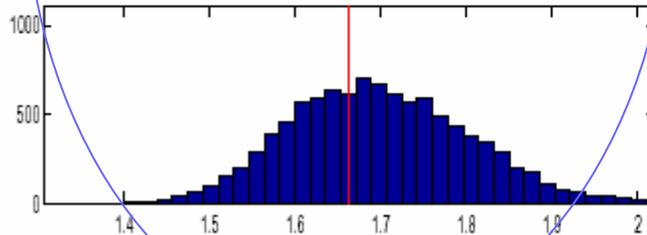
Single grid AUC (2), model: bias  $-0.007$ , std  $0.082$ ,  $\text{sqrt}(\text{MSE})$   $0.083$



Hybrid: bias  $0.015$ , std  $0.102$ ,  $\text{sqrt}(\text{MSE})$   $0.103$

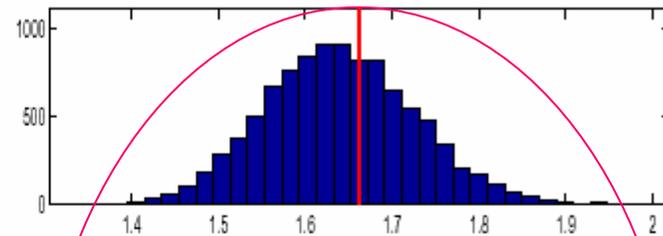


Splines: bias  $0.036$ , std  $0.103$ ,  $\text{sqrt}(\text{MSE})$   $0.109$

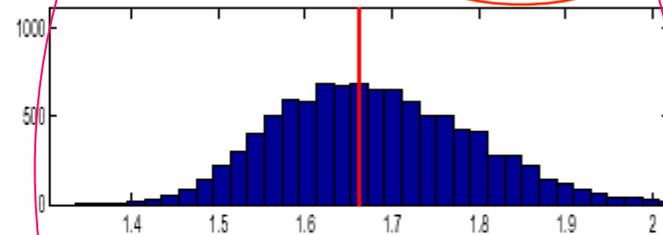


Single grid

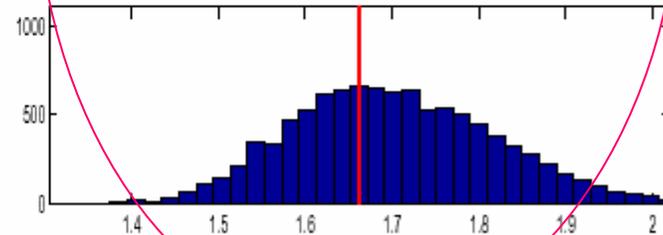
Split grid AUC (2), model: bias  $-0.022$ , std  $0.088$ ,  $\text{sqrt}(\text{MSE})$   $0.090$



Hybrid: bias  $0.018$ , std  $0.113$ ,  $\text{sqrt}(\text{MSE})$   $0.114$



Splines: bias  $0.041$ , std  $0.117$ ,  $\text{sqrt}(\text{MSE})$   $0.124$



Right panel - split grid

Method 2: first average responses at each  $x_i$

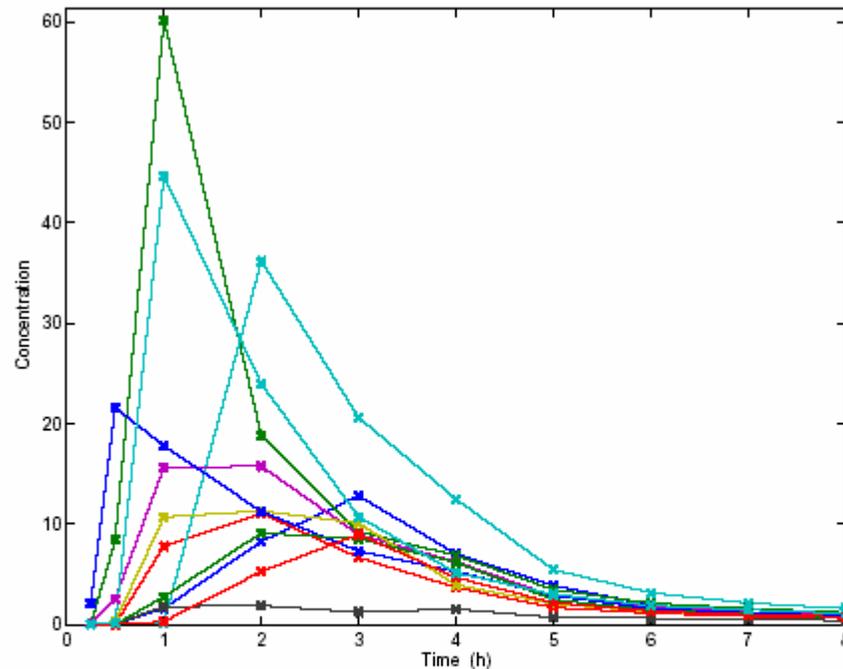
Upper - model-based, middle-hybrid, lower-splines

