

Evaluation of Model-Based Bioequivalence approach for one single sample pharmacokinetic studies

Coralie Tardivon (1), Florence Loingeville (2), Satish Sharan (3), Mark Donnelly (3), Kairui Feng (3), Wanjie Sun (4), Guoying Sun (4), Stella Grosser (4), Liang Zhao (3), Lanyan (Lucy) Fang (3), France Mentre (1), and Julie Bertrand (1)

(1) Université de Paris, IAME, INSERM,F-75018 Paris, France, (2) Faculty of Pharmacy, Univ. Lille, EA 2694, Public Health: Epidemiology and Healthcare quality, 59000 Lille, France, (3) Office of Research and Standards, Office of Generic Drugs, Center for Drug Evaluation and Research, U.S. Food and Drug Administration, 10903 New Hampshire Ave, Silver Spring, MD 20993, USA, (4) Office of Biostatistics, Office of Translational Sciences, Center for Drug Evaluation and Research, U.S. Food and Drug Administration, 10903 New Hampshire Ave, Silver Spring, MD 20993, USA

Introduction

- Bioequivalence (BE) studies are key to the development and approval of generic drugs
- Traditionally, BE studies with pharmacokinetic (PK) endpoints are conducted using a two-way crossover study design and the two one-sided test (TOST) is performed using estimates of area under the concentration-time curve (AUC) and maximal concentration (Cmax) obtained by non-compartmental analysis (NCA).
- In a typical PK BE studies for ophthalmic drug products, only one sample of aqueous humor is collected from one eye per patient.
- Parallel (P) design studies
 - subjects assigned to one pre-specified sampling times t_j with $j = 1, \dots, J$
 - C_{ij} the concentration of subject $i = 1, \dots, N_j$ at t_j
 - total number of samples (n_{tot}) = $\sum_{j=1}^J N_j$ = study sample size (N)
- Crossover (C) design studies
 - subject with bilateral cataracts randomly assigned one of two treatments to one of two eyes and one sample collected from each eye at the same t_j
 - C_{ijk} the concentration of subject $i = 1, \dots, N_{kj}$ at each period/in each eye $k = 1, 2$
 - $n_{tot} = \sum_{k=1}^2 \sum_{j=1}^J N_{kj}$ and $N = n_{tot}/2$

Methods

TOST¹

- β^T = the treatment effect, i.e., the difference in μ_T and μ_R , which are the average means of the test and reference products for $\log(AUC)$ or $\log(C_{max})$
- $H_0 : \beta^T = \mu_T - \mu_R \geq \delta$ or $\beta^T = \mu_T - \mu_R \leq -\delta$ with δ a pre-specified BE margin.

$$\frac{\hat{\beta}^T + \delta}{SE(\hat{\beta}^T)} \geq u_{1-\alpha} \quad \text{and} \quad \frac{\hat{\beta}^T - \delta}{SE(\hat{\beta}^T)} \leq -u_{1-\alpha}$$

where $\hat{\beta}^T$ and $SE(\hat{\beta}^T)$ are the β^T estimate and its standard error and $u_{1-\alpha}$ is the $1 - \alpha$ quantile of a reference distribution.

- $\delta = \log(1.25) = -\log(0.8)$ and the significance level $\alpha = 0.05$ according to regulation authorities \rightarrow The typical BE acceptance criteria is for the 90% confidence interval (CI) around the geometric mean ratio (GMR) of AUC or Cmax to be included in the [80; 125]% interval.

