

Introduction to population pharmacokinetics *"pharmacometrics"*

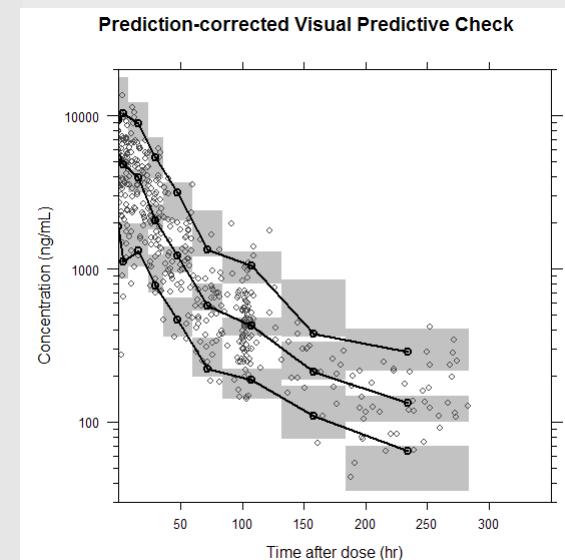
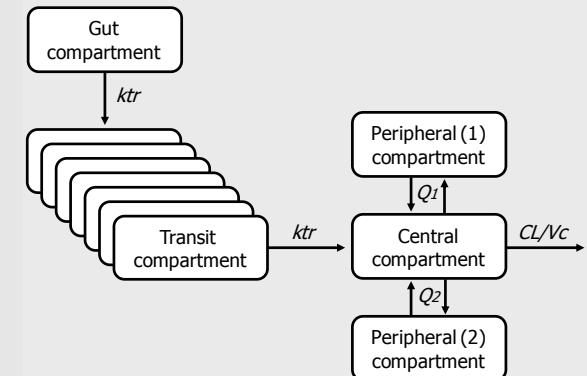
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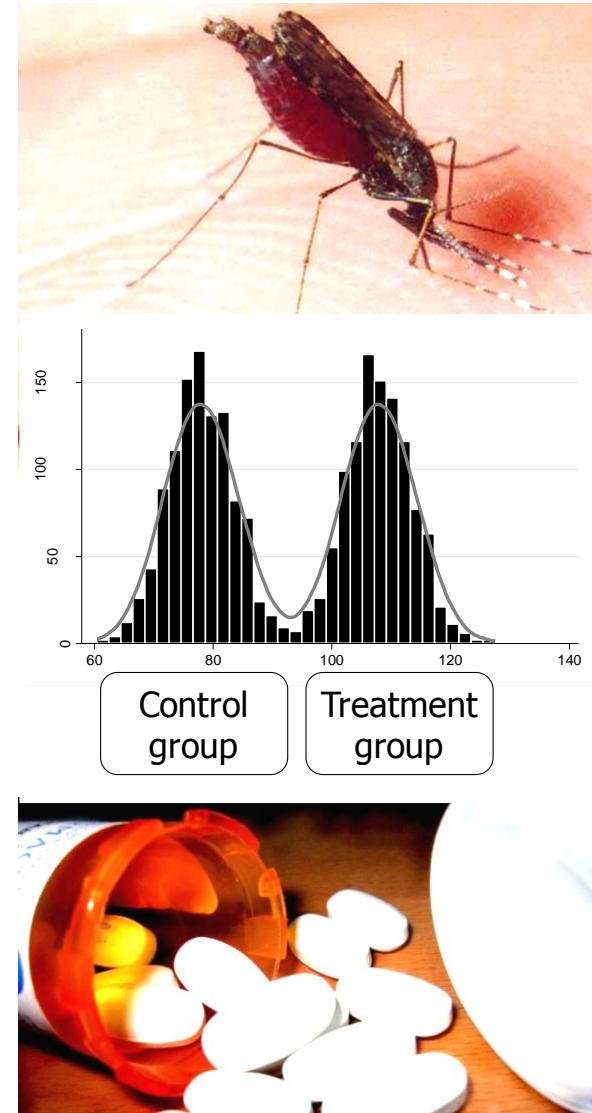


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TROPICAL MEDICINE RESEARCH PROGRAMME



Outline

- Introduction to pharmacometrics
- Structural modelling
 - Disposition kinetics
 - Semi-mechanistic models
 - Absorption models
- Variability
 - Inter-individual variability
 - Residual variability
- Covariate modelling
- Model diagnostics
- Antimalarial examples



Introduction to pharmacometrics

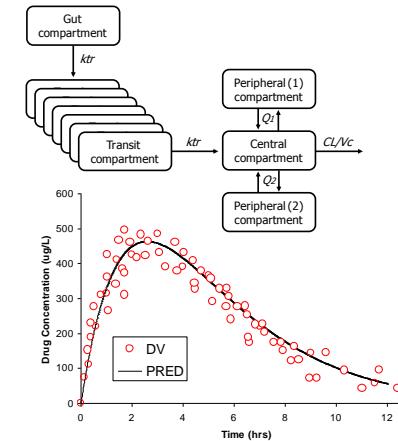
Pharmacometrics:

"the science of developing and applying mathematical and statistical models to characterize, understand and predict a drug's pharmacokinetics, pharmacodynamics and biomarker-outcome behavior"^[1]

- Pharmacokinetics
"what the body does to the drug"
- Pharmacodynamics
"what the drug does to the body"
- Biomarker-outcome behavior
disease progression, relationship between biomarkers and clinical endpoints etc. ~

“All models are wrong but some are useful...”

George Box, PhD

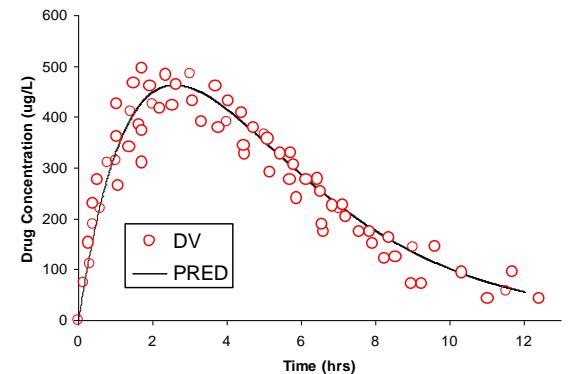
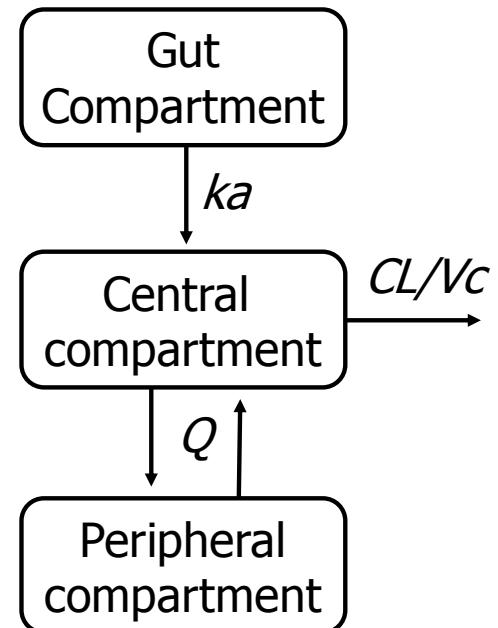


[1] Ette, E.I. and P.J. Williams, Pharmacometrics: The Science of Quantitative Pharmacology. 2007: John Wiley & Sons.

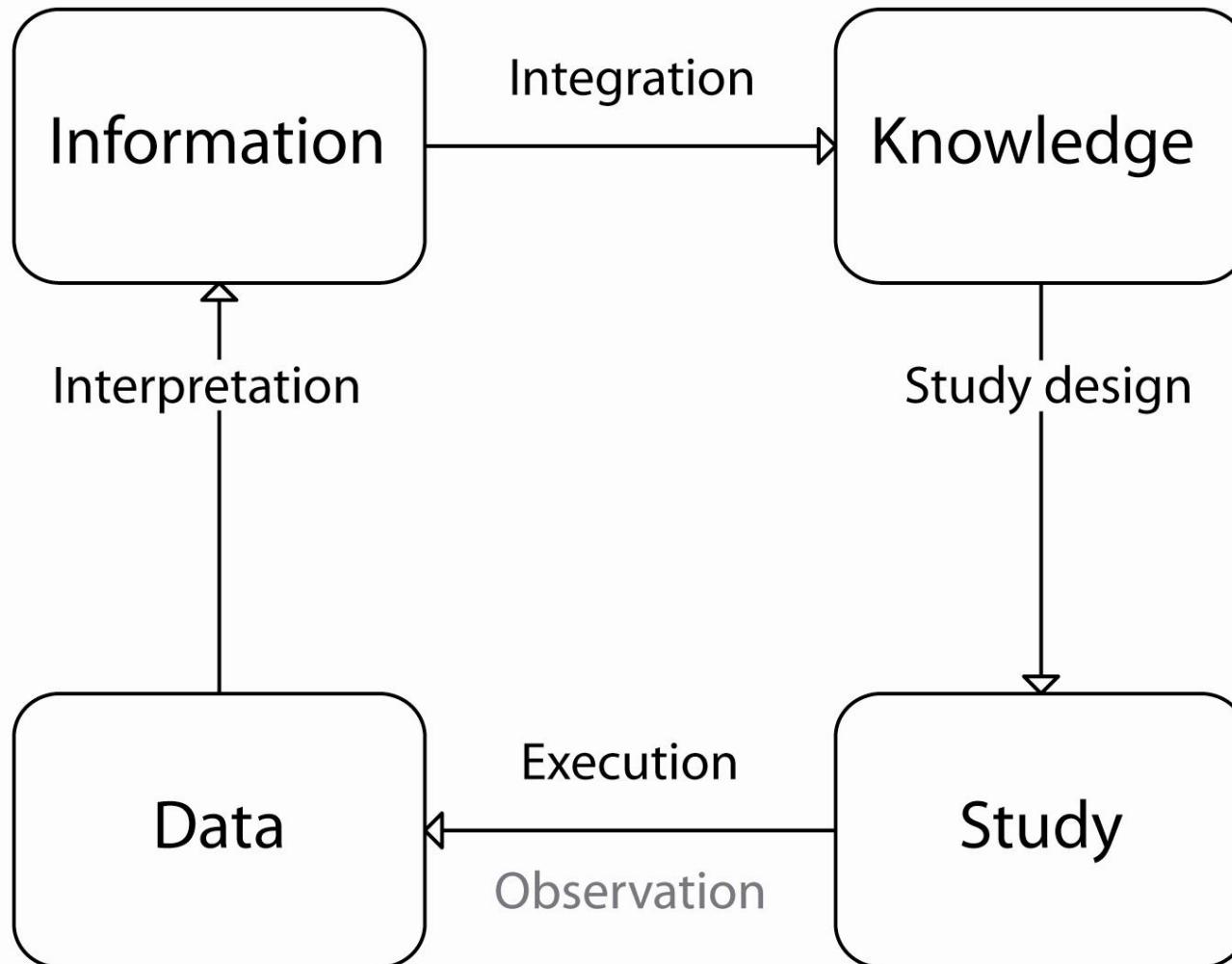


Introduction to pharmacometrics

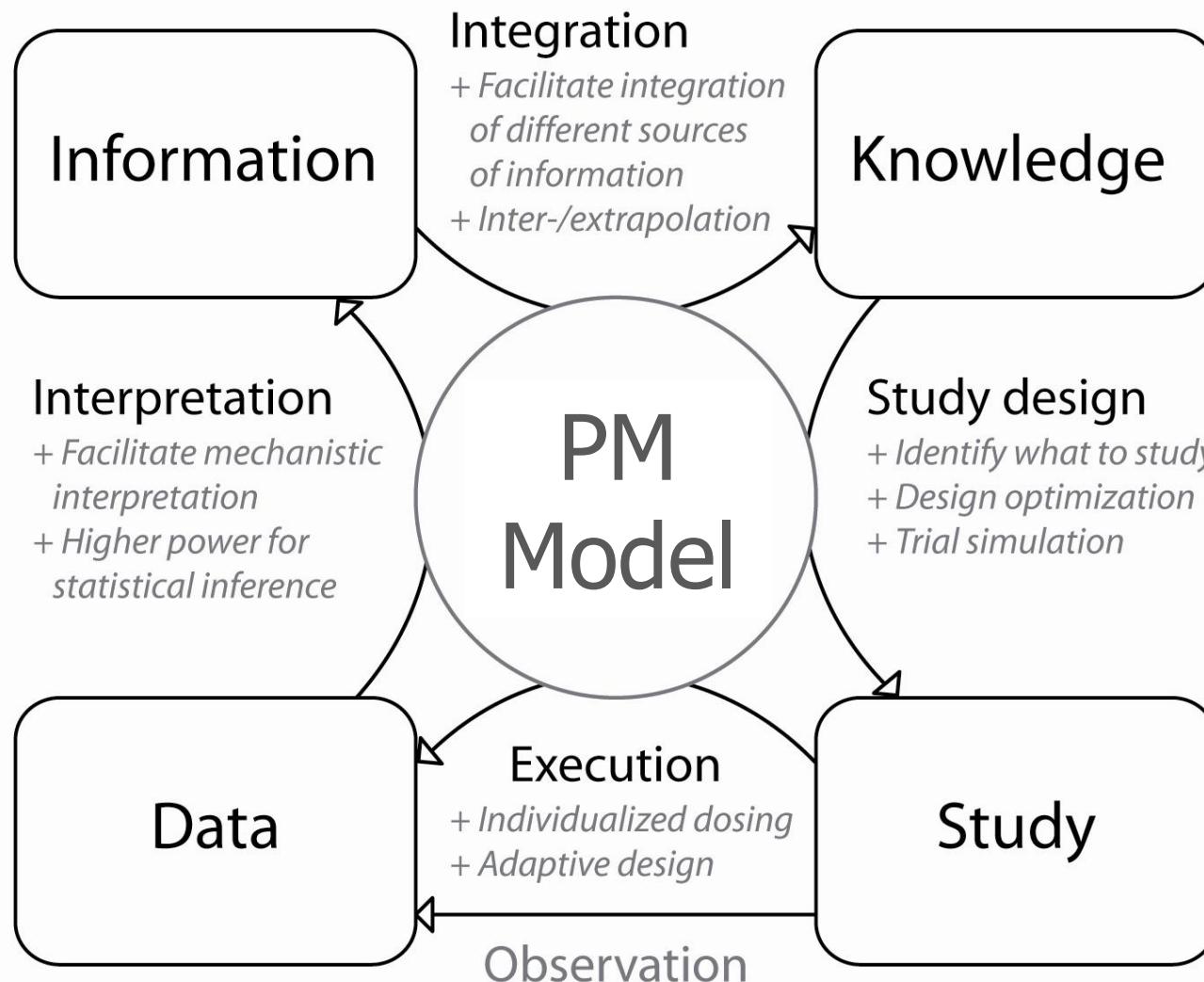
- Model-based view
 - Set of mathematical relationships
 - Separate components to describe complex systems
- To improve the description of pharmacological data
- To give a mechanistic understanding of the drug/human interaction (learning *vs* confirming)
- To explore and optimize dose regimens
- To explore and optimize future clinical trials