Costs:

$$2nNc_s + Nc_p$$

$$nNc_s + Nc_p$$

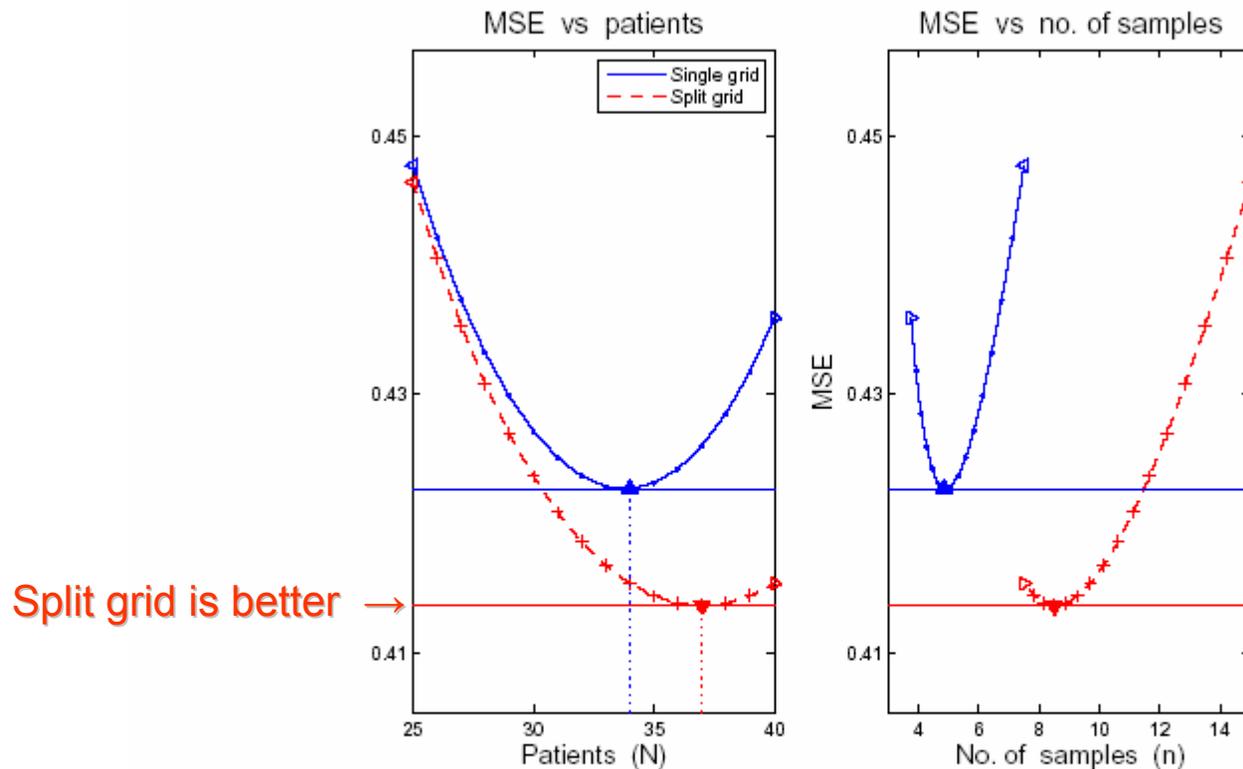
# How to select “meaningful” parameters



Concentration-time curves from a real study

- $f(x, \theta) = A - B(x - x_0)^2$ ,  $\max_x f(x, \theta) = f(x_0, \theta) = A$ ,  $|f''| \equiv 2B$
- $f(0, \theta) = 0$ ,  $x_0 = 1 \implies A = B$ . From the plot:  $x_0 \approx 1$ ,  $\bar{A}_j \sim 40 \implies |f''| \approx 80$
- Range of values:  $50 \approx \max_x f(x, \theta_j) - \min_x f(x, \theta_j) \approx 5 \times std \implies$  selected  $\sigma + s \sim 10$

# MSE as a function of $N$ (left) and $n$ (right), fixed $C_{total}$



Parameters:  $c_s = 100$ ,  $c_p = 500$ ,  $C_{total} = 50000$ ,  $s = 2.4$ ,  $\sigma = 9$ ,  $f'' = 100$

- Single grid:  $N_{opt} = 34$ ,  $n_{opt} = 5$ ,  $MSE_{opt} \approx 0.425$  ( $2n_{opt}=10$  samples/subject)
- Split grid:  $N_{opt} = 37$ ,  $n_{opt} = 8$ ,  $MSE_{opt} \approx 0.415$

# Concluding remarks

- Model-based designs: superior to empirical
- Empirical approach: reasonable performance
- Split grids (“sparse” sampling): may perform quite well (method 2)
- Cost-based designs: more meaningful comparison

## References

- [1] Atkinson, A.C., Chaloner, K., Herzberg, A.M., and Juritz, J. (1993) Optimal experimental designs for properties of a compartmental model, *Biometrics*, **49**, 325-337.
- [2] Cook, R.D., Fedorov, V.V. (1995), Constrained optimization of experimental design, *Statistics*, **26**, 129-178.
- [3] Elfving, G. (1952), Optimum allocation in linear regression theory. *Annals of Mathematical Statistics*, **23**, 255-262.
- [4] Fedorov, V., Gagnon, R., and Leonov, S. (2002), Design of experiments with unknown parameters in variance. *Applied Stochastic Models in Business and Industry*, **18** (3), 207-218.
- [5] Fedorov, V., Gagnon, R., Leonov, S. and Wu, Y. (2006), Optimal Design of Experiments in Pharmaceutical Applications. In: Dmitrienko, A., Chuang-Stein, C., D'Agostino, R. (eds.), *Pharmaceutical Statistics*, SAS Press (to appear).
- [6] Fedorov, V.V., and Hackl, P. (1997), *Model-Oriented Design of Experiments*. Springer, New York.
- [7] Gagnon, R., and Leonov, S. (2005), Optimal population designs for PK models with serial sampling. *J. Biopharm. Stat.*, **15** (1), 143-163.
- [8] Mentré, F., Mallet, A. and Baccar, D. (1997), Optimal design in random-effects regression models, *Biometrika*, **84** (2), 429-442.
- [9] Retout, S., and Mentré, F. (2003), Further developments of the Fisher information matrix in nonlinear mixed effects models with evaluation in population pharmacokinetics. *J. Biopharm. Stat.*, **13** (2), 209-227.

# Numerical integration, examples