Model-based (MB) TOST²

- Based on a nonlinear mixed effect model (NLMEM) analysis of the data
- Crossover (C) design studies

$$C_{ijk} = f(t_j, \phi_{ijk}) + g(t_j, \phi_{ijk})\epsilon_{ijk} \\ \log(\phi_{ijkl}) = \log(\lambda_i) + \beta_l^T T_{ijk} + \beta_l^{P'} P_k + \beta_l^{S'} S_{ij} + \eta_{ijl} + \kappa_{ijkl}$$

- $f(\cdot)$ the structural model and $g = a + bf(\cdot)$ the error model
- ϕ_{ijkl} is the l^{th} element of the PK parameter η_p -vector of individual i at time t_j and occasion k
- λ_i the i^{th} element of the fixed effect η_p -vector for the covariate reference class
- T_{ijk} , P_k and S_{ij} the treatment, period and sequence covariate vectors
- β_l^T , $\beta_l^{P'}$ and $\beta_l^{S'}$ the coefficients of treatment, period and sequence effect vectorfor the l^{th} individual parameter
- η_{ijl} the l^{th} element of the random effect vector η_{ij} for subject i at time t_j capturing the between subject variability (BSV)
- κ_{ijkl} the l^{th} element of the vector of random effects κ_{ijk} for subject i at time t_j and period k , capturing the within subject variability (WSV)
- $\eta_{ij} \sim N(0, \Omega)$ and $\kappa_{ijk} \sim N(0, \Gamma)$ independent with ω_l^2 and γ_l^2 the l^{th} diagonal element of Ω and Γ
- $\epsilon_{ijk} \sim N(0, \sigma^2)$ the independent residual errors

- Parallel (P) design studies

$$C_{ij} = f(t_j, \phi_{ij}) + g(t_j, \phi_{ij})\epsilon_{ij} \\ \log(\phi_{ijl}) = \log(\lambda_i) + \beta_l^T T_{ij} + \eta_{ijl},$$

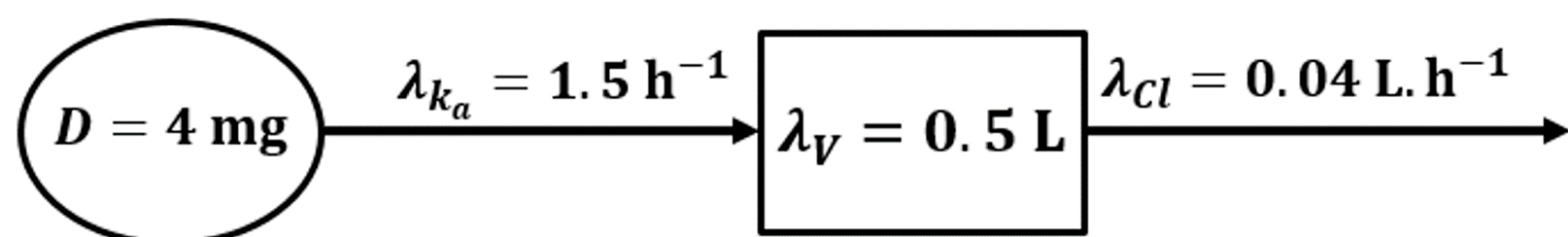
- β_{AUC}^T and $\beta_{C_{max}}^T$ derived from functions of the λ and β^{T^2}
- $VAR(\beta_{AUC}^T)$ and $VAR(\beta_{C_{max}}^T)$ are derived using the delta-method using the inverse of the observed Fisher Information Matrix (FIM) with 90% CI $= \pm u_{1-\alpha} SE$
- NLME modeling was performed using Monolix 2018R2

Obiective

To evaluate MB-TOST, by clinical trial simulation, for the analysis of BE crossover (C) and parallel (P) design 1 single point pharmacokinetic studies

Simulation study

- PK model of concentrations of the anti-asthmatic drug theophylline, a narrow therapeutic index, however conventional BE limits are used for the analysis



- Limit of Quantification at 0.2 mg/L
- Designs
 - each of the N subjects provides one sample in one (parallel, P) or both (crossover, C) eyes at one sampling time chosen among a set of 10 or 5 possible sampling times:

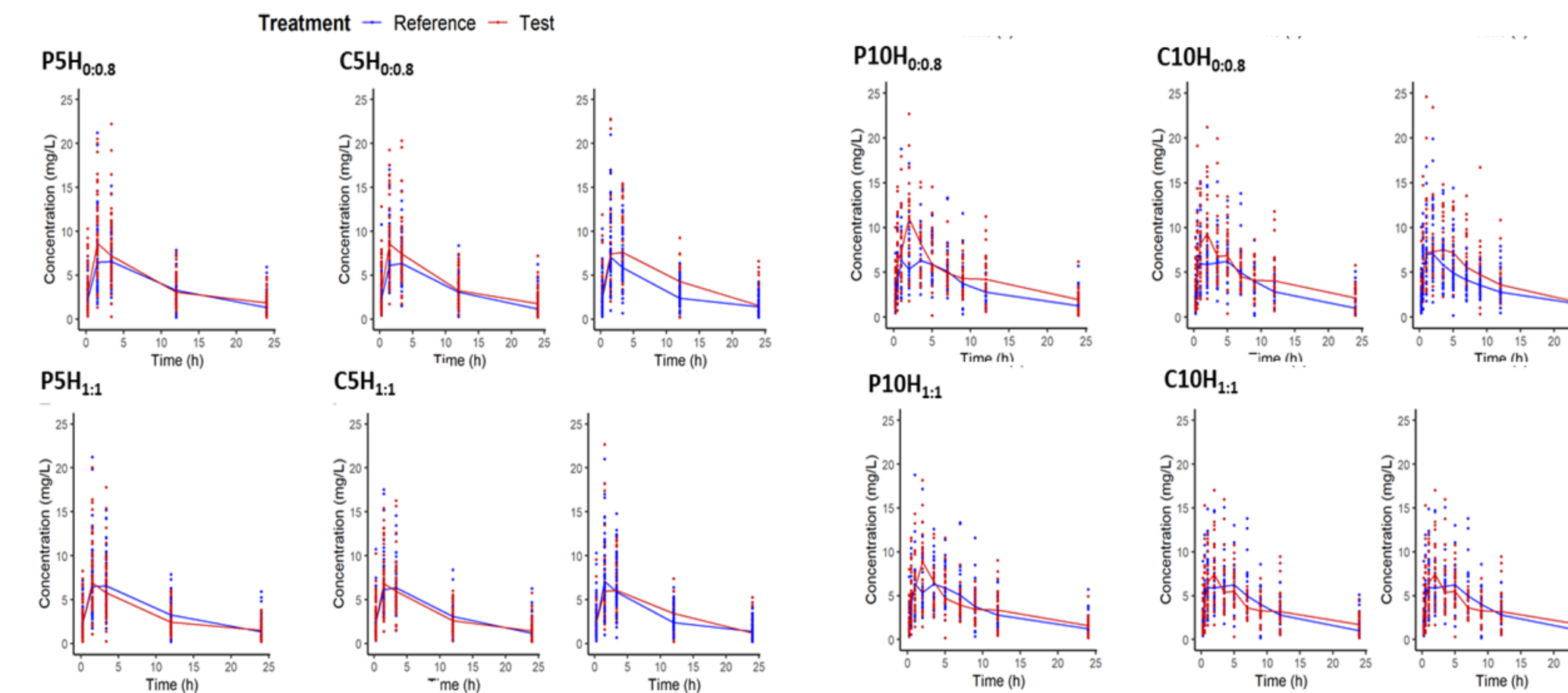
Design	N	Total sample size	Sampling times (h)	Subjects per sampling time
Parallel	500	500	{0.25, 0.5, 1, 2, 3.5, 5, 7, 9, 12, 24}	50
	500	500	{0.25, 1.5, 3.35, 12, 24}	100
Crossover	500	1 000	{0.25, 0.5, 1, 2, 3.5, 5, 7, 9, 12, 24}	50
	500	1 000	{0.25, 1.5, 3.35, 12, 24}	100

	BSV			WSV			Error model	
	ω_{k_a} (%)	$\omega_{V/F}$ (%)	$\omega_{Cl/F}$ (%)	γ_{k_a} (%)	$\gamma_{V/F}$ (%)	$\gamma_{Cl/F}$ (%)	a (mg/L)	b (%)
Parallel	52	52	52	-	-	-	0.1	10
Cross-over	50	50	50	15	15	15	0.1	10

