



# PODE 2008

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Optimization of sampling times  
for a combined PK/PD model:  
optimal design as a reference point

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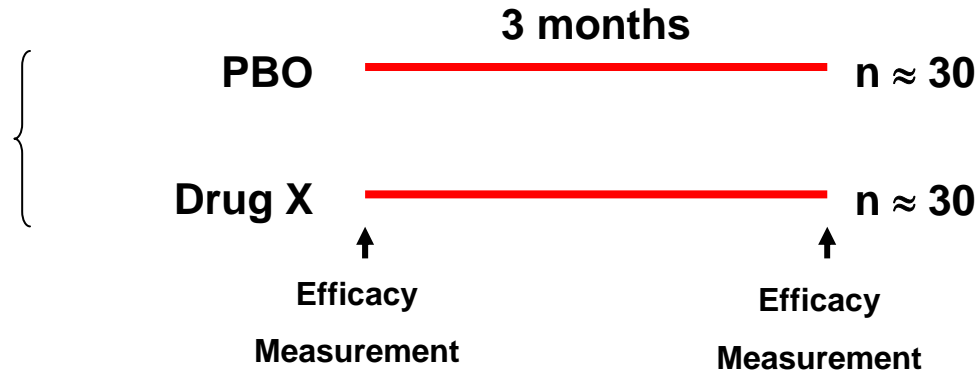
# Outline

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- Background: clinical problem
- Original sampling design
- Optimization of sampling times
- Comparison options

# Study Design

Inclusion:  
High risk  
CVD

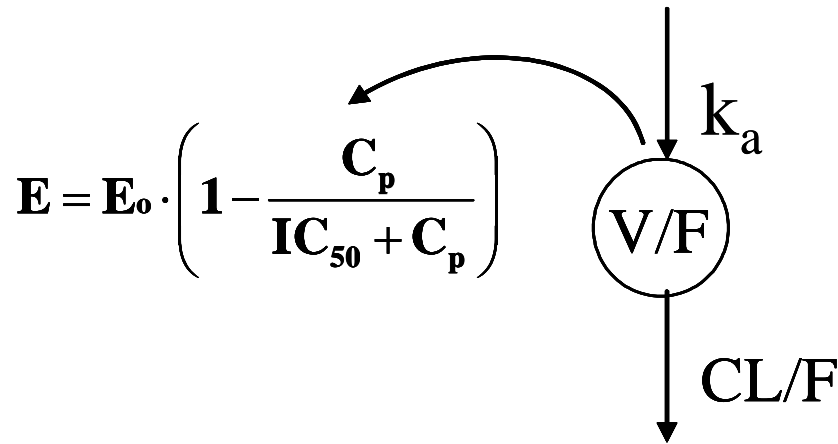


## Endpoints

- Safety
- Efficacy
- PK
- PK/PD

# Drug X PK/PD Modeling & Simulation

## Final PK/PD Model



$k_a$ : first-order absorption rate constant ( $h^{-1}$ )