Introduction to pharmacometrics



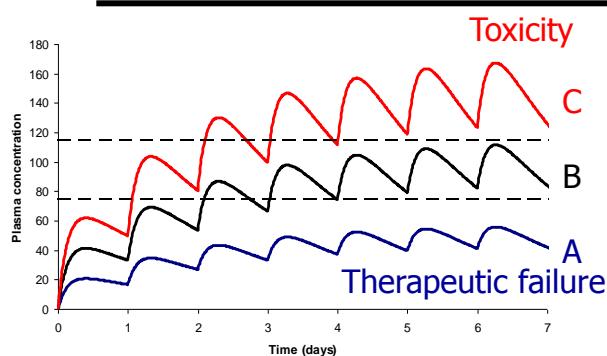
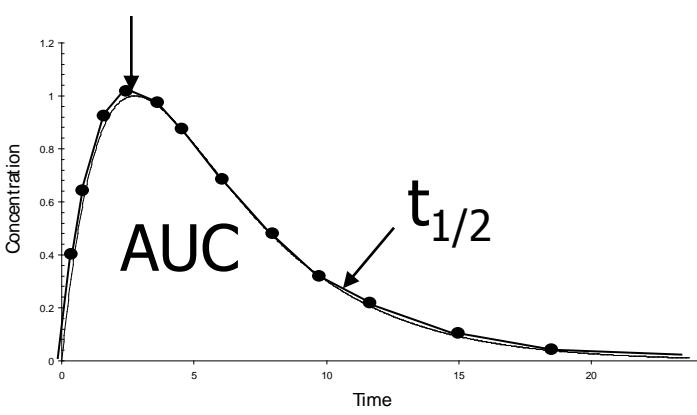
Introduction to pharmacometrics



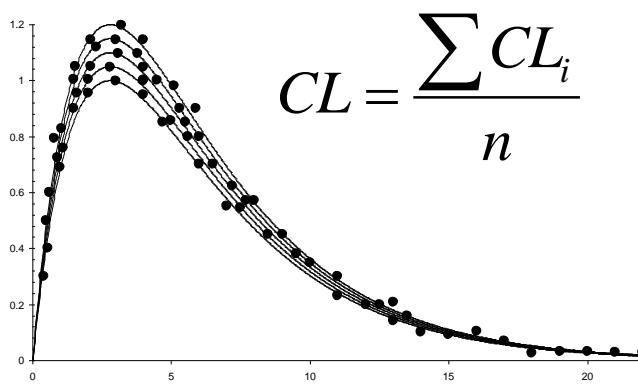
Introduction to pharmacometrics

Population pharmacokinetics (POP-PK)

Non-compartmental analysis

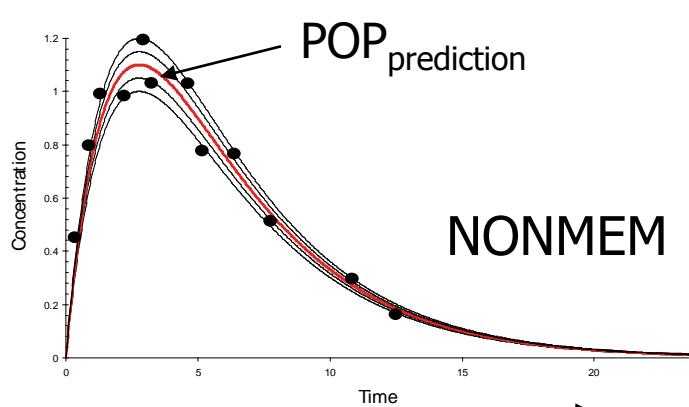


Standard two stage

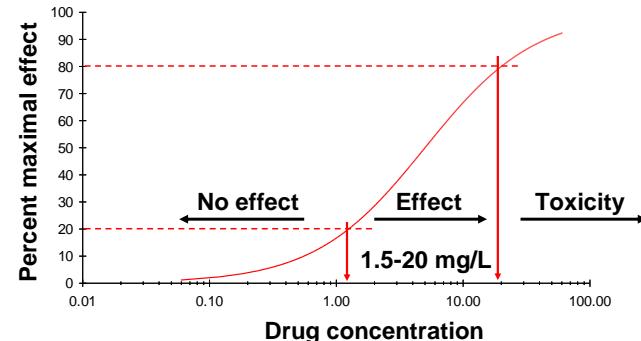


$$CL = \frac{\sum CL_i}{n}$$

Mixed effects modelling



Complexity



Introduction to pharmacometrics

Nonlinear mixed-effects model

Covariate
model

Structural
model

Random effects
model

Fixed effects

- Individual parameter estimates (CL, Ka, V)
- Sampling-schedules
- Dosing
- Covariates
- Formulation

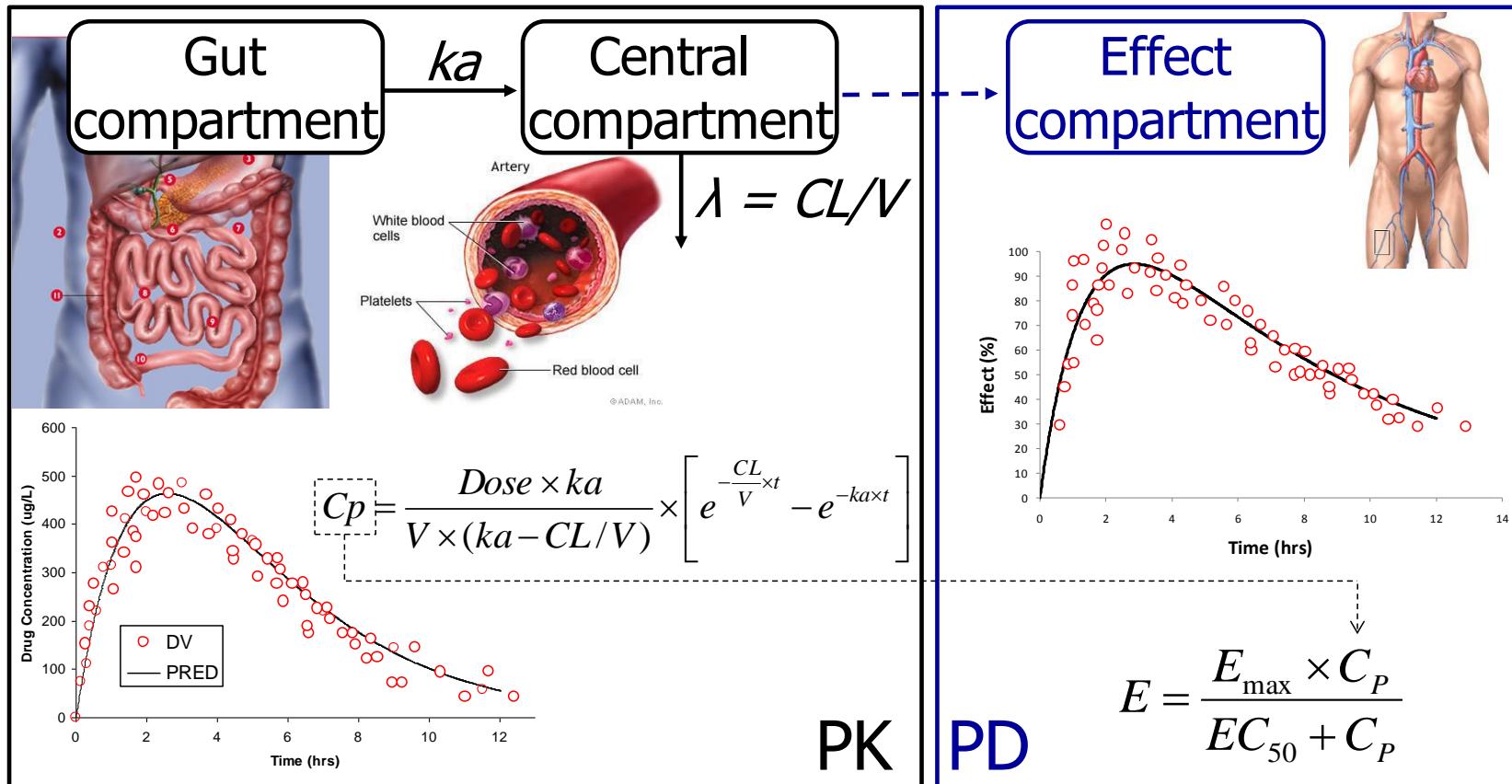
Random effects

- Measurement errors
- Inter-individual random effects
- Intra-individual random effects
- Model-misspecification
- Unknown factors

Introduction to pharmacometrics

■ Pharmacometrics (population PK/PD)

-The aim of the pharmacometric model is to describe pharmacological responses quantitatively and qualitatively



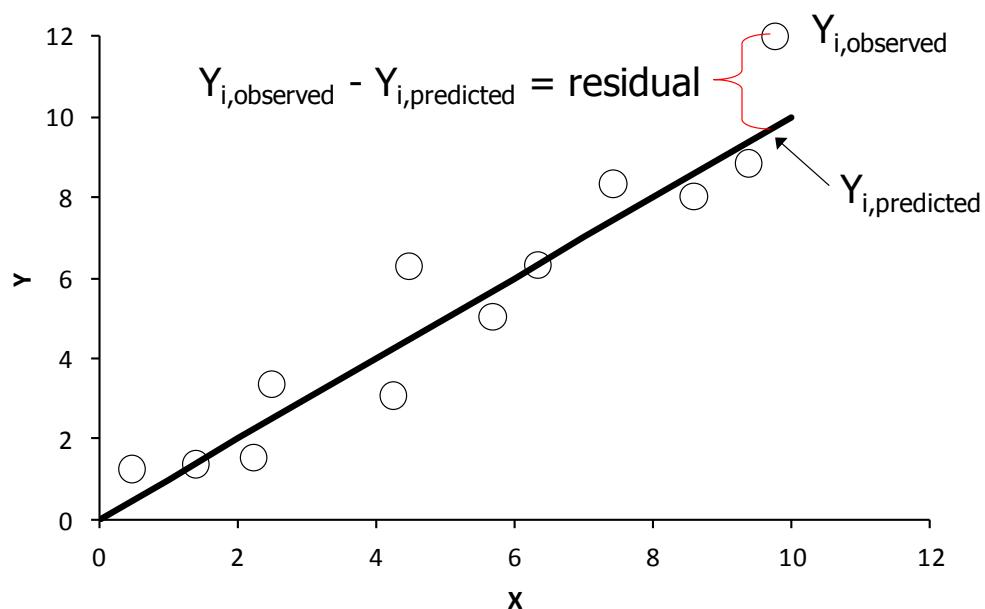
Introduction to pharmacometrics

Linear regression

$$Y = a \times x + b$$

Minimisation of squared residuals (SS):