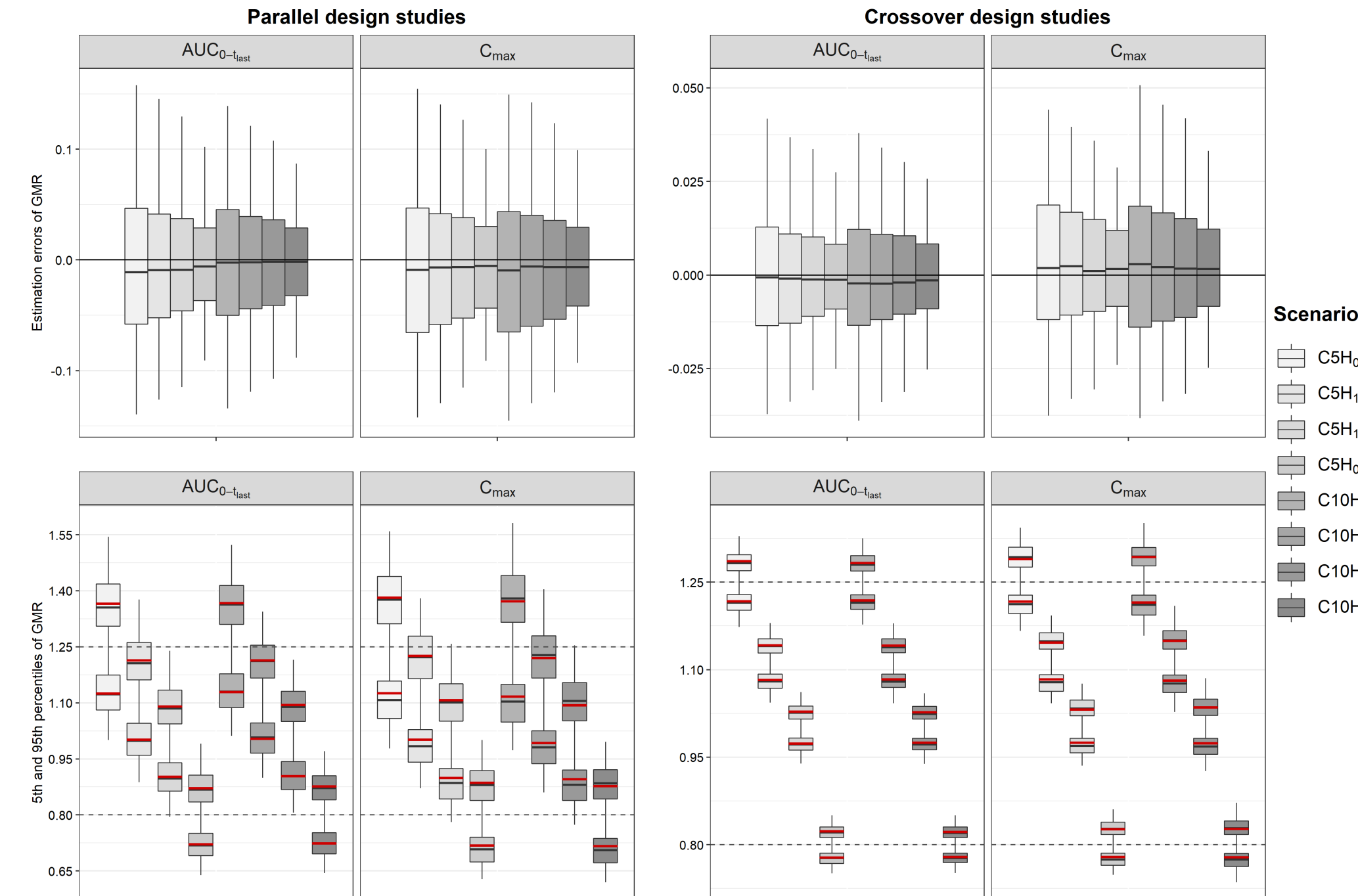
- Under $H_0 : \beta^T = \log(0.8)$ and $\beta^T = \log(1.25)$ to assess type I error
- Under $H_1 : \beta^T = \log(0.9)$ and $\beta^T = \log(1)$ to assess the power
- 16 scenarios evaluated with 500 simulated data sets for each scenario \rightarrow 95% prediction interval around 0.05 = [0.033-0.073]