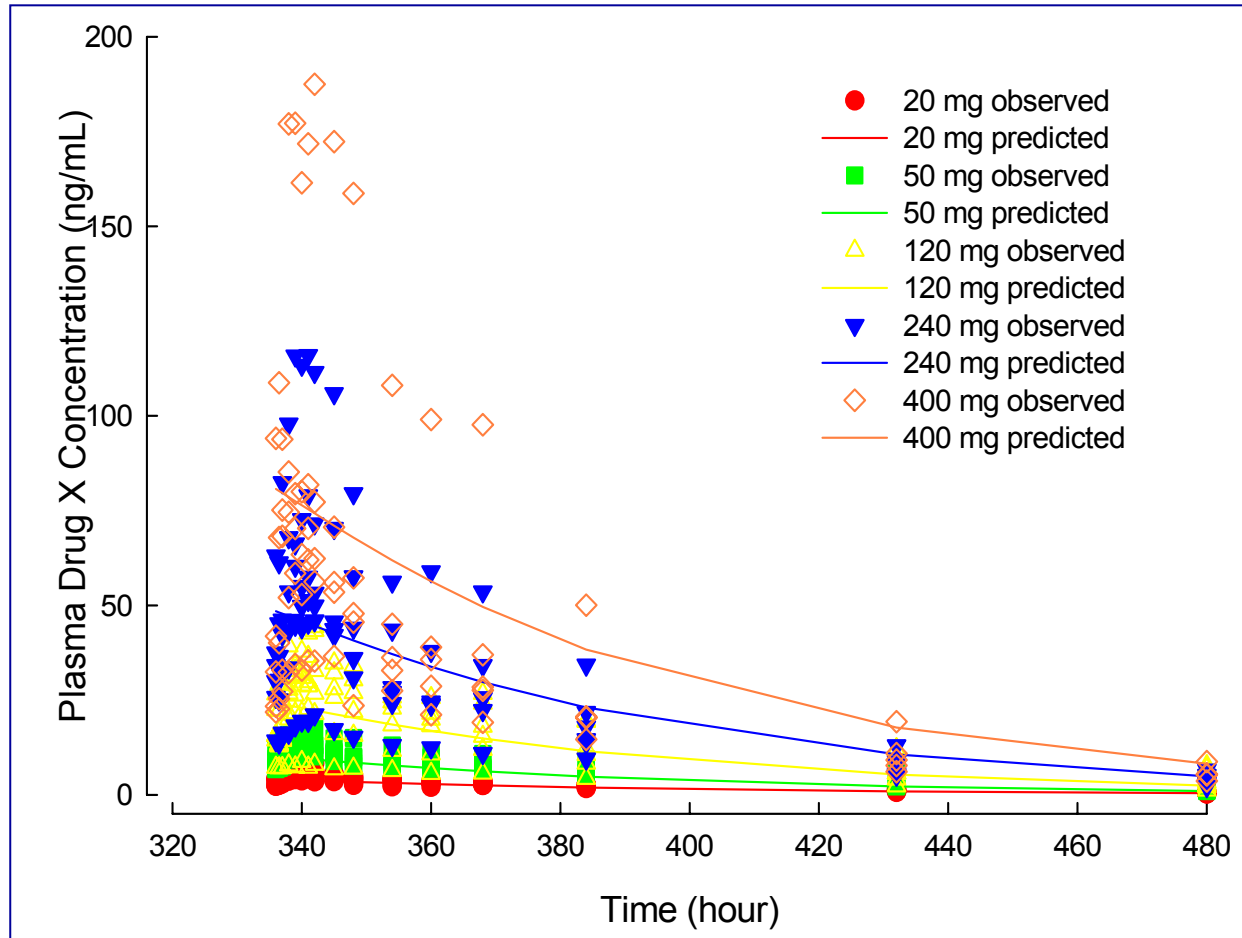
$V/F$ : apparent volume of distribution (L)

$CL/F$ : apparent systemic clearance (L/h)

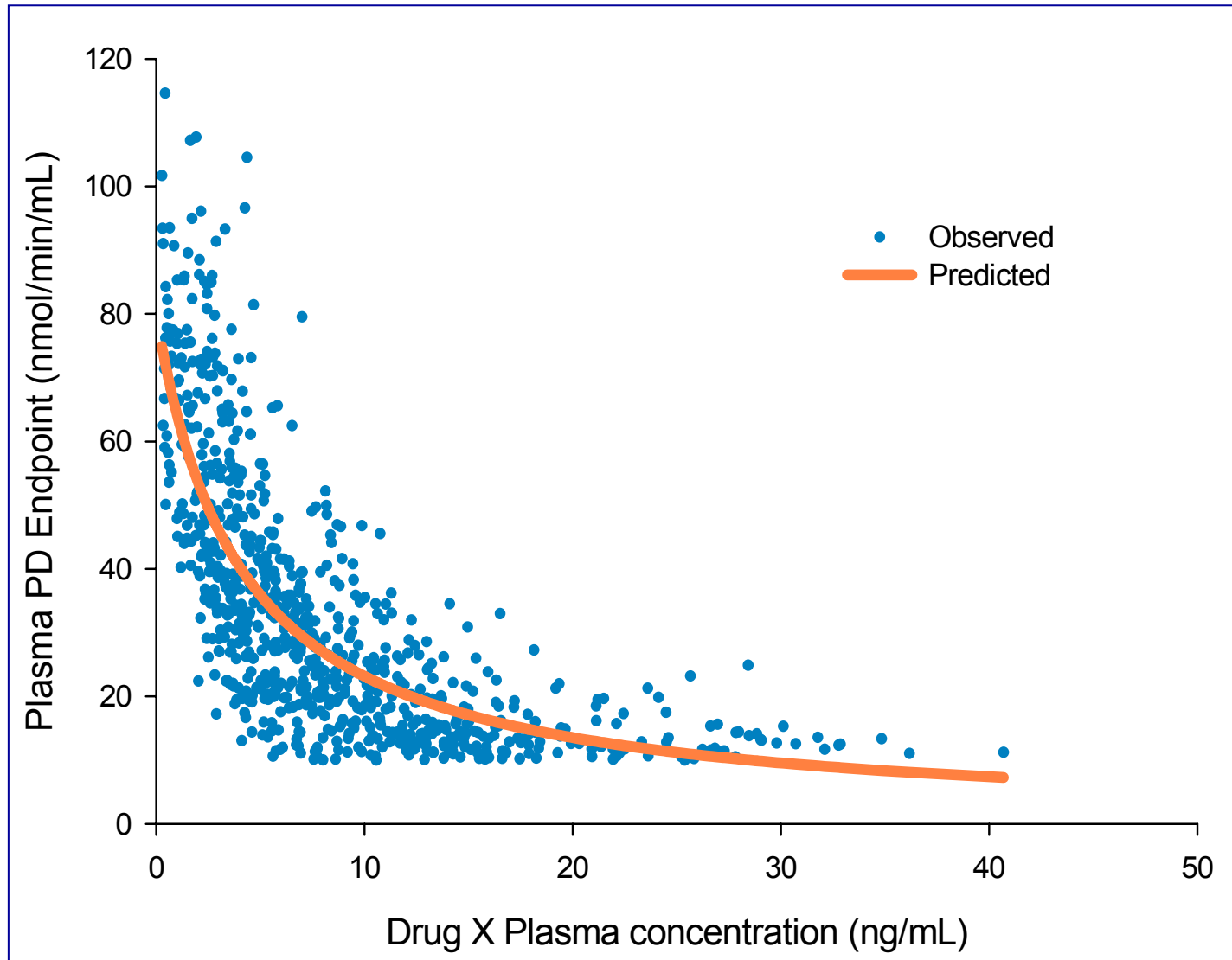
$E_o$ : PD endpoint at baseline (nM/min/mL)