$$\sum [Y_{i,\text{observed}} - Y_{i,\text{predicted}}]^2$$

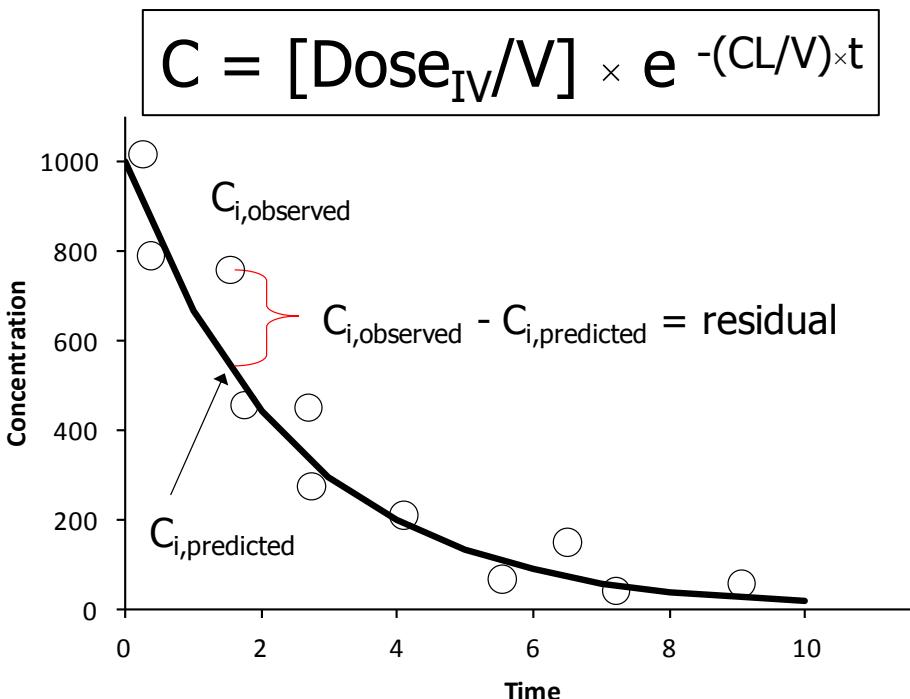


$$C = C_0 \times e^{-k \times t}$$

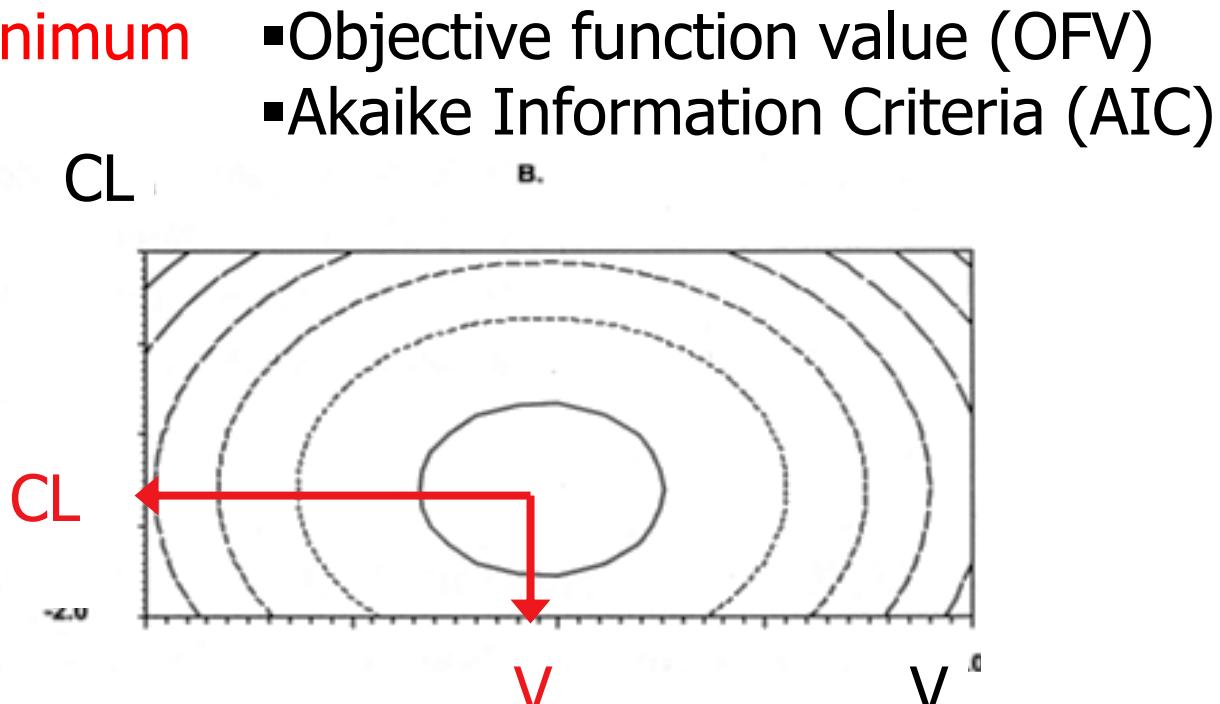
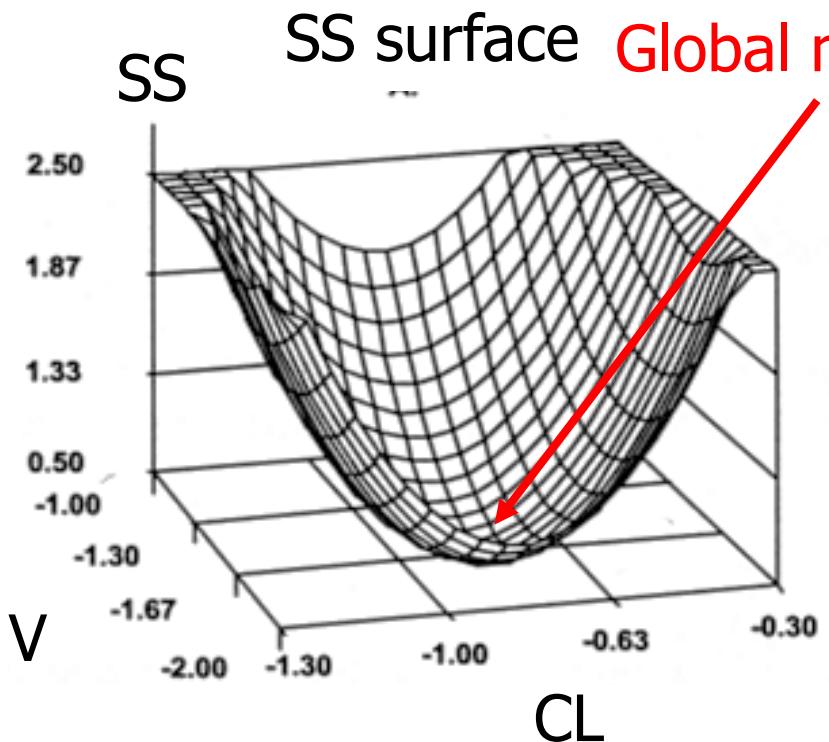
$$C_0 = \text{Dose}_{\text{IV}}/V$$

$$k = CL/V$$

Reparametrisation:



Introduction to pharmacometrics



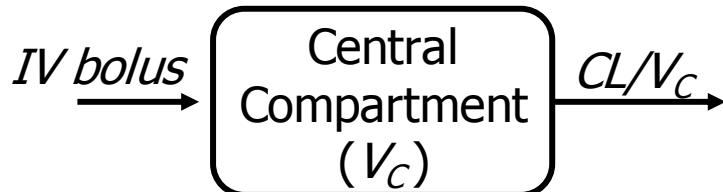
- Objective function value (OFV)
- Akaike Information Criteria (AIC)

- New combinations of parameter values are tested iteratively until convergence is reached.
- The best model parameters are those that correspond to the lowest SS (loglikelihood in nonlinear mixed-effects modelling)

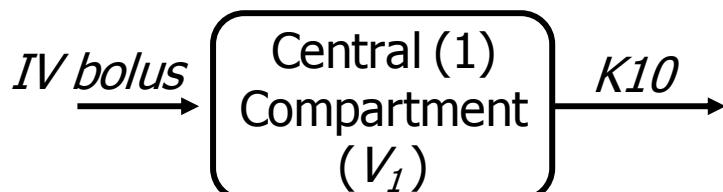


Structural modelling

1-compartment disposition model (IV administration)

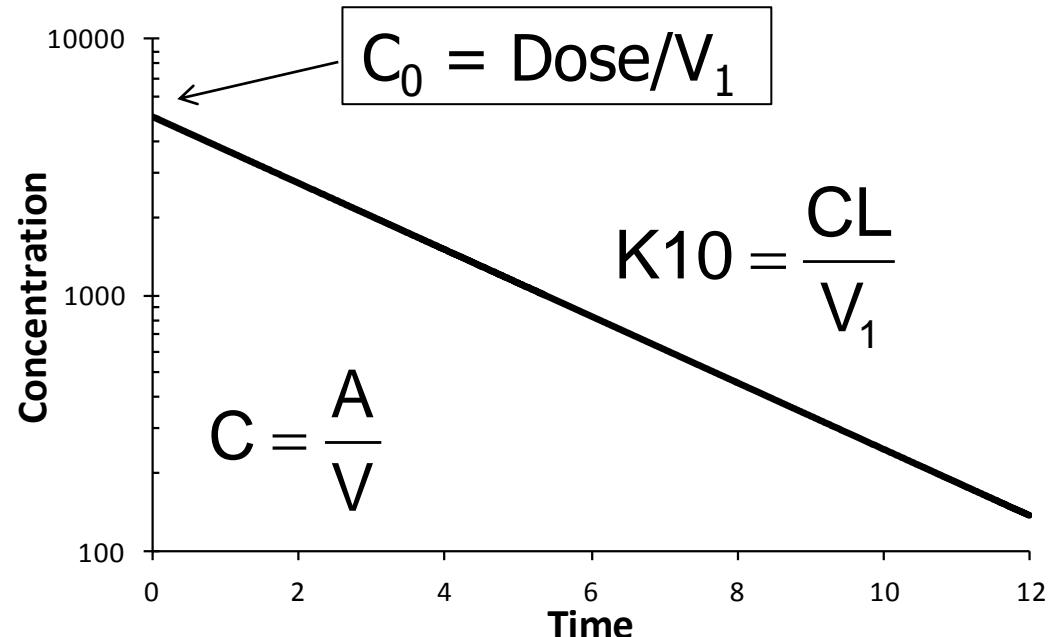


$$\frac{dA}{dT} = -\frac{CL}{V_C} \times A$$



$$\frac{dA}{dT} = -K10 \times A$$

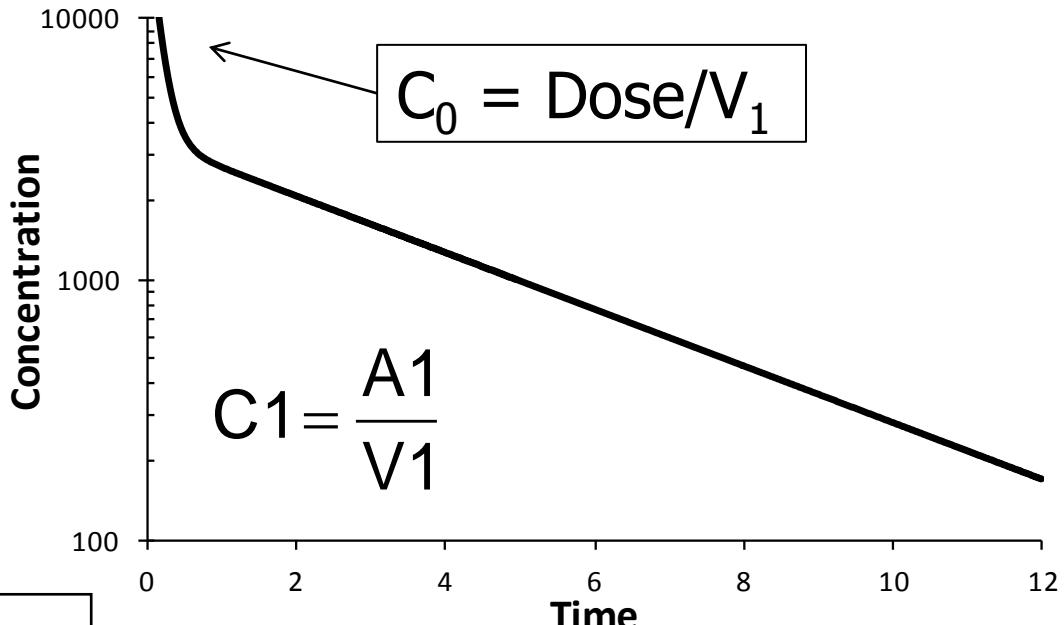
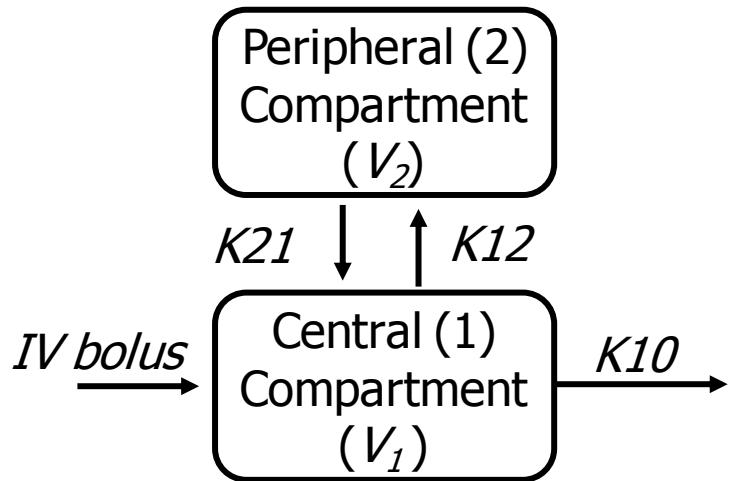
$$A(0) = \text{Dose}$$



$$t_{1/2} = \frac{\ln 2}{K10} = \frac{\ln 2 \times V_1}{CL}$$

Structural modelling

2-compartment disposition model (IV administration)



$$\frac{dA_1}{dT} = -K_{10} \times A_1 - K_{12} \times A_1 + K_{21} \times A_2$$

$$A_1(0) = \text{Dose}$$

$$\frac{dA_2}{dT} = K_{12} \times A_1 - K_{21} \times A_2$$

$$A_2(0) = 0$$

$$K_{10} = \frac{CL}{V_1}$$

$$K_{12} = \frac{Q}{V_1}$$

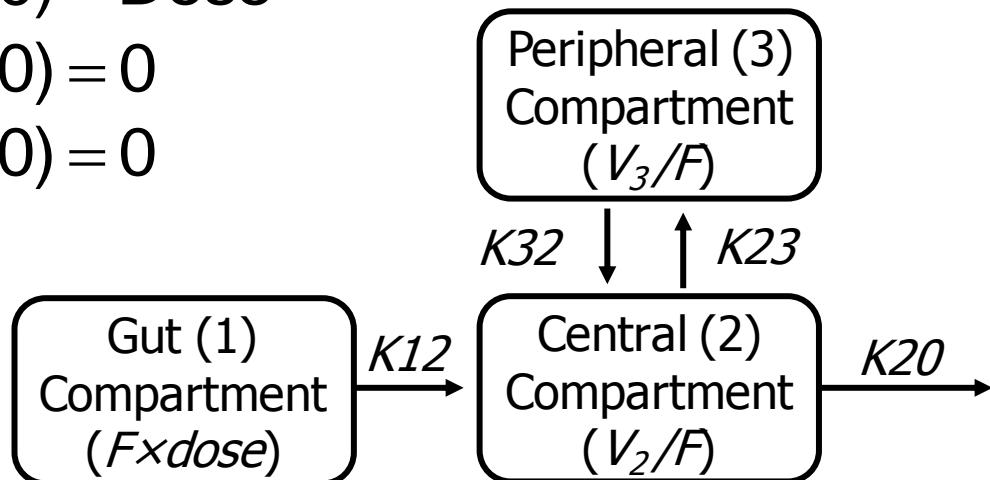
$$K_{21} = \frac{Q}{V_2}$$

Structural modelling

2-compartment disposition model (PO administration)

$$\begin{aligned} A_1(0) &= \text{Dose} \\ A_2(0) &= 0 \\ A_3(0) &= 0 \end{aligned}$$

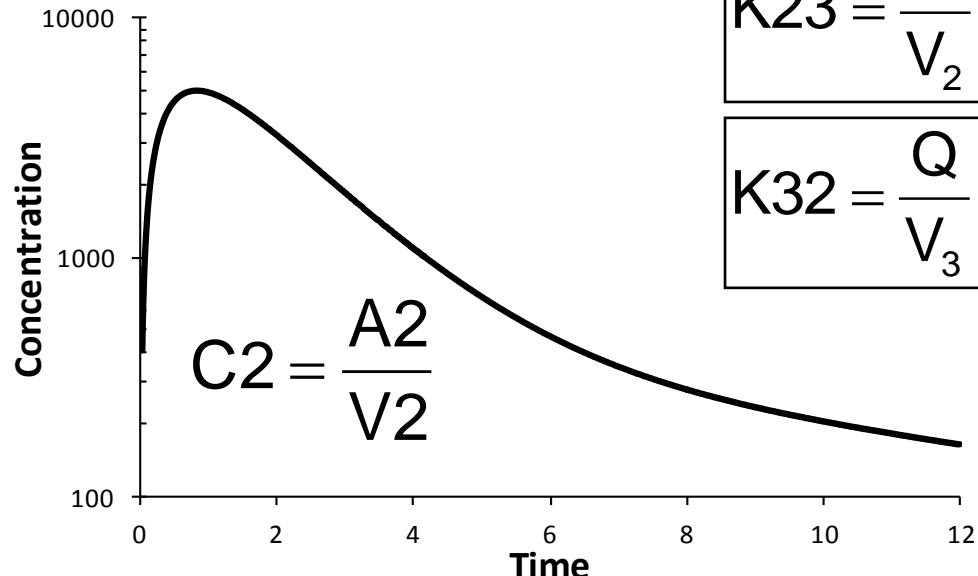
$$\frac{dA_3}{dT} = K_{23} \times A_2 - K_{32} \times A_3$$



$$K_{20} = \frac{CL}{V_2}$$

$$K_{23} = \frac{Q}{V_2}$$

$$K_{32} = \frac{Q}{V_3}$$



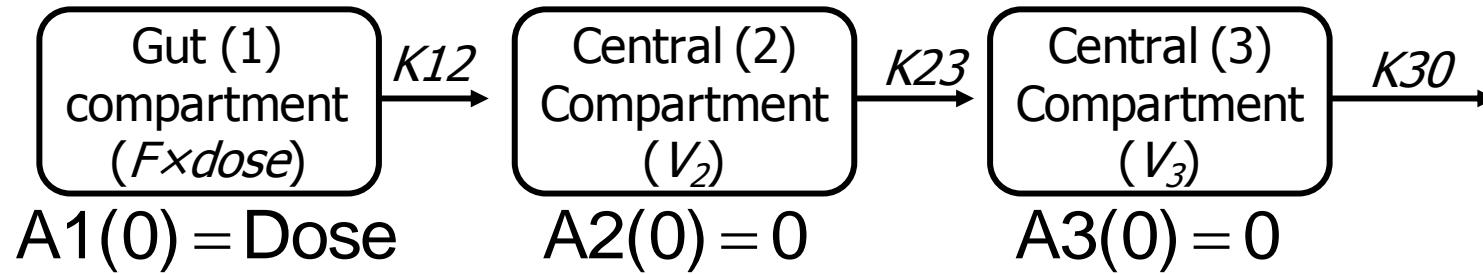
$$\frac{dA_1}{dT} = -K_{12} \times A_1$$

$$K_{12} = K_a$$

$$\frac{dA_2}{dT} = K_{12} \times A_1 - K_{23} \times A_2 + K_{32} \times A_3 - K_{20} \times A_2$$

