

Two-stage adaptive designs in nonlinear mixed-effects models: an evaluation by simulation for a pharmacokinetic (PK) and pharmacodynamic (PD) model in oncology

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# CONTEXT

Optimal design in population PKPD is based on prior information on the models and on the parameters. Adaptive designs [1,2] are a promising alternative to local or robust designs [3]. Two-stage designs are easier to implement than fully adaptive designs and can be as efficient [4].

# **OBJECTIVES**

- To compare by simulation one and two-stage designs using a PKPD model in oncology
- To study the influence of the size of each cohort in two-stage designs

# **METHODS**

## Two-Stage design

Assumptions

# RESULTS



For PK, good results for all designs

*Figure 4:* Boxplot of REE for ka and CL and relative bias (RB)

- prior information about the parameters and model available - same elementary design  $\xi$  for all patients in each cohort

### Notation

- M<sub>F</sub>= Population Fisher Information Matrix
- $\Psi^0$ : prior parameters
- $\Psi^*$  : true parameters

**Design optimisation** 

- $\xi^0$ : optimized design obtained with  $\Psi^0$ for N<sub>1</sub> subjects
- $\widehat{\Psi}_1$  : estimated parameters from data  $Y_1$ with design  $\xi^0$  and N<sub>1</sub> subjects
- $\xi^2$ : optimized design obtained with  $\Psi_1$ for N<sub>2</sub> subjects
- $\widehat{\Psi}_2$  : estimated parameters from data  $Y_1$ and  $Y_2$  (obtained with design  $\xi^2$  for  $N_2$  subjects)



 $\widehat{\Psi}_1$  (from  $Y_1$ )

**COHORT 1** 

Model M

Initial parameters  $\Psi^0$ 

*Figure 1: Two-stage design* 

**COHORT 2** 

Model M

 $\widehat{\Psi}_1$ 

Design

optimisation

Estimation

 $\widehat{\Psi}_2$  (from  $Y_1$  and  $Y_2$ )

kout

<u>First stage</u>: from a priori  $\Psi^0_{j}$   $\xi^0$  maximizes determinant of

 $\mathsf{M}_{\mathsf{F}}(\Psi^{0},\mathsf{N}_{1}\xi) = \mathsf{N}_{1}\mathsf{M}_{\mathsf{F}}(\Psi^{0},\xi)$ 

ka

<u>Second stage</u>: using estimated  $\widehat{\Psi}_1, \xi^2$  maximizes determinant of

 $\mathsf{M}_{\mathsf{F}}(\widehat{\Psi}_{1},\mathsf{N}_{1}\xi^{0} + \mathsf{N}_{2}\xi) = \mathsf{N}_{1}\mathsf{M}_{\mathsf{F}}(\widehat{\Psi}_{1},\xi^{0}) + \mathsf{N}_{2}\mathsf{M}_{\mathsf{F}}(\widehat{\Psi}_{1},\xi)$ 

ksyn

**NB:** this procedure is implemented in PFIM 4.0 released in April 2014 [7, 8]





Figure 2: PKPD Model

Effect





*Figure 5:* Boxplot of REE for kout and IC50 and relative bias (RB)