$IC_{50}$ : Drug X plasma concentration causing 50% inhibition of PD endpoint (ng/mL)

# PK



# PK/PD



# Final PK/PD Sampling Scheme

Sample Collection Timepoint <sup>1,2</sup>	Treatment				
	Baseline / Randomization	Week 4	Week 6	Week 8	Week 10
Pre-dose (Trough concentration)	X	X		X	
0.5-5 hours after dose (Absorption phase)		X		X	
5-9 hours after dose (Peak concentration)					X
9-22 hours after dose (Elimination phase)			X <sup>3</sup>		

1. If the subject is withdrawn early, a blood sample for PK and PD should be collected prior to discharge from the study, if possible
2. For each PK sample, a PD sample will be drawn at the same time to assess the plasma PD endpoint
3. Subjects should be reminded to take their study medication around lunch time for the 2 days prior to clinic visit

## 4 samples to be selected

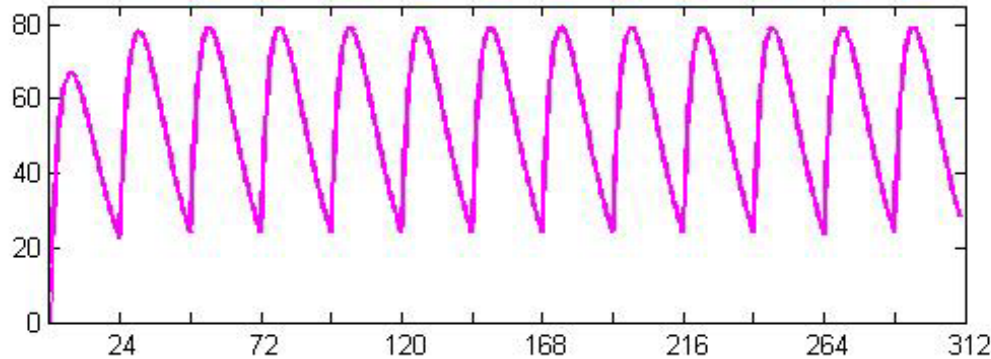
- Week 4, between [0.5, 5] h
- Week 6, between [ 9, 22] h
- Week 8, between [0.5, 5] h
- Week 10, between [ 5, 9] h

## Forced samples:

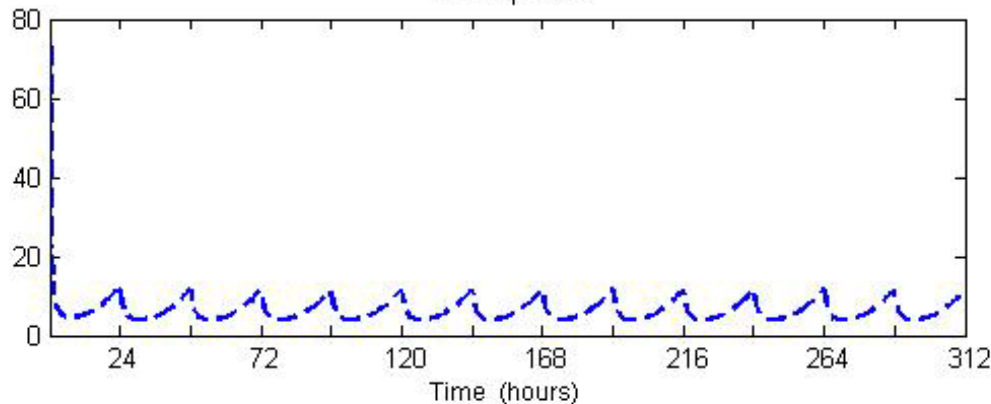
- PD trough (0 h)
- Trough PK/PD, weeks 4 and 8