Structural modelling

1-compartment disposition metabolite model (PO administration)



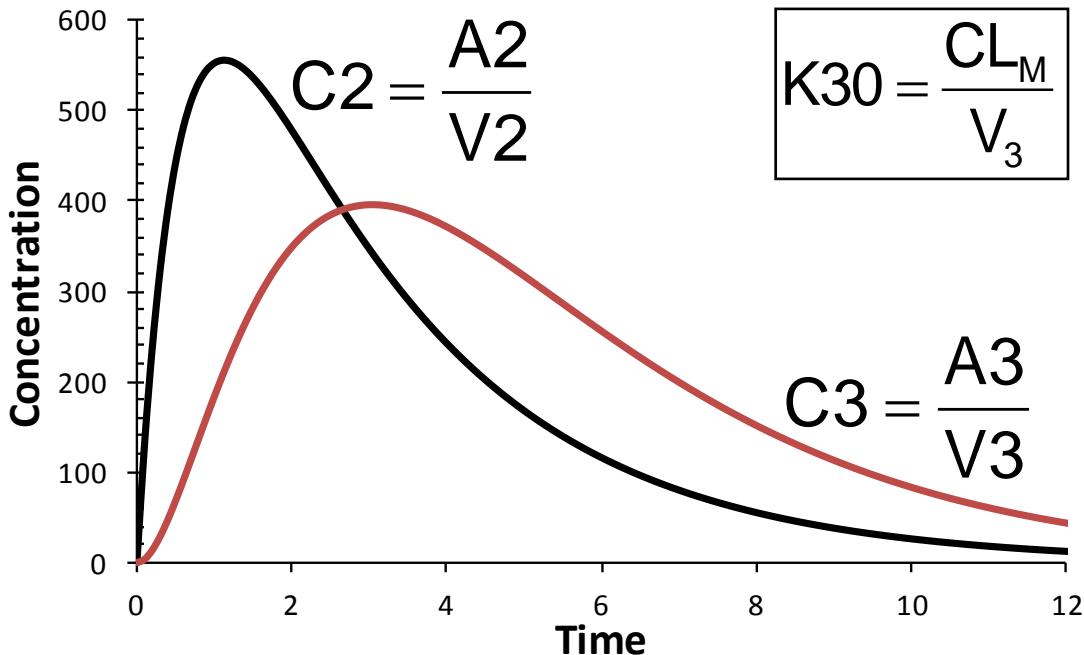
$$K_{12} = K_a$$

$$K_{23} = \frac{CL_p}{V_2}$$

$$\frac{dA_1}{dT} = -K_{12} \times A_1$$

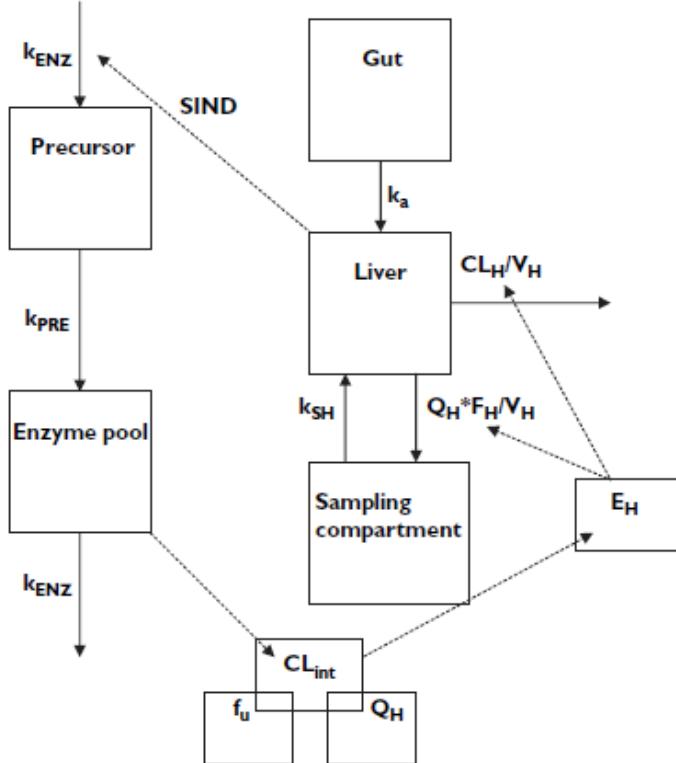
$$\frac{dA_2}{dT} = K_{12} \times A_1 - K_{23} \times A_2$$

$$\frac{dA_3}{dT} = K_{23} \times A_2 - K_{30} \times A_3$$



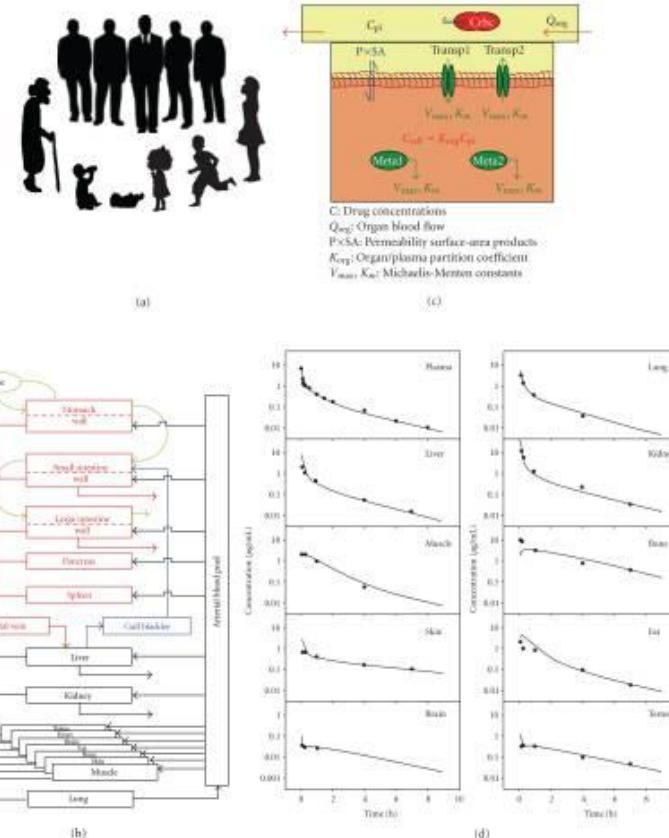
Structural modelling

Semi-physiological model describing the metabolic auto-induction and saturable first-pass hepatic extraction of artemisinin^[1]



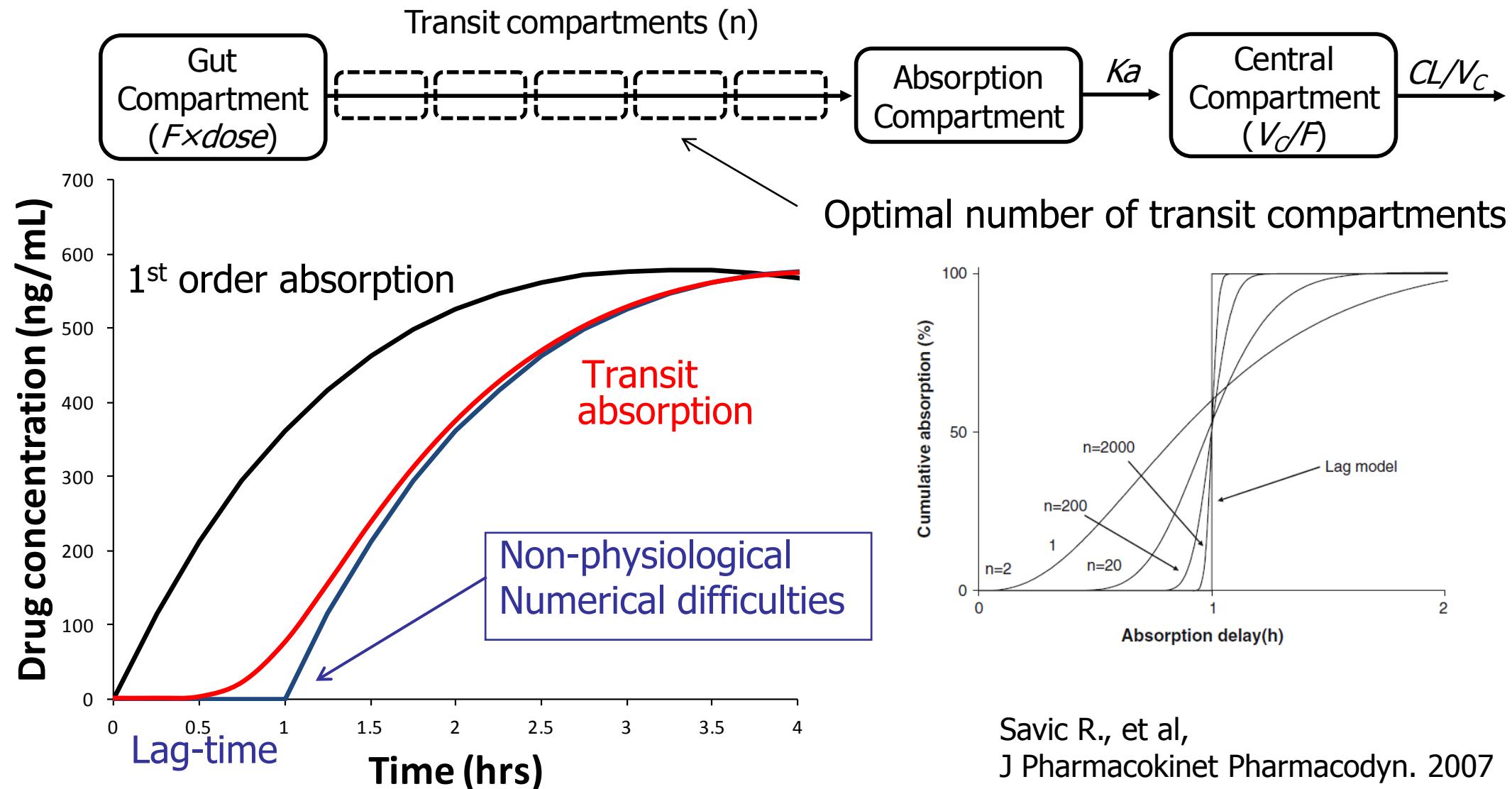
[1] Gordi T., et al, Br J Clin Pharmacol. 2005

Physiologically based pharmacokinetic modeling: methodology, applications, and limitations with a focus on its role in pediatric drug development. [2]



[2] Khalil F. & Laer S., J Biomed Biotechnol 2011

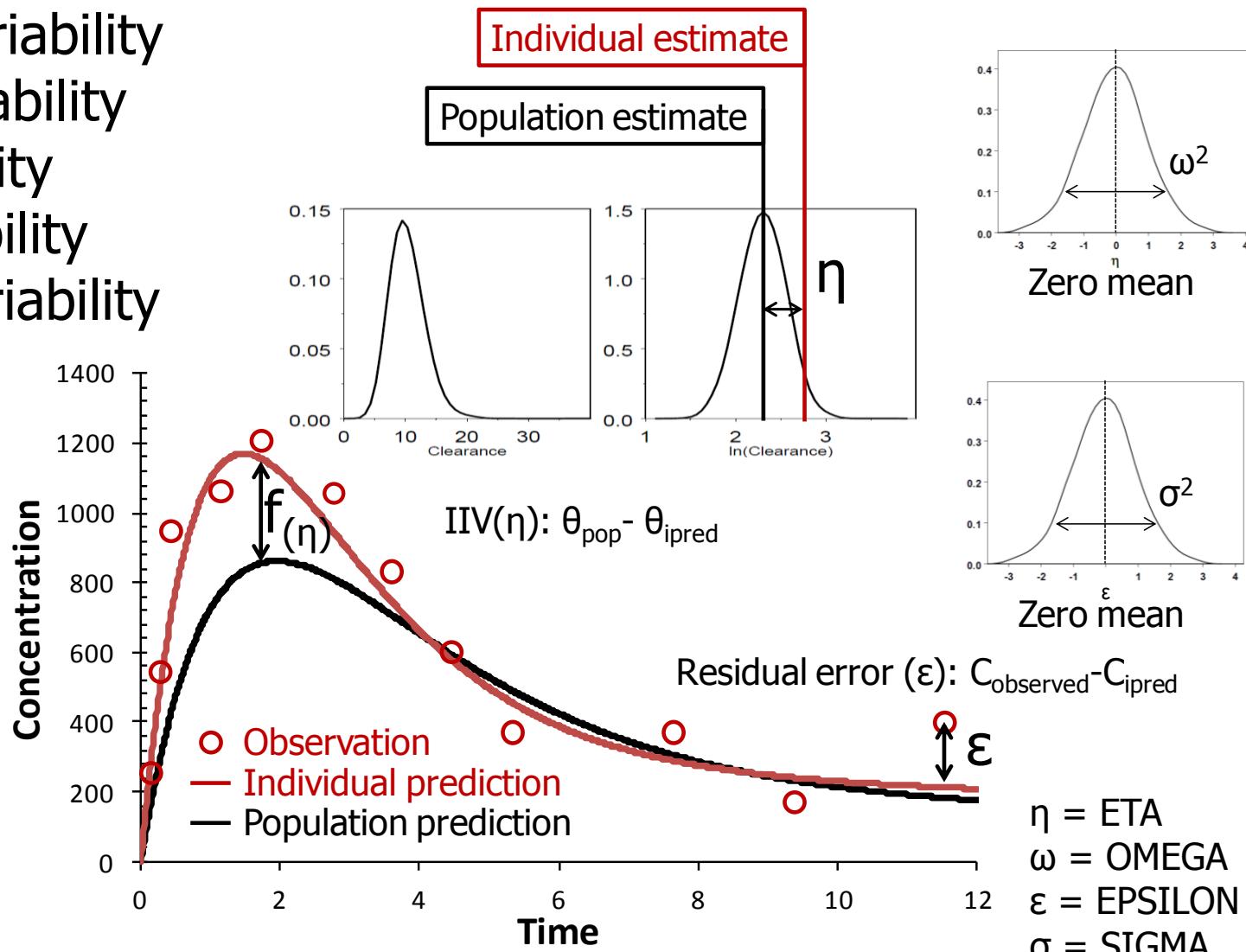
Structural modelling



Variability

Two main sources of variability

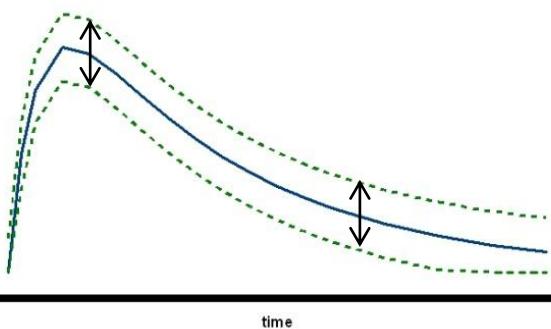
- Residual random variability
-unexplained variability
- Inter-individual variability
-between subject variability



