



Caroline Bazzoli, Dubois Anne, Thu Thuy Nguyen, France Mentré

UMR 738 INSERM and University Paris Diderot, Paris, France.

Context

- **Nonlinear mixed effect modeling or population analysis**
 - pharmacokinetic (PK) /pharmacodynamic (PD) data
- **Population analyses often based on limited sampling strategy**
 - ethical and / or financial reasons
- **Methodology developed to ensure informative population design**
 - based on the Fisher information matrix (M_F)
 - expression of M_F using a first order Taylor expansion of the model [1]
- **Implementation in a R function PFIM [2]**
 - R function for population design evaluation and optimization
- **Extension of this methodology for multiple response models [3]**
 - for models with parameters quantifying influence of discrete covariates [4]
 - for models including within-subject variability [5]
- **Implementation in a new version PFIM 3.2 (released in January 2010)**

Objective

- To illustrate the use of PFIM 3.2 using an example on the PK and the PD of warfarin, an oral anticoagulant [6, 7]

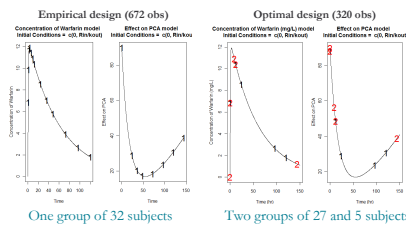
Joint PK/PD model of warfarin

- **PK: total racemic warfarin plasma concentration**
 - single oral dose of 100 mg
 - one compartment model, first order absorption and elimination
 - exponential modeling of the random effects
- **PD: effect on prothrombin complex activity (PCA)**
 - turnover model with inhibition of the input
 - exponential modeling of the random effects

PK/PD design on Warfarin

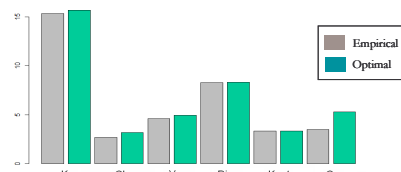
- **Evaluation of the empirical design**
 - one group of 32 subjects
 - 13 sampling times for PK and 7 sampling times for PD
- **Design optimization with the Federov-Wynn algorithm**
 - 32 subjects with only 5 sampling times per subject
 - common to both responses
 - sampling times from empirical design (PK + PD)

Figure 1. Empirical design versus optimal design



→ 2.1 less samples with optimal design than empirical design

Figure 2. Comparison of predicted RSE for fixed effects (%)



→ Relative standard errors (RSE) in the same range for the fixed effects

Pharmacogenetic on warfarin PK

- **Single nucleotide polymorphism (SNP) CYP2C9**
 - SNP on the gene of a cytochrome involved in the warfarin metabolism
 - influence of the genetic covariate on the clearance
 - clearance decrease of 50% for subjects with a mutant genotype
- **Evaluation of the optimized PK/PD design with the effect of the genetic covariate on clearance**
 - predicted power of the comparison Wald test (type I error=5%)
 - number of subjects needed (given power=90%)

Table 1. Covariate effect parameters

Covariate	Parameter Associated	Categories	Proportions of subjects in each category (%)	β
CYP2C9	CL	Wild genotype (ref)	60	$\log(0.5)=-0.69$ or $\log(0.8)=-0.22$
		Mutant genotypes	40	

Figure 3. PK/PD design evaluation output for $\beta = \log(0.5) = -0.69$

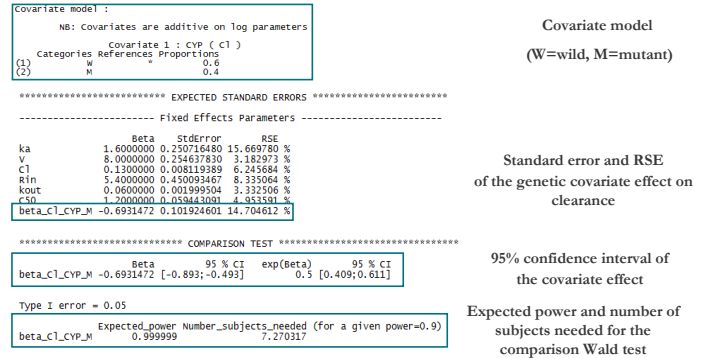


Table 2. Results on genetic covariate effect

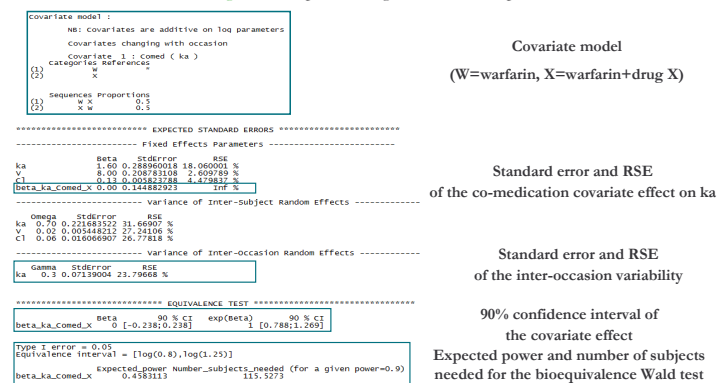
β	SE (RSE %)	95% CI(β)	exp(β)	95% CI(exp(β))	Expected power	Number of subjects needed
-0.69	0.10 (15)	[-0.89; -0.49]	0.50	[0.41; 0.61]	1	8
-0.22	0.10 (43)	[-0.41; -0.03]	0.80	[0.66; 0.97]	0.63	64

→ Increase of the number of subjects needed when the effect on the clearance decreases

Two-way crossover PK study on warfarin

- **Planification of a new study to assess the absence of interaction of drug X on warfarin ka**
 - two-period, two-sequence balanced crossover trial
 - inter-occasion variability on ka: $\gamma^2_{ka}=0.3$ (CV=55%)
 - expected effect of the co-medication on ka: $\beta=\log(1)=0$
- **Evaluation of the empirical PK design**
 - 32 subjects
 - sampling times
 - 0.5, 1, 2, 3, 6, 9, 12, 24, 36, 48, 72, 96 and 120 hours
- **Predicted power of the bioequivalence Wald test (type I error=5%)**
- **Number of subjects needed (given power=90%)**

Figure 4. Empirical design evaluation output



→ To achieve a power of 90%, 116 subjects with the same sampling design would be needed to perform the bioequivalence test

Conclusion

- Illustration of the choice of the design and the number of subjects needed to achieve a given power of the Wald test of discrete covariate for complex PK/PD model
- Great potential of PFIM 3.2 to optimize parallel or crossover designs and to control expected power of a Wald test for comparison or bioequivalence
- PFIM 3.2 freely available at www.pfim.biostat.fr

Reference

- [1] Mentré F, Mallet A, Baccar D. *Biometrika*. 1997..
- [2] Retout S, Mentré F. *Journal of Biopharmaceutical Statistics*. 2003.
- [3] Bazzoli C, Retout S and Mentré F. *Statistics in Medicine*. 2009.
- [4] Retout S, Comets E, Samson A, Mentré F. *Statistics in Medicine*. 2007.
- [5] Nguyen TT, Bazzoli C and Mentré F. *American Conference on Pharmacometrics*. 2009 (Poster).
- [6] O'Reilly RA, Aggeler PM. *Circulation*. 1968.
- [7] O'Reilly RA, Aggeler PM, Leong LS. *The Journal of Clinical Investigation*. 1963.