# PK/PD curves

Doses: loading 250 mg, maintenance 250 mg, every 24 h



PD response



Main goal: validate proposed design

- 4 “flexible” candidate times
- Given frequency e.g. every 30 min
  1. Day 4, [0.5, 5] h: 10 points
  2. Day 6, [0.5, 5] h: 10 points
  3. Day 6, [5, 9] h: 9 points
  4. Day 6, [9, 22]h: 17 points





# Nonlinear models, multiple responses

- Predictor  $\mathbf{x} = (x_1, x_2, \dots, x_k)$  - sequence of sampling times,
- Measurements  $\mathbf{Y} = [y(x_1), \dots, y(x_k)]$  - vector,
- Response  $\boldsymbol{\eta}(\mathbf{x}, \boldsymbol{\theta}) = [\eta(x_1, \boldsymbol{\theta}), \dots, \eta(x_k, \boldsymbol{\theta})]$  - vector

**Key:**  $\boldsymbol{\mu}(\mathbf{x}, \boldsymbol{\theta})$  - information matrix of a  $k$ -dimensional sequence  $\mathbf{x}$

# Optimal design

Information matrix :  $n_i$  patients on seq.  $\mathbf{x}_i \implies \mathbf{M}_N(\boldsymbol{\theta}) = \sum_{i=1}^N n_i \boldsymbol{\mu}(\mathbf{x}_i, \boldsymbol{\theta})$

Variance of the MLE:  $\text{Var}(\hat{\boldsymbol{\theta}}) \approx \mathbf{M}_N^{-1}(\boldsymbol{\theta})$

$\mathbf{M}(\xi, \boldsymbol{\theta}) = \frac{\mathbf{M}_N(\boldsymbol{\theta})}{N} = \sum_i w_i \boldsymbol{\mu}(\mathbf{x}_i, \boldsymbol{\theta})$  - normalized information, per observation

$\xi = \{w_i, \mathbf{x}_i\}$  - normalized design;  $w_i = n_i/N$  - weights

$\mathbf{D}(\xi, \boldsymbol{\theta}) = \mathbf{M}^{-1}(\xi, \boldsymbol{\theta})$  - normalized variance-covariance matrix

Restrictions on the number of optimal sequences: NONE

# Optimal design (cont.)

Criterion of optimality  $\Psi(\xi, \theta) \rightarrow \min_{\xi}$ : minimization with respect to

- weights  $w_i, 0 \leq w_i \leq 1, \sum_i w_i = 1$
- admissible sampling sequences  $\mathbf{x}_i \in \mathbf{X}$  - design region.

Locally optimal designs:

D-criterion:  $\Psi = |\mathbf{D}(\xi, \theta)|$ ; A-criterion:  $\Psi = \text{tr}[\mathbf{A}\mathbf{D}(\xi, \theta)]$

**Equivalence Theorem:** *Kiefer, Wolfowitz (1960), Fedorov (1972)* -  
background for algorithms

# Information matrix for sequence $\mathbf{x}$

Gaussian  $\mathbf{Y}$  :  $\mathbf{E}[\mathbf{Y}|\mathbf{x}] = \boldsymbol{\eta}(\mathbf{x}, \boldsymbol{\theta})$ ,  $\text{Var}[\mathbf{Y}|\mathbf{x}] = \mathbf{S}(\mathbf{x}, \boldsymbol{\theta})$

$\boldsymbol{\mu}(\mathbf{x}, \boldsymbol{\theta})$  - information matrix of a single ( $k$ -dimensional) sequence  $\mathbf{x}$ :

$$\mu_{\alpha\beta}(\mathbf{x}, \boldsymbol{\theta}) = \frac{\partial \boldsymbol{\eta}}{\partial \theta_{\alpha}} \mathbf{S}^{-1} \frac{\partial \boldsymbol{\eta}}{\partial \theta_{\beta}} + \frac{1}{2} \text{tr} \left[ \mathbf{S}^{-1} \frac{\partial \mathbf{S}}{\partial \theta_{\alpha}} \mathbf{S}^{-1} \frac{\partial \mathbf{S}}{\partial \theta_{\beta}} \right], \quad \odot$$

$\mathbf{S} = \mathbf{S}(\mathbf{x}, \boldsymbol{\theta})$ ,  $\boldsymbol{\eta} = \boldsymbol{\eta}(\mathbf{x}, \boldsymbol{\theta})$  [*Muirhead (1982), Magnus and Neudecker (1988)*]

If  $\boldsymbol{\eta}$ ,  $\mathbf{S}$  defined (approximated)  $\Rightarrow$  get  $\boldsymbol{\mu}$   $\Rightarrow$  run the algorithm

Vector  $\mathbf{Y}$  combines PK and PD responses

# Information matrix for sequence $\mathbf{x}$ (cont.)

- Data  $y(x_{ij}) = \eta(x_{ij}, \gamma_i) [1 + \varepsilon_{ij}^p] + \varepsilon_{ij}^a, \quad j = 1, \dots, k_i. \quad (1)$

$$\varepsilon_{ij}^a \sim N(0, \sigma_a^2), \quad \varepsilon_{ij}^p \sim N(0, \sigma_p^2)$$