Variability

$$y_{ij} = f_i + \varepsilon_{ij}$$

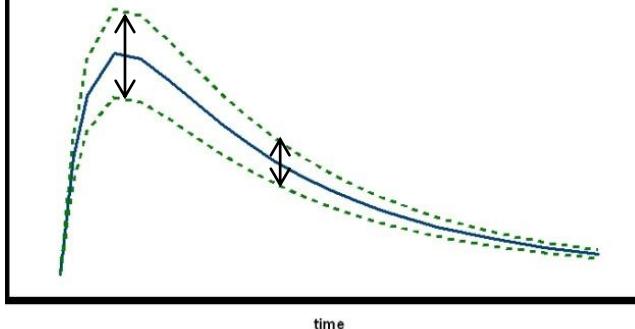
[Additive]



Homoscedastic error
-the residual variability
is constant

$$y_{ij} = f_i \times (1 + \varepsilon_{ij})$$

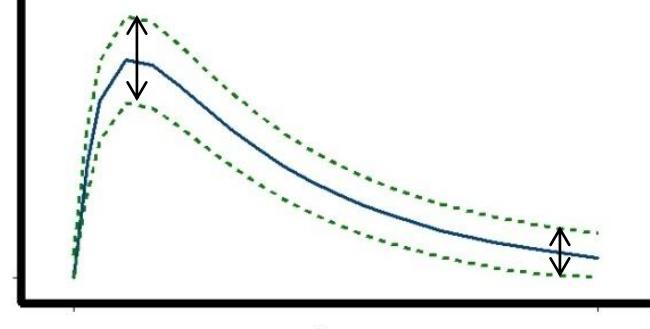
[Proportional]



Heteroscedastic error
-the residual variability
is proportional to the
size of the variable (i.e.
concentration)

$$y_{ij} = f_i \times (1 + \varepsilon_{1ij}) + \varepsilon_{2ij}$$

[Combined]



Slope-intercept model
-the residual variability
is proportional at high
predictions and
constant at low

Covariate modelling

Covariate modelling

- Identify patient sub-groups at potential risk
- Increase the predictive performance of the model
- Increase the understanding of a studied system
- Increase the mechanistic interpretation of the model

Covariates

- Demographics (pregnancy, BMI)
- Lab values (bilirubin, AGP)
- Disease parameters (parasitemia)
- Therapy related (co-medication)
- Environmental (smoking)

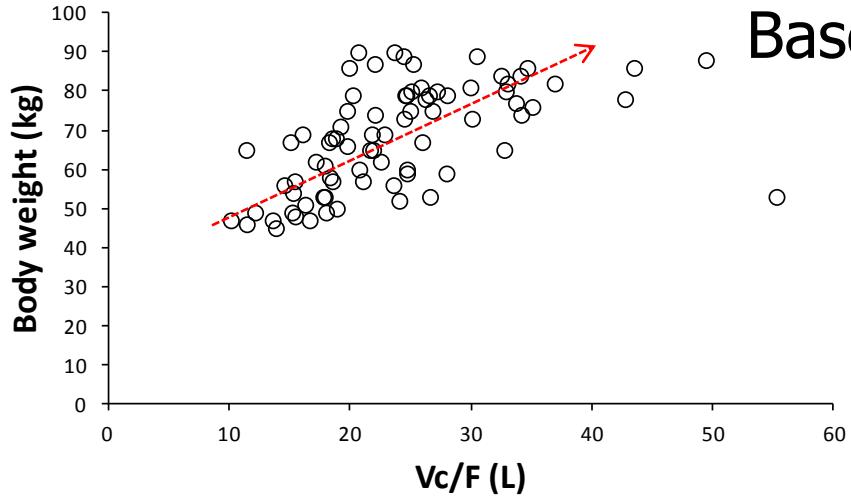
Covariate modelling: Stepwise forward addition and backward elimination

(automated functionality in Pearl-speaks-NONMEM: SCM)

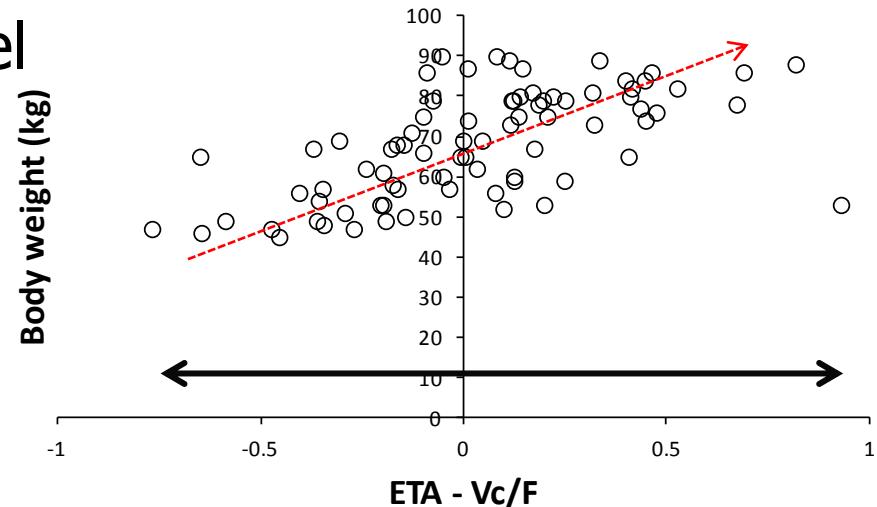
http://psn.sourceforge.net/pdfdocs/scm_userguide.pdf



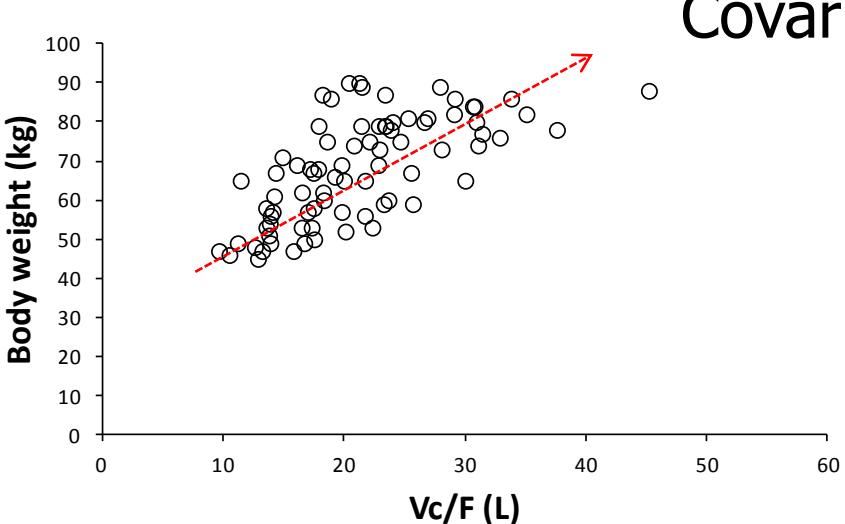
Covariate modelling



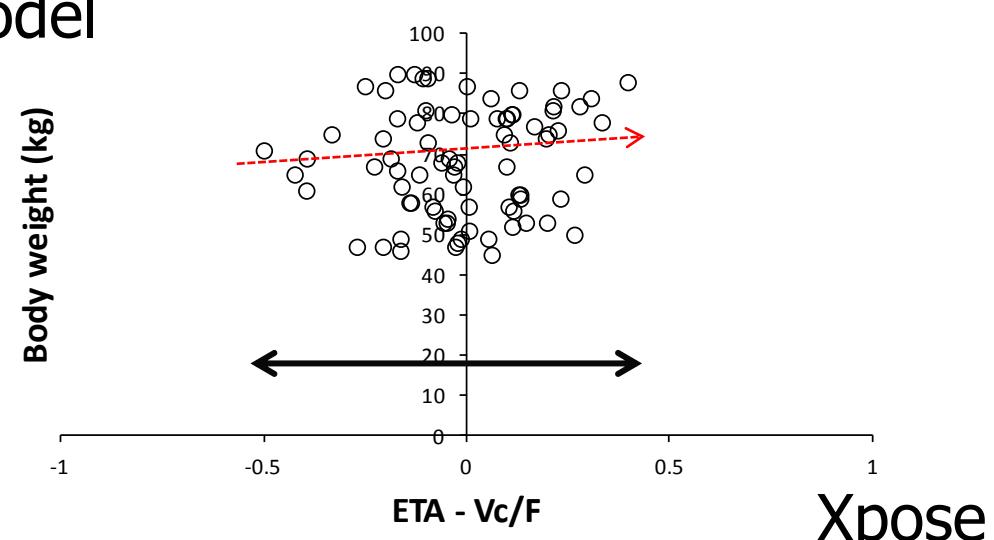
Base model



Base model



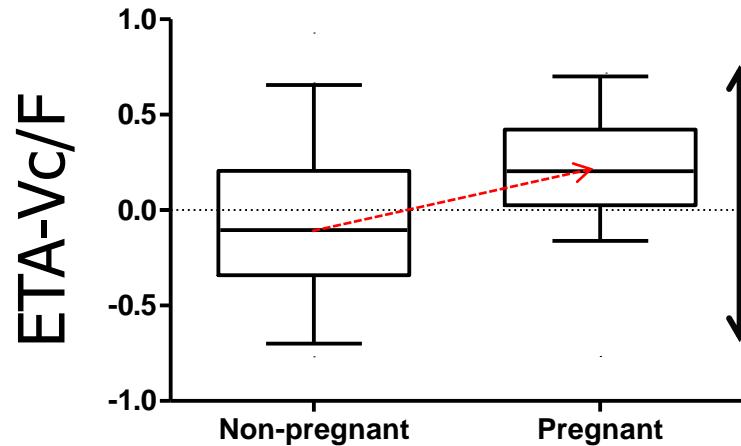
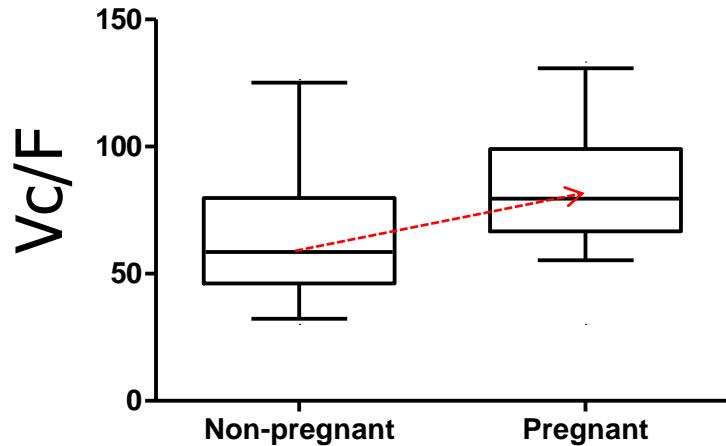
Covariate model



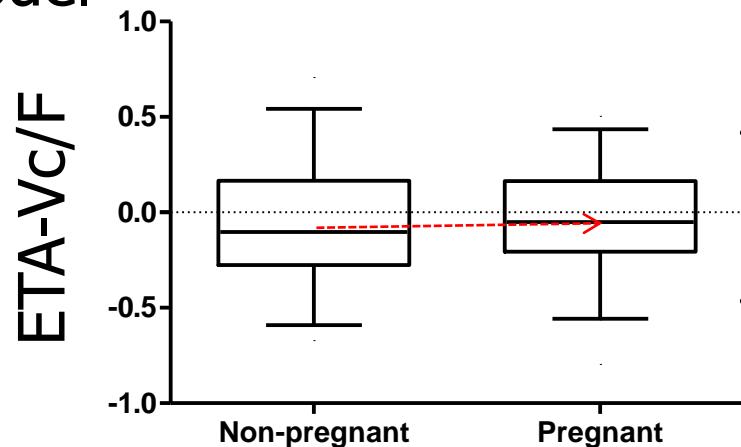
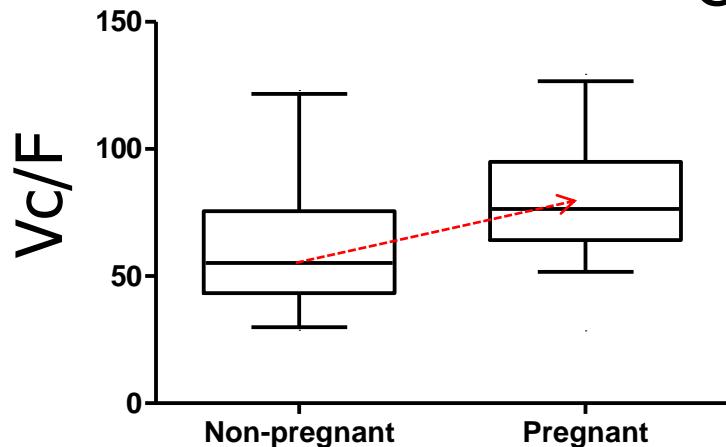
Xpose

Covariate modelling

Base model



Covariate model



Xpose

Covariate modelling

Covariate modelling: Stepwise forward addition and backward elimination

Basic structural model

Scientifically plausible covariates

Stepwise forward addition ($p < 0.05$)