		RRMSE % (standardized RRMSE)				
Parameters	Ψ*	ξ*	$\xi^0$	$\xi^{0*}$	$\xi_{25-25}$	
$k_a(h^{-1})$	2	5.8	5.6 (0.97)	5.7 (0.98)	5.0 (0.86)	
V (L)	100	9.9	9.9 (1.00)	9.9 (1.00)	9.3 (0.94)	
CL(L/h)	10	12.5	12.4 (0.99)	12.5 (1.00)	12.5 (1.00)	
$\omega_V^2$	0.49	22.7	22.5 (0.99)	22.5 (0.99)	22.2 (0.98)	
$\omega_{CL}^2$	0.49	24.3	24.5 (1.01)	24.2 (1.00)	24.1 (0.99)	
$\sigma_{slope.PK}$	0.2	10.2	10.2 (1.00)	10.0 (0.98)	9.9 (0.97)	
$k_{out}(h^{-1})$	0.2	23.2	54.5 (2.35)	25.6 (1.10)	24.3 (1.05)	
<i>IC</i> <sub>50</sub> (mg/L)	0.3	22.1	91.1 (4.12)	30.4 (1.38)	30.3 (1.37)	
$\omega_{k_{out}}^2$	0.49	72.9	59.9 (0.82)	59.5 (0.82)	61.2 (0.84)	
$\omega_{IC50}^2$	0.49	72.4	709.9 (9.81 <b>)</b>	95.7 (1.32)	99.0 (1.37)	
$\sigma_{inter.PD}$	0.2	7.2	6.5 (0.90)	6.5 (0.90)	6.3 (0.88)	
Mean Standardized						
RRMSE		1.00	2.18	1.04	1.02	

- For PD, REE and RB are very high with  $\xi^0$  compared with the other designs
- For the two-stage design  $\xi_{25-25}$  results of REE and RB are close to those of  $\xi^*$
- Relative RRMSE shows again good results of the two-stage design  $\xi_{25-25}$ , except somehow for IC50 and  $\omega_{IC50}^2$  but much better than those of

- Model developed for a novel oral transforming growth factor  $\beta$  (TGF –  $\beta$ ) inhibitor [5,6]
- PK parameters: ka, V, CL
- PD parameters: kout, IC50
- True parameters  $\Psi^*$  in Table 1
- Prior parameters  $\Psi^0 \neq \Psi^*$ : CL=40 L/h ( × 4), kout=2 h<sup>-1</sup> (× 10)



**Figure 3:** Simulated PK (left) and PD (right) models with parameters  $\Psi^0$  and  $\Psi^*$ 

## **Evaluated designs**

• N= 50 patients

### **One-stage designs**

- Rich design, n=6 sampling times:  $\xi_{rich} = (0.1, 0.5, 1.5, 4, 6, 12)$
- Sparse designs, n=3 sampling times among the 6 of  $\xi_{rich}$ :

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#### **Table 1:** RRMSE of final estimated parameters from N<sub>1</sub>+N<sub>2</sub>=50 patients

Influence of the size of each cohort in two-stage design

		RRMSE % (standardized RRMSE)				
Parameters	Ψ*	$\xi_{10-40}$	$\xi_{15-35}$	$\xi_{25-25}$	$\xi_{35-15}$	$\xi_{40-10}$
$k_a(h^{-1})$	2	5.5 (0.95)	5.6 (0.97)	5.0 (0.86)	5.3 (0.91)	5.6 (0.97)
V (L)	100	9.4 (0.95)	9.7 (0.98)	9.3 (0.94)	9.5 (0.96)	9.7 (0.98)
CL(L/h)	10	12.4 (0.99)	12.5 (1.00)	12.5 (1.00)	12.5 (1.00)	12.5 (1.00)
$\omega_V^2$	0.49	22.3 (0.98)	22.0 (0.97)	22.2 (0.98)	22.1 (0.97)	22.2 (0.98)
$\omega_{CL}^2$	0.49	23.9 (0.98)	24.5 (1.01)	24.1 (0.99)	23.9 (0.98)	24.9 (1.02)
$\sigma_{slope.PK}$	0.2	10.7 (1.05)	10.0 (0.98)	9.9 (0.97)	9.9 (0.97)	9.9 (0.97)
$k_{out}(h^{-1})$	0.2	28.7 (1.24)	26.2 (1.13)	24.3 (1.05)	32.2 (1.39)	33.3 (1.44)
<i>IC</i> <sub>50</sub> (mg/L)	0.3	49.1 (2.22)	36.0 (1.63)	30.3 (1.37)	45.7 (2.07)	57.0 (2.58)
$\omega_{k_{out}}^2$	0.49	60.0 (0.82)	63.4 (0.87)	61.2 (0.84)	59.3 (0.81)	63.3 (0.87)
$\omega_{IC50}^2$	0.49	104.5 (1.44)	102.4 (1.41)	99.0 (1.37)	197.7 (2.73)	247.2 (3.41)
$\sigma_{inter.PD}$	0.2	6.3 (0.88)	6.8 (0.94)	6.3 (0.88)	6.5 (0.90)	6.5 (0.90)
Mean Standardized						
RRMSE		1.14	1.08	1.02	1.25	1.37