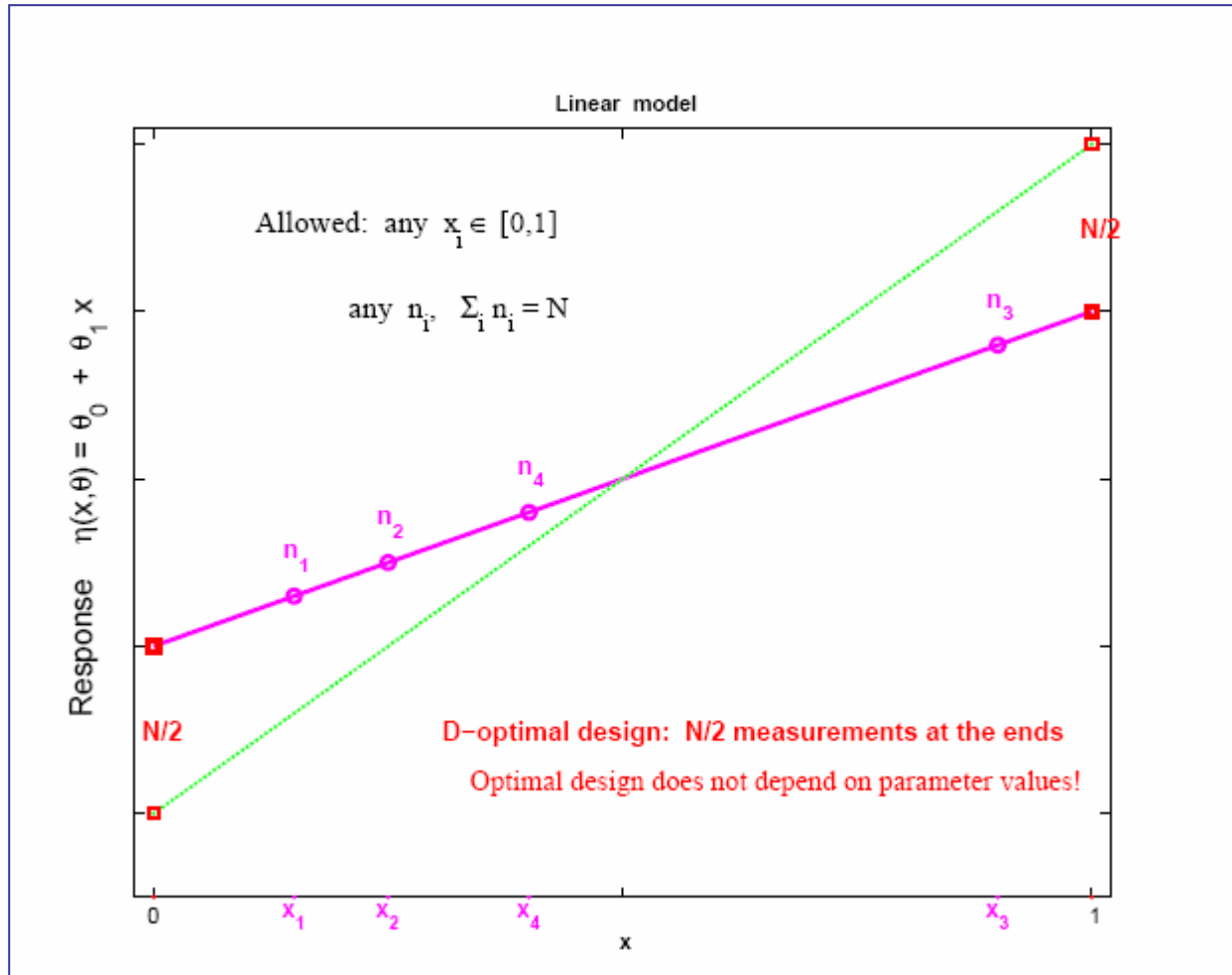
First-order approximation of variance matrix  $\mathbf{S}$ , model (1): for normal  $\gamma$

$$S(\mathbf{x}, \boldsymbol{\theta}) \simeq \mathbf{F} \boldsymbol{\Lambda} \mathbf{F}^T + \sigma_p^2 \text{Diag}[\boldsymbol{\eta}(\mathbf{x}, \boldsymbol{\theta}) \boldsymbol{\eta}^T(\mathbf{x}, \boldsymbol{\theta}) + \mathbf{F} \boldsymbol{\Lambda} \mathbf{F}^T] + \sigma_A^2 \mathbf{I}_k,$$

$$\mathbf{F} = \mathbf{F}(\mathbf{x}, \gamma^0) = \left[ \frac{\partial \boldsymbol{\eta}(\mathbf{x}, \boldsymbol{\theta})}{\partial \gamma_\alpha} \right] \Big|_{\gamma = \gamma^0} \quad - \quad (k \times m_\gamma) \text{ matrix}$$