Screen all covariates
- Add the covariate with lowest OFV

Screen all covariates
- Add the covariate with lowest OFV

Screen all covariates
- Add the covariate with lowest OFV

Reduced final covariate model

Remove non-significant covariates

Full covariate model
- No significant covariates left

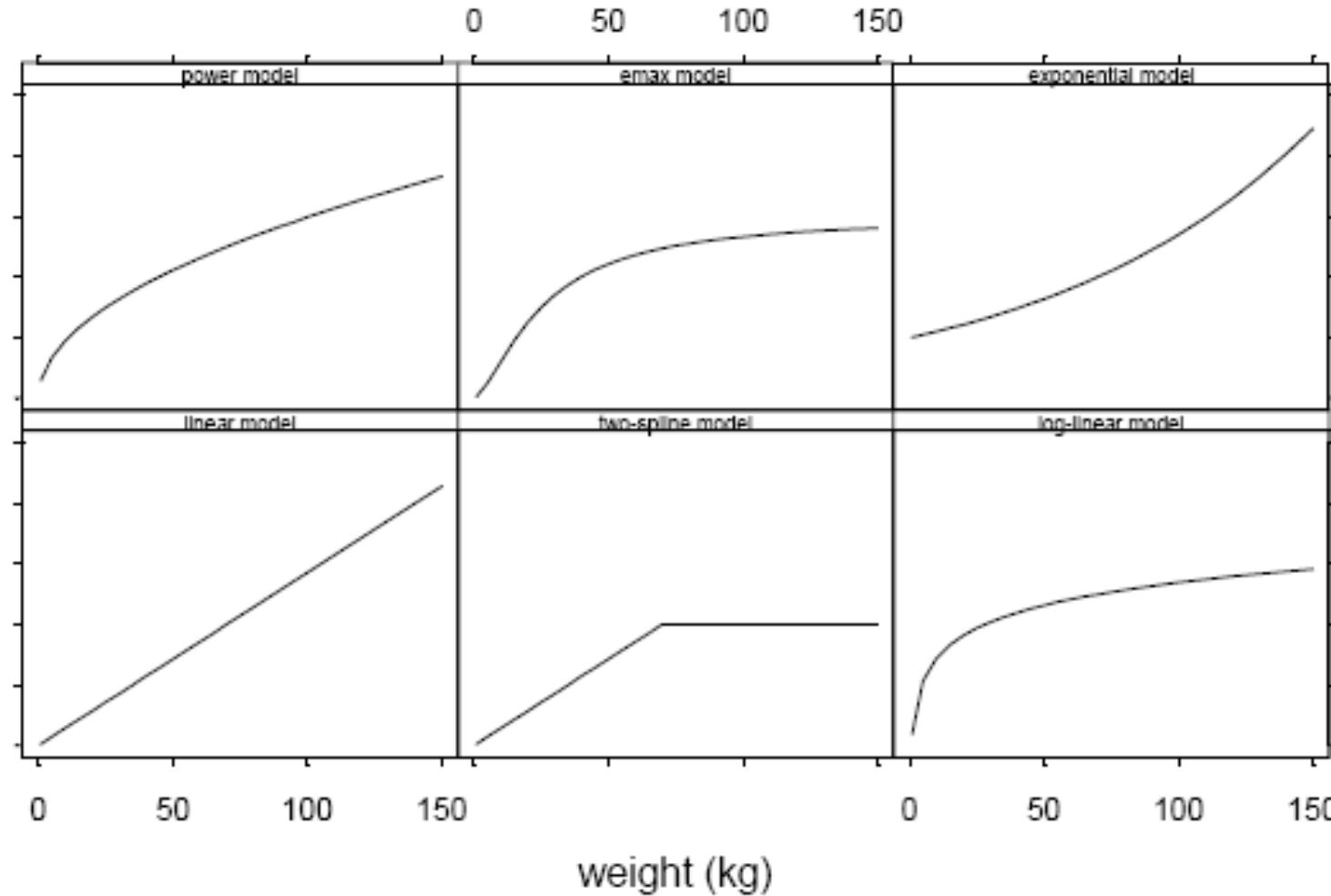
Backward elimination ($p < 0.01$)



Covariate modelling

Covariate relationships

Typical value of P



Can be implemented automatically in PsN

Covariate modelling

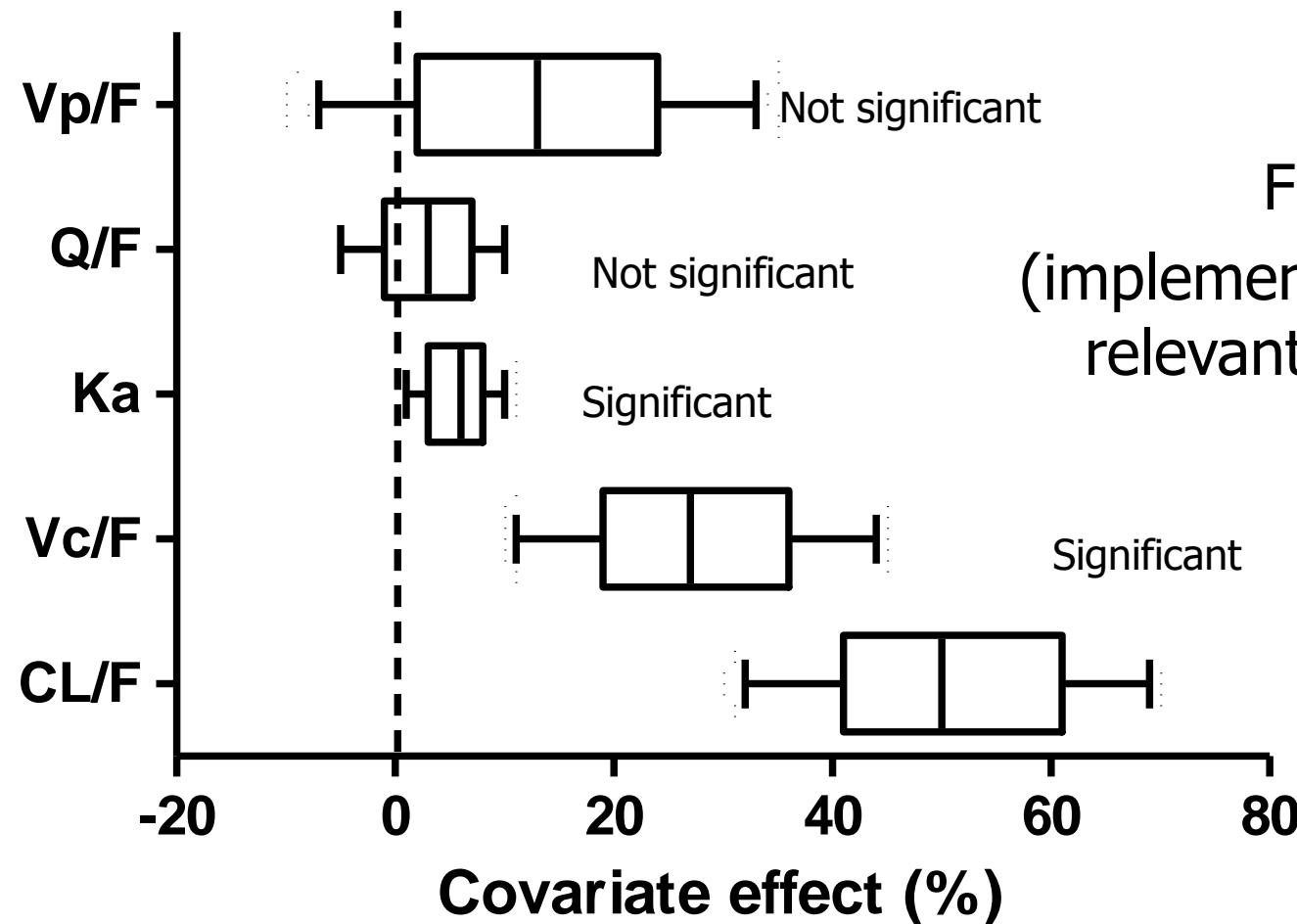
Covariate modelling										
	Population estimate (% RSE) [IIV]									ΔOFV
Model	CL/F (L/h)	V _C /F (L)	Q _I /F (L/h)	V _{P1} /F (L)	K _a (h ⁻¹)	RUV	Cov 1	Cov 2	Cov 3	
Base model	70.1 (12.5) [31.5]	32.1 (19.5) [59.5]	10.8 (14.9) [-]	108 (14.8) [-]	0.763 (4.97) [45.8]	0.295 (5.47) [-]	X	X	X	
Forward addition										
Covariate 1-CL	60.3 (10.7) [21.5]	32.6 (19.5) [59.5]	10.4 (14.9) [-]	111 (14.8) [-]	0.763 (4.97) [45.8]	0.296 (5.47) [-]	33.0 (24.5)			-25.6
Covariate 2-V _c	60.5 (10.5) [21.5]	22.1 (12.5) [39.5]	10.7 (14.9) [-]	112 (14.8) [-]	0.761 (4.97) [45.8]	0.283 (5.47) [-]	32.0 (24.5)	46.8 (35.6)		-20.2
Covariate 3-CL	60.1 (10.3) [20.5]	22.2 (12.5) [39.5]	10.9 (14.9) [-]	110 (14.8) [-]	0.761 (4.97) [45.8]	0.285 (5.47) [-]	32.0 (24.5)	46.8 (35.6)	5.8 (55.6)	-5.3
...										
Backward elimination										
Covariate 1	70.2 (13.5) [30.5]	22.2 (12.5) [39.5]	10.9 (14.9) [-]	110 (14.8) [-]	0.761 (4.97) [45.8]	0.285 (5.47) [-]	X (35.6)	46.8 (55.6)	15.8 (55.6)	24.5
Covariate 2	60.2 (10.5) [20.5]	29.2 (14.5) [59.5]	10.9 (14.9) [-]	110 (14.8) [-]	0.761 (4.97) [45.8]	0.285 (5.47) [-]	32.0 (24.5)	X (55.6)	15.8 (55.6)	20.4
Covariate 3	60.2 (10.5) [21.5]	22.2 (12.5) [39.5]	10.9 (14.9) [-]	110 (14.8) [-]	0.761 (4.97) [45.8]	0.285 (5.47) [-]	32.0 (24.5)	46.8 (35.6)	X (55.6)	5.3
Final model	60.2 (10.5) [21.5]	22.2 (12.5) [39.5]	10.9 (14.9) [-]	110 (14.8) [-]	0.761 (4.97) [45.8]	0.285 (5.47) [-]	32.0 (24.5)	46.8 (35.6)		



Covariate modelling

"Absence of evidence is not evidence of absence"

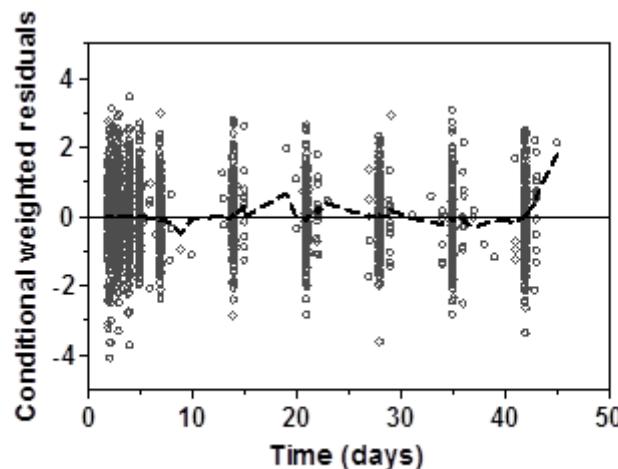
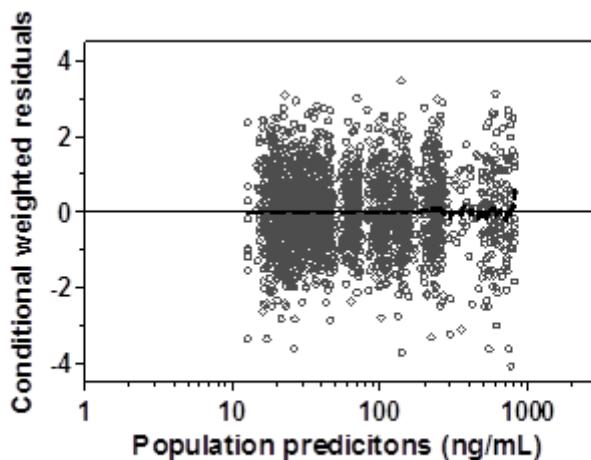
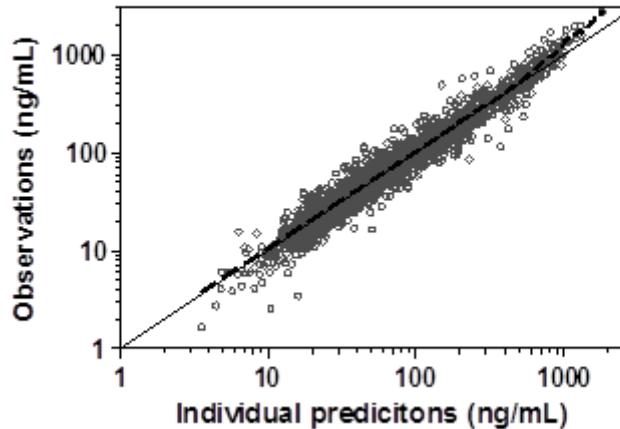
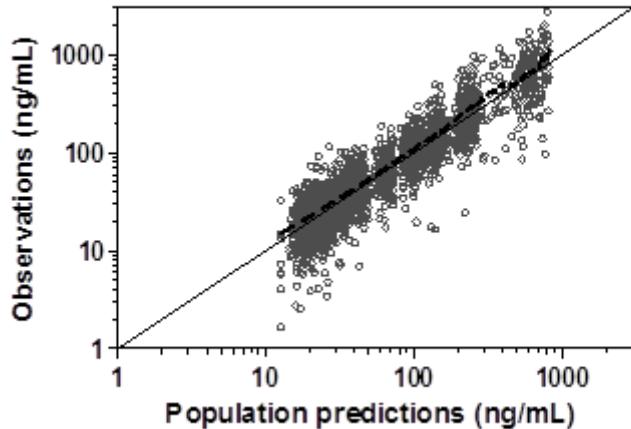
Carl Sagan (1934-1996)



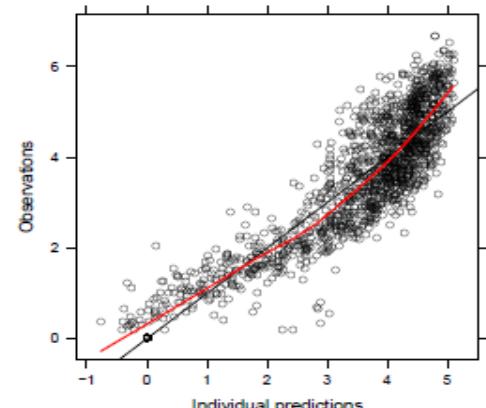
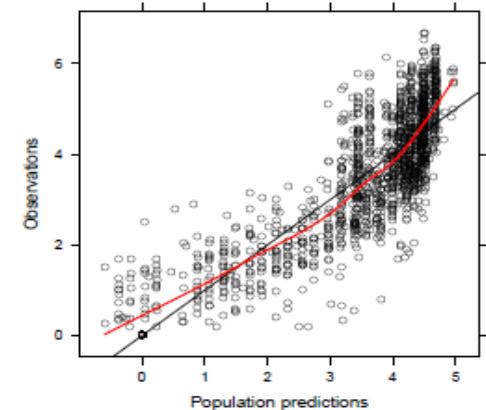
Full covariate model
(implement the group covariate on all relevant parameters and bootstrap)