Results

SIMULATED DATA SET

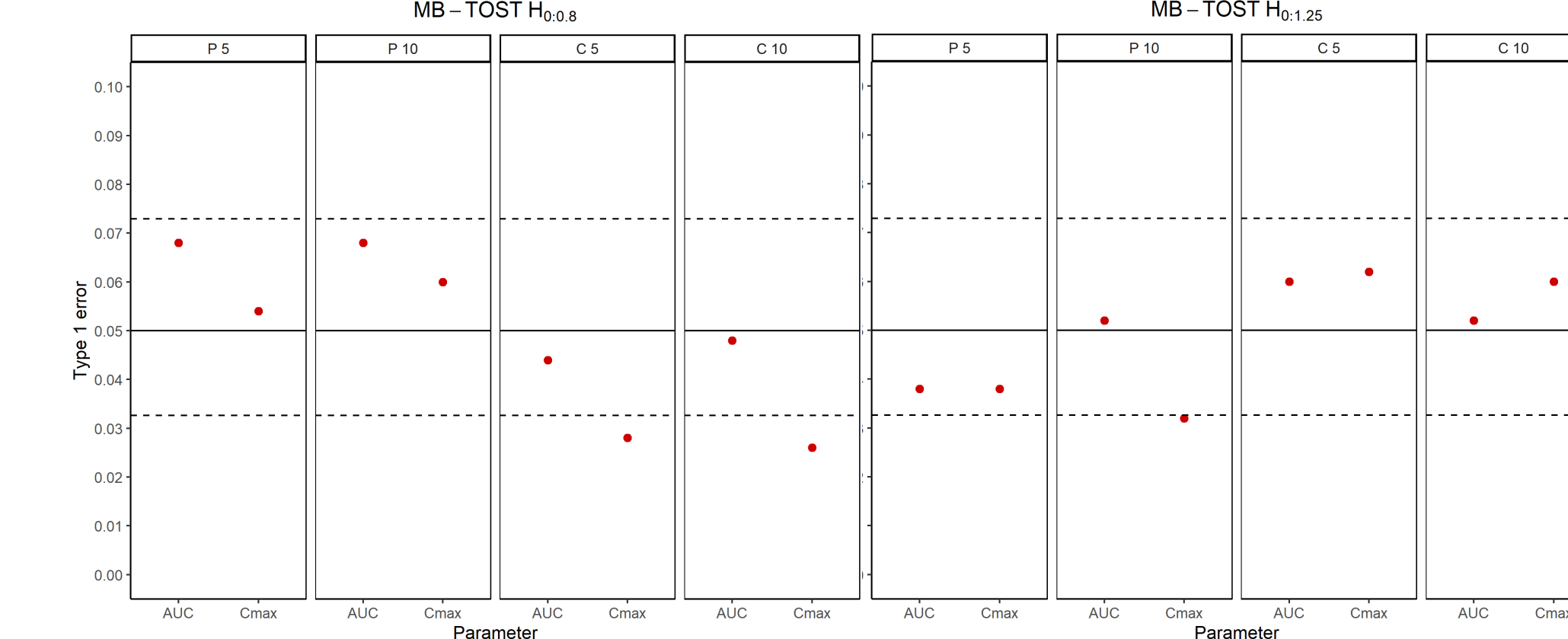


ESTIMATION



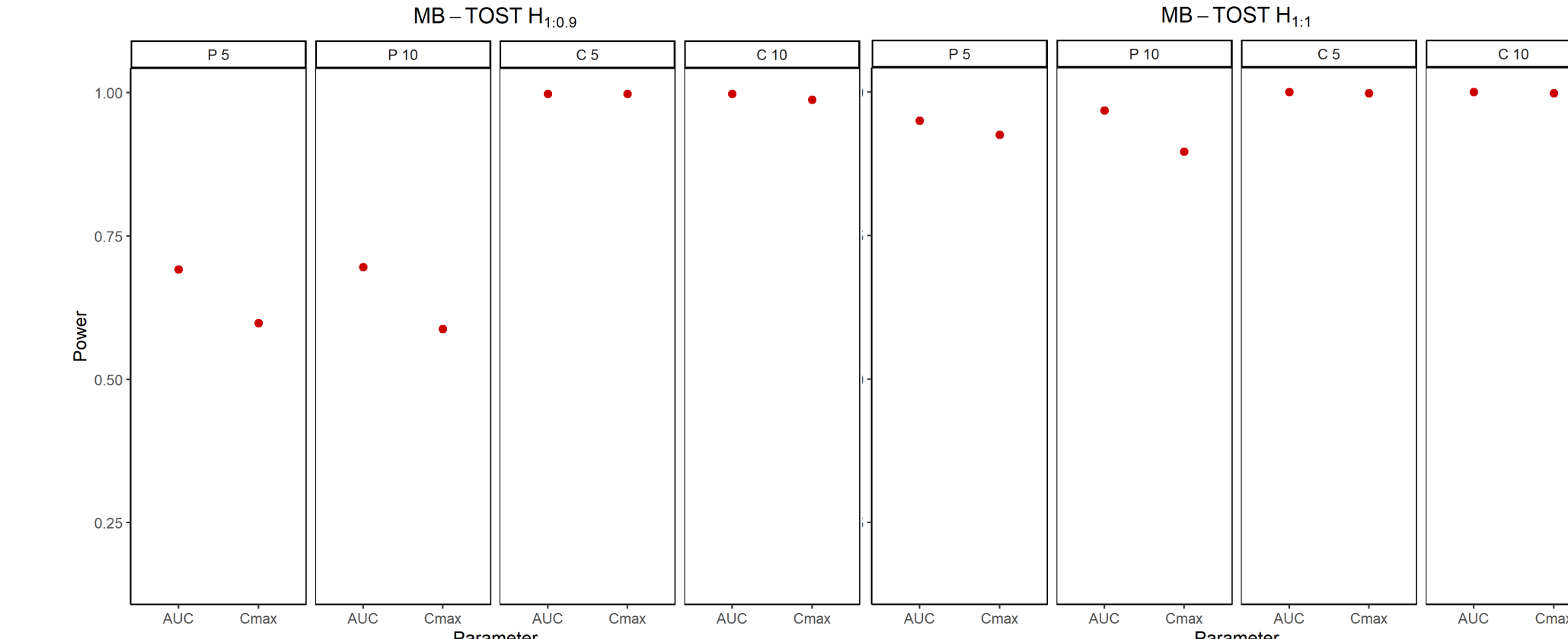
- Model-based GMR for $AUC_{0-t_{last}}$ and C_{max} were unbiased and precise
- \rightarrow validation of the parameter estimation step
- Overestimation of 90% CI for C_{max}
- Crossover studies, as expected, resulted in smaller 90% CI

TYPE I ERROR



- Controlled type 1 errors for AUC under 0.07 on parallel (P) and crossover (C) study designs
- Significantly conservative type 1 errors for C_{max} for scenarios $C5H_{0;0.8}$ and $C10H_{0;0.8}$

POWER



- High power estimates close to 100% on crossover studies
- rather low simulated WSV \rightarrow small 90% CIs

Conclusion

Simulation study shows that MB approaches, when the PK model is accurately specified, can be a good alternative approach for BE studies with only one-time point measured drug concentration.

References

¹ Schuirmann DJ. J Pharmacokinet Biopharm. 1987;15(6):657459680; ² Dubois A, Lavielle M, Gsteiger S, Pigeolet E, Mentré .Stat Med. 2011;30(21):25822600;

Acknowledgements

This work was supported by the U.S. Food and Drug Administration (FDA) under contract 75F40119C10111. The authors thank FDA for this funding. The views expressed here do not necessarily reflect the views or policies of the FDA.