*Retout, Mentré (2003), Gagnon and Leonov (2005)*

# Optimal designs: not necessarily practical

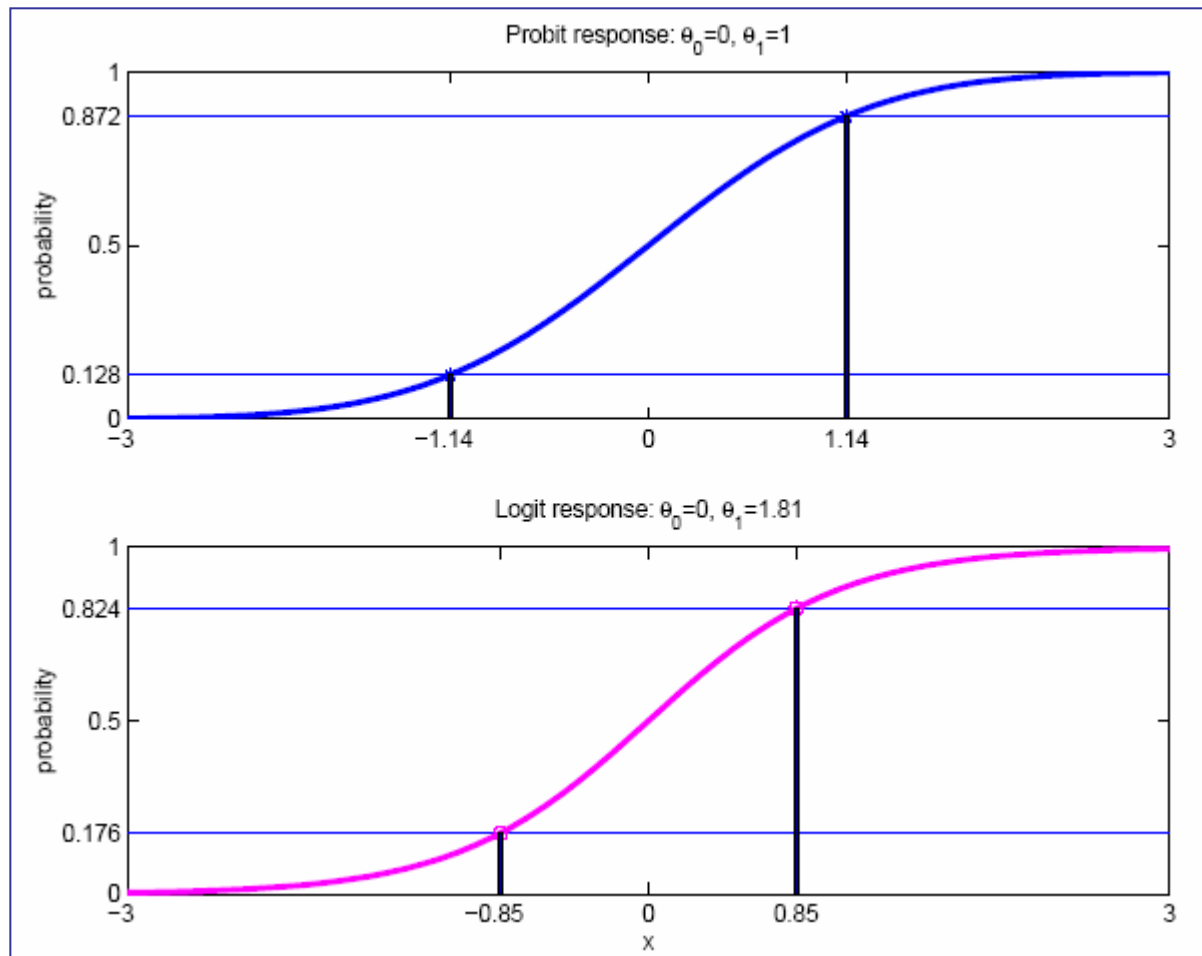


# Optimal designs: not necessarily practical

Binary logistic model:  $P(\text{response}|\theta) = \exp(\theta_0 + \theta_1 x) / [1 + \exp(\theta_0 + \theta_1 x)]$

Two optimal doses with equal weights on z-scale:  $z = \theta_0 + \theta_1 x$  *White (1975)*

$$z^* = \pm 1.54 \text{ (Logit)}, \quad z^* = \pm 1.14 \text{ (Probit)}$$



# One-compartment PK and $E_{max}$ PD

Parameters:  
 $K_a$ ,  $V/F$ ,  $CL/F$  (PK)  
 $E_{max}$ ,  $IC_{50}$  (PD)