Model diagnostics

Basic Goodness-of-fit diagnostics



Substantial and systemic deviations/trends indicate model-misspecification



Xpose



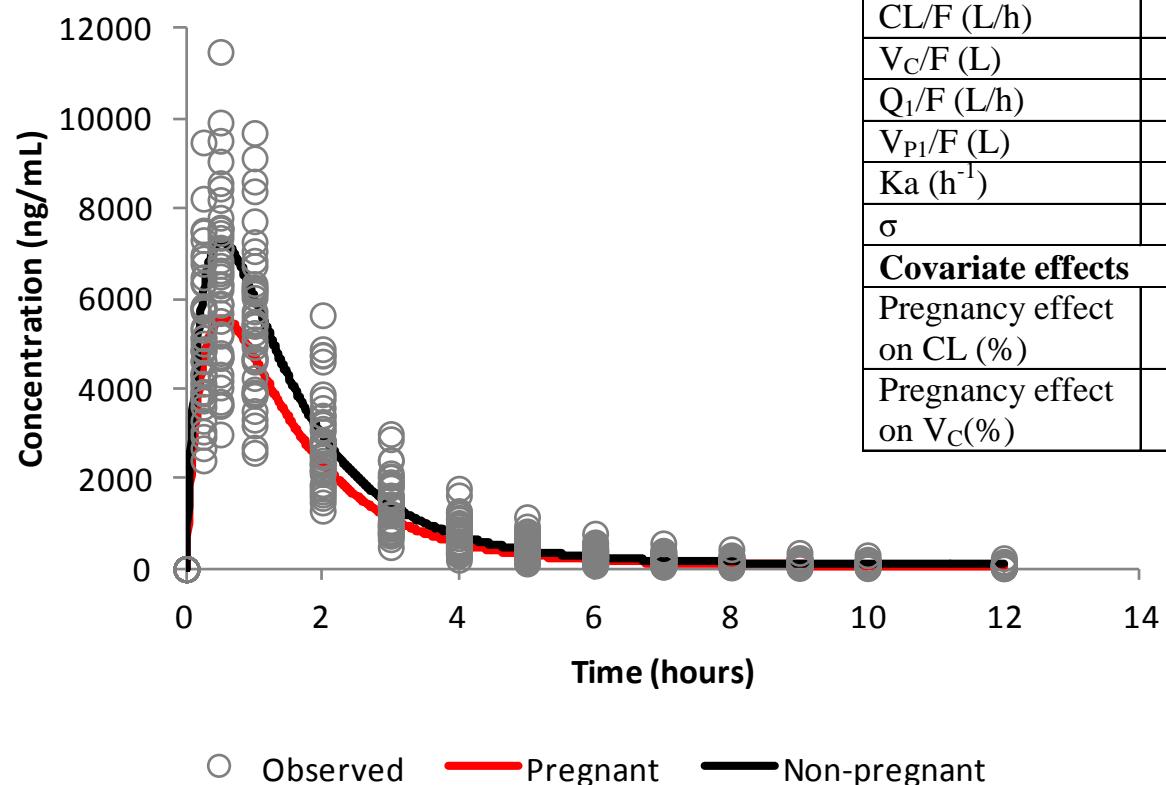
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Model diagnostics

Numerical diagnostics

- Parameter values
- Parameter certainty



NONMEM Bootstrap

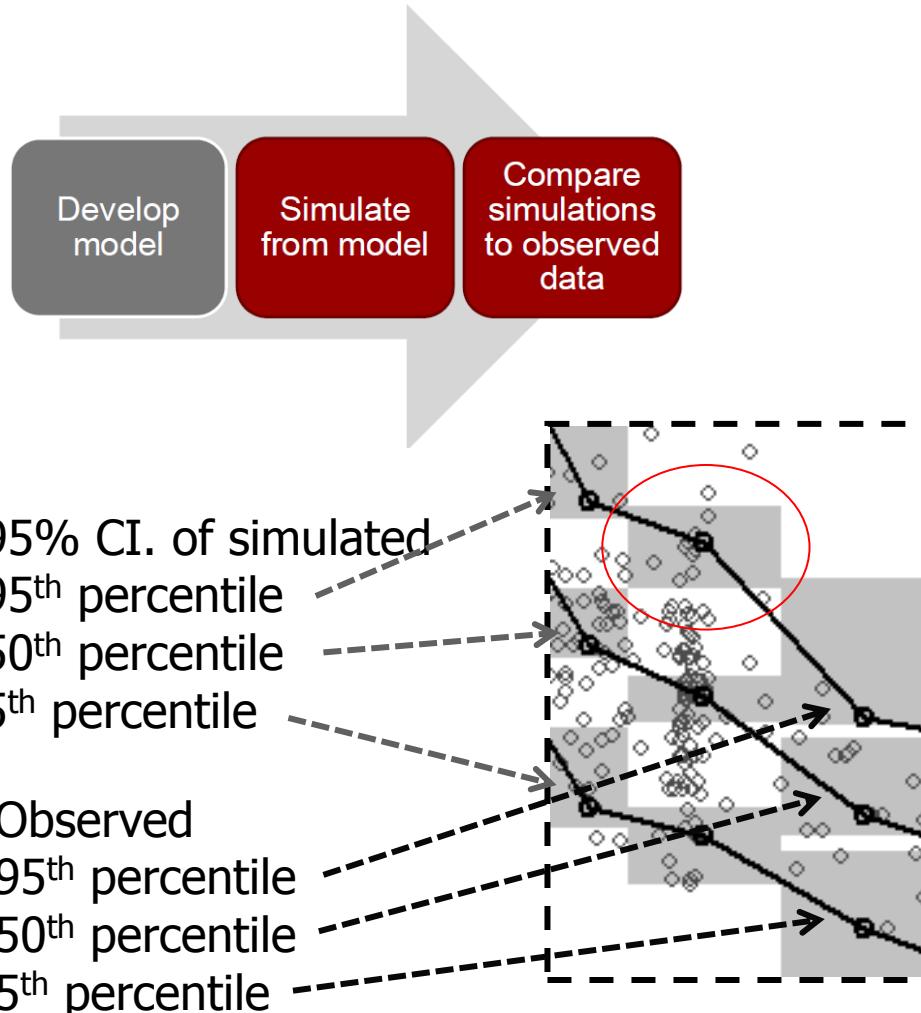
Parameter estimates of the final model		NONMEM	Bootstrap	
	Population estimate ^a (% RSE ^b)	95% CI. ^b	95% CI. ^b	
Typical parameters				
CL/F (L/h)	60.2 (10.5)	49.6-74.2	21.5 (27.0)	14.5-26.2
V _C /F (L)	22.2 (12.5)	18.2-25.6	39.5 (35.7)	21.7-50.7
Q ₁ /F (L/h)	10.9 (14.9)	6.31-13.4	-	-
V _{P1} /F (L)	110 (14.8)	80.3-131	-	-
K _a (h ⁻¹)	0.761 (4.97)	0.592-0.891	45.8 (22.1)	35.4-56.1
σ	0.285 (5.47)	0.255-0.314	-	-
Covariate effects				
Pregnancy effect on CL (%)	32.0 (24.5)	25.1-69.1	-	-
Pregnancy effect on V _C (%)	46.8 (35.6)	18.2-86.0	-	-

- Sample data randomly and re-fit the model for bootstrap diagnostics
- Stratify on important covariates

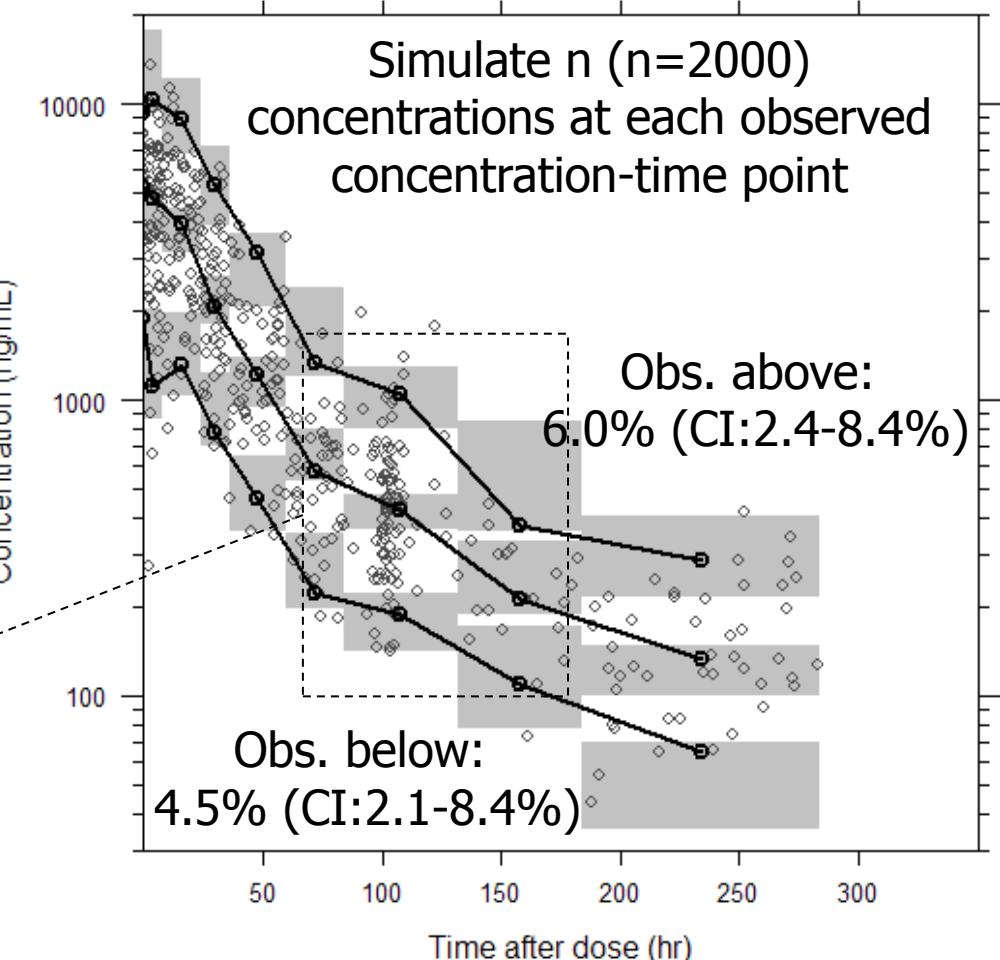
Bootstrap runX.mod -samples=2000

Model diagnostics

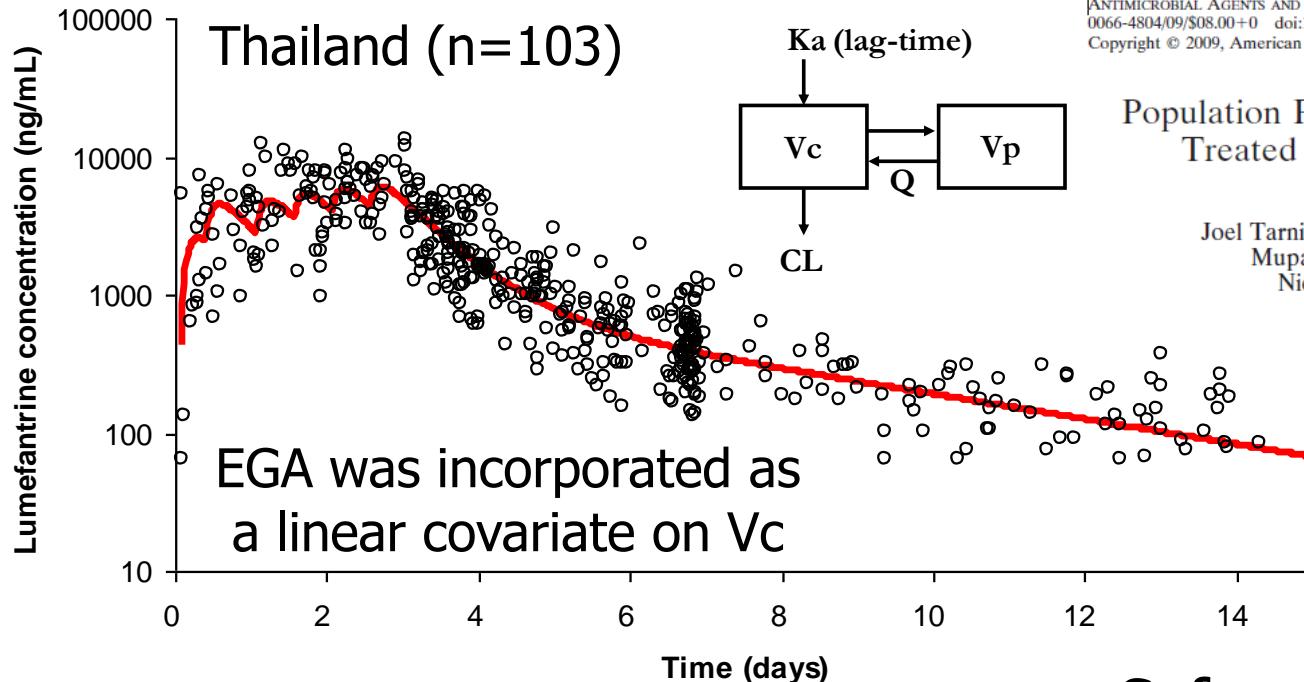
Simulation-based diagnostics



Prediction-corrected Visual Predictive Check



Antimalarial examples



ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, Sept. 2009, p. 3837–3846
0066-4804/09/\$08.00+0 doi:10.1128/AAC.00195-09
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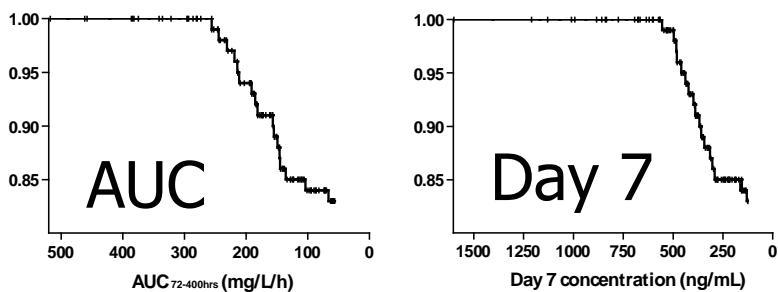
Vol. 53, No. 9

Population Pharmacokinetics of Lumefantrine in Pregnant Women Treated with Artemether-Lumefantrine for Uncomplicated *Plasmodium falciparum* Malaria^V

Joel Tarning,^{1,2,*} Rose McGready,^{1,2,3} Niklas Lindegardh,^{1,2} Elizabeth A. Ashley,³ Mupawjay Pimanpanarak,³ Benjamas Kamannikom,¹ Anna Annerberg,¹ Nicholas P. J. Day,^{1,2} Kasia Stepniewska,^{1,2} Pratap Singhasivanon,⁴ Nicholas J. White,^{1,2} and François Nosten^{1,2,3}