• From the RRMSE, the balanced twostage design  $(\xi_{25-25})$ performed better compared to the other different two-stage designs

**Table 2:** RRMSE of final estimated parameters from N<sub>1</sub>+N<sub>2</sub>=50 patients for the balanced and unbalanced cohort size two-stage designs

	$\xi_{10-40}$	$\xi_{15-35}$	$\xi_{25-25}$	$\xi_{35-15}$	$\xi_{40-10}$
# dif designs	12	8	6	6	6
# data-set with design $\xi^2 = \xi^*$	24	36	49	47	45

• After the first stage, the design  $\xi_{25-25}$  is the one with the greatest number of optimal elementary designs  $\xi^2$ 

 $-\xi^{0} = \{\xi^{0}_{PK} = (0.1, 4, 12); \xi^{0}_{PD} = (0.5, 1.5, 4)\}$  (D-optimal for  $\Psi^{0}$ )  $-\xi^* = \{\xi_{PK}^* = (0.1, 4, 12); \xi_{PD}^* = (4, 6, 12)\}$  (D-optimal for  $\Psi^*$ ) - mixed design  $\xi^{0*}$  (N<sub>1</sub>=25 patients with  $\xi^{0}$ ; N<sub>2</sub>=25 patients with  $\xi^{*}$ )

**Two-stage designs** 

- Balanced:  $\xi_{25-25}$  (N<sub>1</sub>= N<sub>2</sub>=25)
- Various sizes for cohorts 1 and 2:  $\xi_{10-40}$ ,  $\xi_{15-35}$ ,  $\xi_{35-15}$ ,  $\xi_{40-10}$

## **Clinical Trial Simulation**

- For each design: 100 data sets simulated with  $\Psi^*$
- For two-stage design: optimisation of  $\xi^2$  from estimated  $\widehat{\Psi}_1$
- Parameters estimation: SAEM algorithm in MONOLIX 4.3
  - 5 chains, initial estimates:  $\Psi^0$
- Comparison of designs from 100 estimated  $\Psi_2$ : Relative Estimation Error (REE), Relative Bias (RB) and Relative Root Mean Squared Error (RRMSE)

[1] Foo L, Duffull S. Pharm Res (2012)

[2] Dumont C, Chenel M, Mentré F. Comm Stat Simulat Comput (2014) [3] Mentré F et al. CPT Pharmacometrics Syst Pharmacol (2013)

#### equals to $\xi^*$ **Table 3:** Optimal designs $\xi^2$ obtained after the first stage CONCLUSIONS

- With the balanced two-stage design  $\xi_{25-25}$ , results are very close to those of the onestage design using true parameters ( $\Psi^*$ ) and are much better than those using wrong prior parameters ( $\Psi^0$ )
- The balanced  $\xi_{25-25}$  was the best two-stage design compared to unbalanced cohort size, especially if the second cohort was of small size
- Perspectives
  - to compare two-stage design with three-stage and five-stage designs —
  - to use robust approach for first stage
  - to expand the approach for dose-finding

[4] Fedorov V, Wu Y, Zhang R. Stat Med (2012) [5] Gueorguieva I et al. Comput Methods Programs Biomed (2007) [6] Gueorguieva I et al. Br J Clin Pharmacol (2014)

## [7] <u>www.pfim.biostat.fr</u>

[8] Mentré F et al. PAGE 23 (2014) Abstr 3032 [www.page-meeting.org/?abstract=3032]

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