1-compartment PK model and Emax PD model

**PK PARAMETERS**

Typical values:  Random

$K_a$	0.12	<input type="checkbox"/>
$V2$	1180	<input checked="" type="checkbox"/>
$CL$	189	<input checked="" type="checkbox"/>
$E_{max}$	79.9	<input checked="" type="checkbox"/>
$IC_{50}$	4.08	<input checked="" type="checkbox"/>

Population Covariance (Etas)

$K_a$	$V2$	$CL$	$E_{max}$	$IC_{50}$
0	0	0	0	0
	0.263	0.208	0	0
		0.195	0	0
			0.112	0
				0.0294

Distribution: Log-normal

**RESIDUAL VARIANCE:**

PK	Additive: known	0	PD	Additive: known	0.1
	Proport.: parameter	0.0425		Proport.: parameter	0.12

**DOSES**

Loading, mg/kg: 250

Repeated: YES

Maintenance: 250 mg/kg

Every: 24 h

**CANDIDATE SAMPLING TIMES**

Sample	1	2	3	4	Freq. (h)
Week	2	2	2	2	1
Day	4	6	6	6	
Hours	[0.5 5]	[0.5 5]	[5 9]	[9 22]	

PD only (h): 0

Forced samples: YES

PK/PD: [240 288]

Costs:  $C_e + k^*C_s$

$C_e$ : 1  $C_s$ : 0

**RESULTS**

	Optimal sequences				Weights
1	3.50	3.50	5.00	22.00	1.000
2					
3					
4					

Candidate sequences: Total 2520, Processed All done, Iteration 10

**EFFICIENCY**

Average design 0.952 Mean 0.950 Median 0.956

ALGORITHM: Iterations, max 200; Init. sequences 6; Step size, coeff. 1; Weight cut-off 0.05

Measure:  PK,  PD

Buttons: HELP, About, Measure, ALGORITHM, RUN, Design Efficiency, QUIT

Candidate sampling times



# No PD samples option

1-compartment PK model and Emax PD model

**PK PARAMETERS**

Typical values: Ka 0.12, V2 1180, CL 189, Emax 79.9, IC50 4.08

Population Covariance (Etas): Ka 0, V2 0.263, CL 0.208, Emax 0.195, IC50 0

Distribution: Log-normal

**RESIDUAL VARIANCE:**

PK: Additive: known (0), Proport.: parameter (0.0425)

PD: Additive: known (0.1), Proport.: parameter (0.12)

**DOSES**

Loading, mg/kg: 250

Repeated: YES, Maintenance: 250 mg/kg, Every: 24 h

**CANDIDATE SAMPLING TIMES**

Sample	1	2	3	4	Freq. (h)
Week	2	2	2	2	1
Day	4	6	6	6	
Hours	[0.5 5]	[0.5 5]	[5 9]	[9 22]	0

Forced samples: YES, PK/PD [240 288]

Costs: Ce + k\*Cs, Ce 1, Cs 0

**RESULTS**

Optimal sequences	Weights
1 3.50 3.50 5.00 22.00	1.000
2	
3	
4	

Candidate sequences: Total 2520, Processed All done, Iteration 10

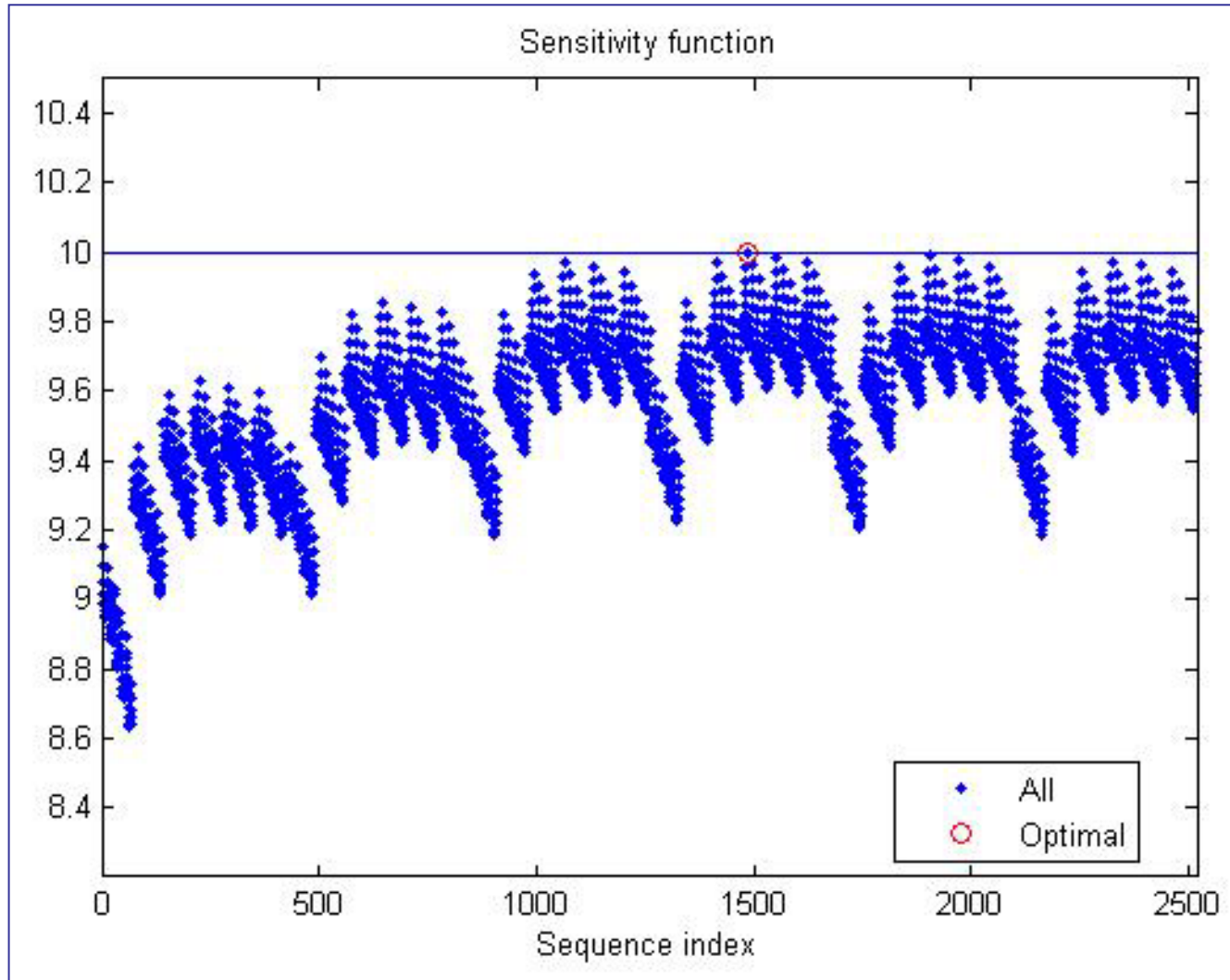
**EFFICIENCY**

Average design 0.903, Mean 0.900, Median 0.909

Buttons: HELP, About, Measure (PK, PD), ALGORITHM (Iterations, max 200; Init. sequences 6; Step size, coeff. 1; Weight cut-off 0.05), RUN, Design Efficiency (Sampling windows, Delta 0.5, Compare), QUIT

No PD samples

# Sensitivity function



# Efficiency analysis: best and worst sequences

- BEST SEQUENCES:

No.	Effic.	Wk 2,D4	Wk 2,D6	Wk 2,D6	Wk 2,D6
1	1.000	3.50	3.50	5.00	22.00
2	0.999	4.50	3.50	5.00	22.00
3	0.999	3.50	4.50	5.00	22.00
4	0.998	4.50	4.50	5.00	22.00
5	0.997	5.00	3.50	5.00	22.00
6	0.997	3.50	5.00	5.00	22.00
7	0.997	2.50	3.50	5.00	22.00
8	0.997	3.50	2.50	5.00	22.00
9	0.996	3.50	3.50	6.00	22.00
10	0.996	5.00	4.50	5.00	22.00

- WORST SEQUENCES:

No.	Effic.	Wk 2,D4	Wk 2,D6	Wk 2,D6	Wk 2,D6
1	0.817	0.50	0.50	9.00	17.00
2	0.818	0.50	0.50	9.00	16.00
3	0.819	0.50	0.50	9.00	18.00
4	0.820	0.50	0.50	9.00	15.00
5	0.822	0.50	0.50	9.00	19.00
6	0.824	0.50	0.50	9.00	14.00
7	0.826	0.50	0.50	9.00	20.00
8	0.829	0.50	0.50	9.00	13.00
9	0.831	0.50	0.50	9.00	21.00
10	0.833	0.50	0.50	8.00	17.00

EFFICIENCY OF INDIVIDUAL SEQUENCES: mean 0.950, median 0.956

EFFICIENCY OF AVERAGE DESIGN 0.952



# Sensitivity analysis

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- Comparison with "average" design within sampling windows
  - Currently 5 times are selected uniformly in each sampling window (average value across  $5^4 = 625$  sequences)
- Comparison with "average" design within Delta-vicinity of D-optimal designs
  - D-optimal times +/- Delta



# Conclusions

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- Original design: quite efficient
- Optimal design: used as a reference point
  - Serial dilution (bioassays)
  - Dose response modeling (linear, binary logistic models)

# References

- Fedorov, V.V., Gagnon, R., Leonov, S., Wu, Y. (2007), Optimal design of experiments in pharmaceutical applications. In: Dmitrienko, A., Chuang-Stein, C., D'Agostino, R. (Eds), *Pharmaceutical Statistics*, SAS Books by Users series, SAS Press, Cary, NC, pp. 151-195.
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