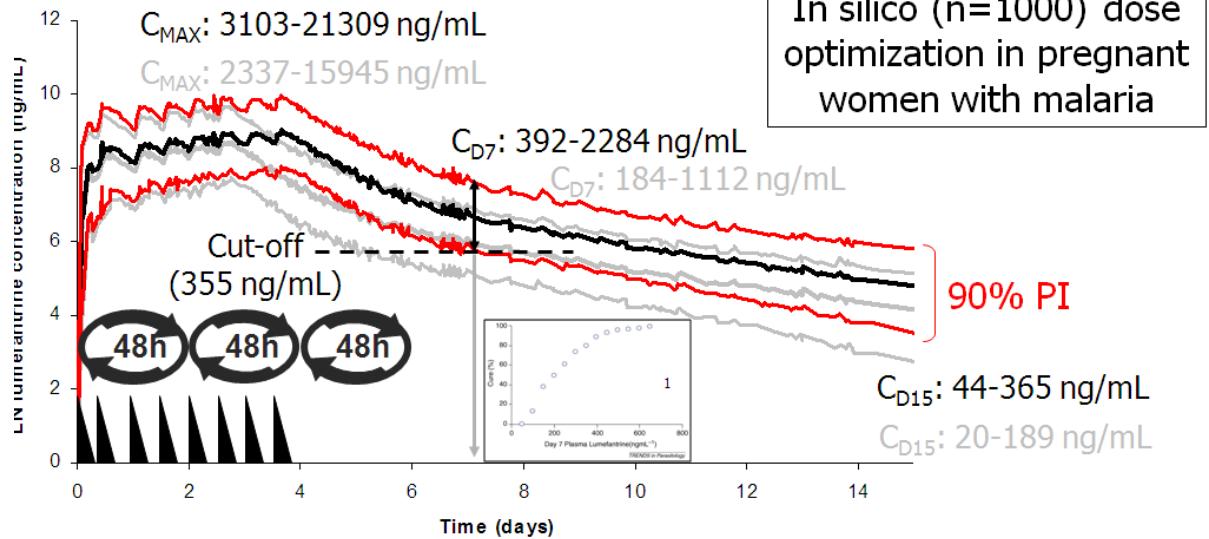
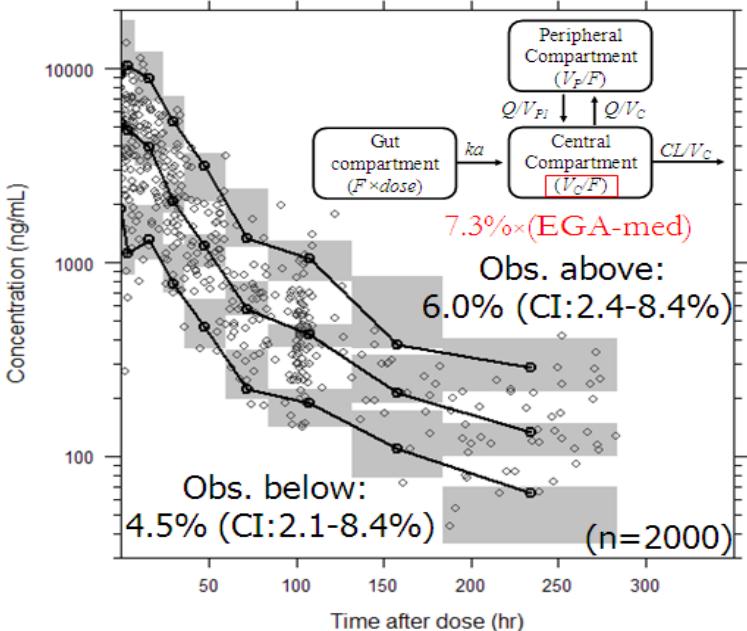
Cumulative risk of recrudescence



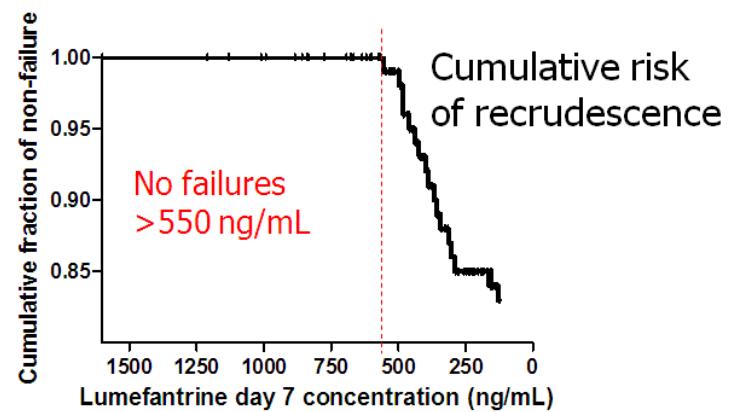
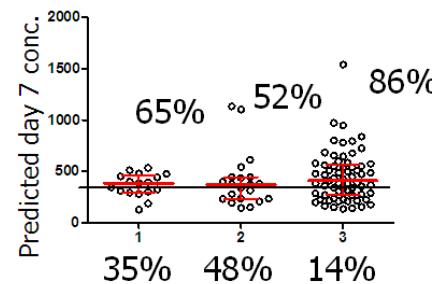
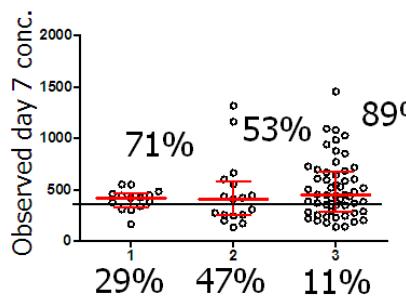
- Safe and effective artemether-lumefantrine treatment in adults
- Specific problem of low cure rates (84%) in pregnant women
- What dose is the right dose → M&S

Antimalarial examples

Prediction-corrected Visual Predictive Check



1: recrudescence, 2: re-infection, 3: non-failures



Antimalarial examples

Population pharmacokinetics and pharmacodynamics of piperaquine in children with uncomplicated falciparum malaria

Joel Tarning^{1,2*}, Issaka Zongo³, Fabrice A. Somé³, Noel Rouamba³, Parikh Sunil⁴, Philip J. Rosenthal⁴, Warunee Hanpitakpong¹, Natthapong Jongrak¹, Nicholas P. J. Day^{1,2}, Nicholas J. White^{1,2}, Francois Nosten^{1,2,5}, Jean-Bosco Ouedraogo³, Niklas Lindegardh^{1,2}

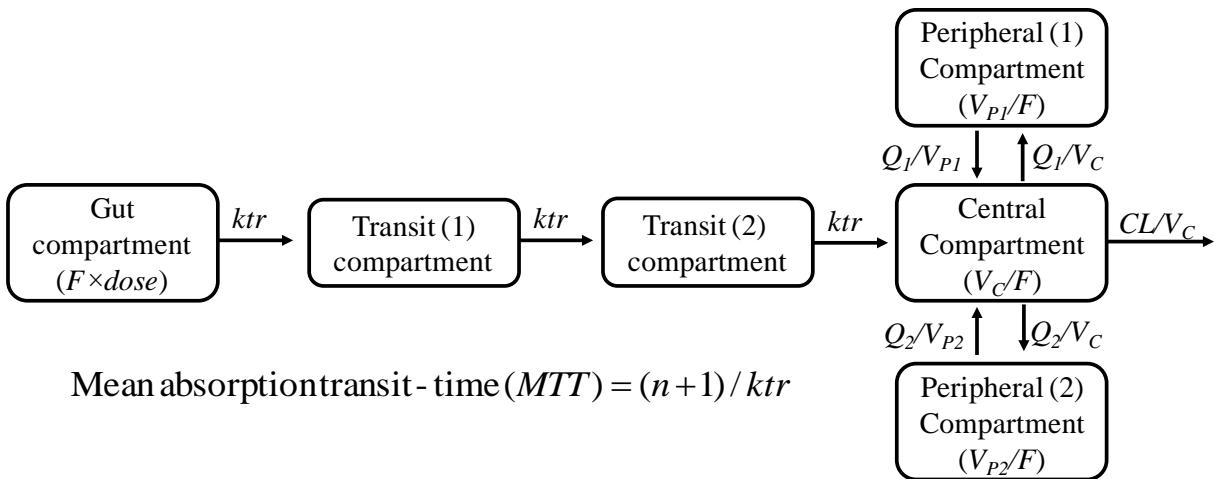
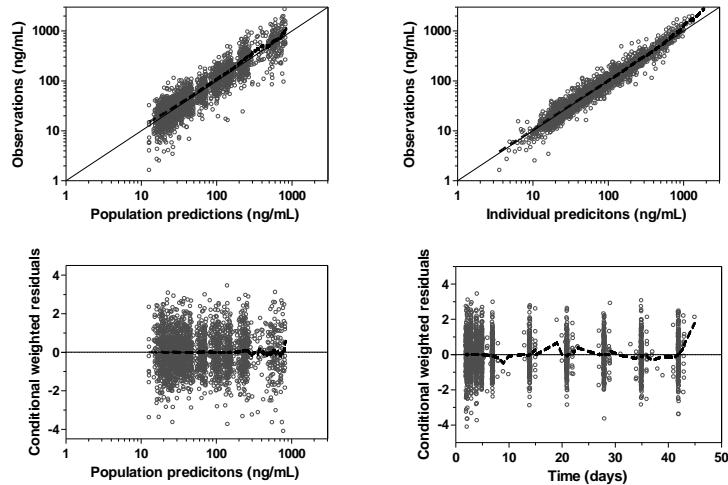
- 236 children (2-10 years) from Burkina Faso received a weight-based dose of DHA-PQ
- Capillary blood sampling (6 weeks)
- Nonlinear mixed-effects modeling



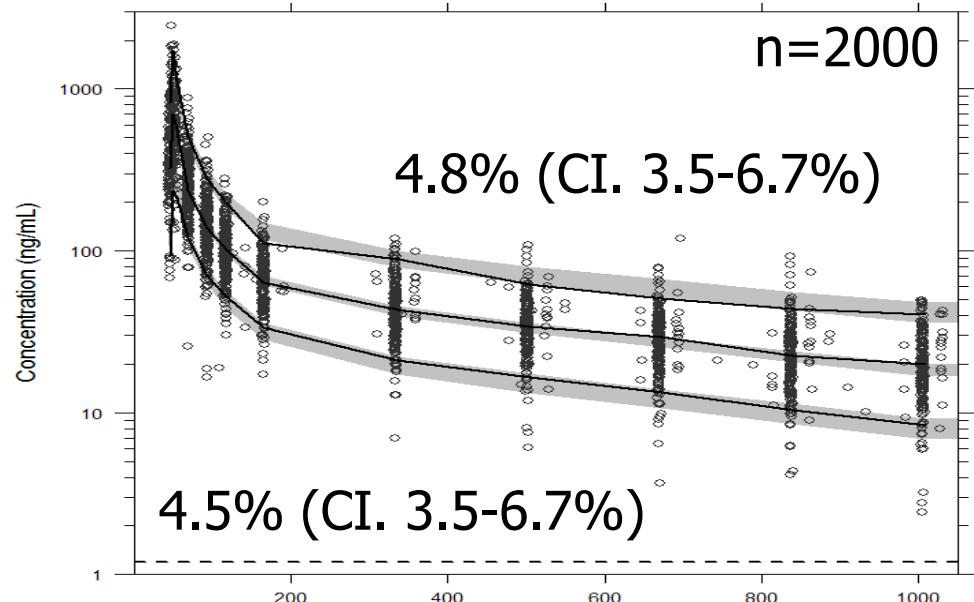
To define the population pharmacokinetic of piperaquine in the treatment of *falciparum* infection in children



Antimalarial examples

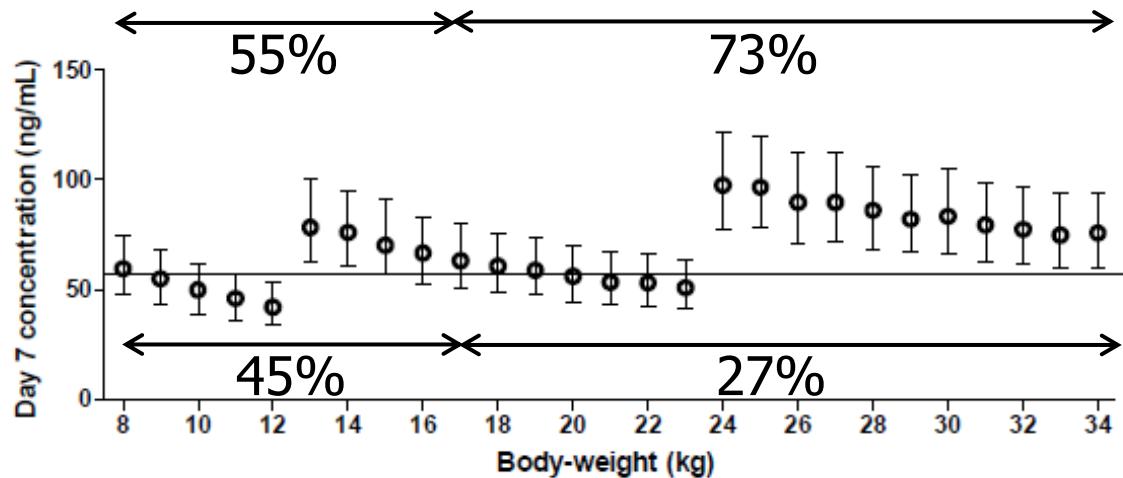


$$\text{Mean absorption/transit-time (MTT)} = (n+1) / k_{tr}$$

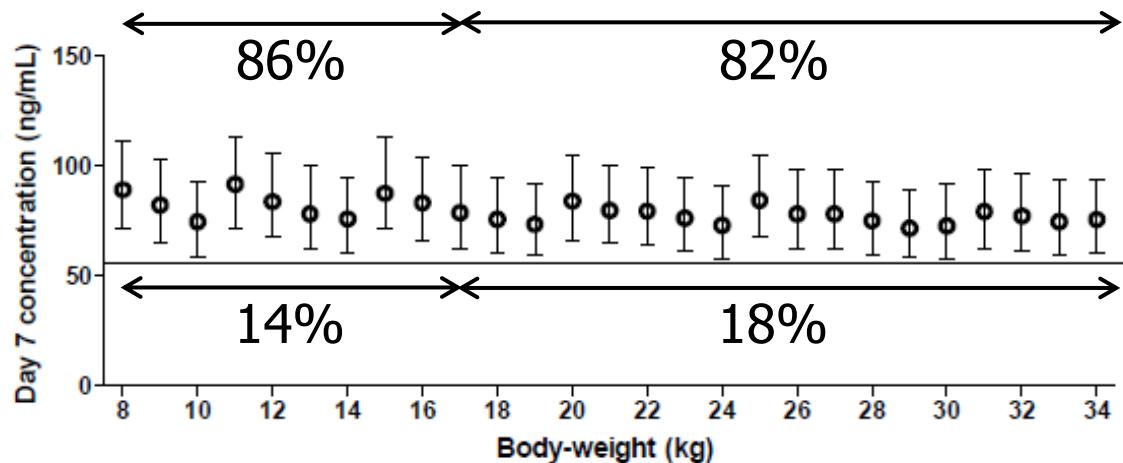


Time-to-event analysis:
The risk of a new malaria infection increased with 5.9% per 1 ng/mL decrease in day 7 concentration (HR 0.94, 95% CI 0.92 to 0.96)

Antimalarial examples



Manufacturer recommendations:
To wide binning of doses
resulting in many under-dosed
children



In silico dose-optimization using
the final model

Antimalarial examples

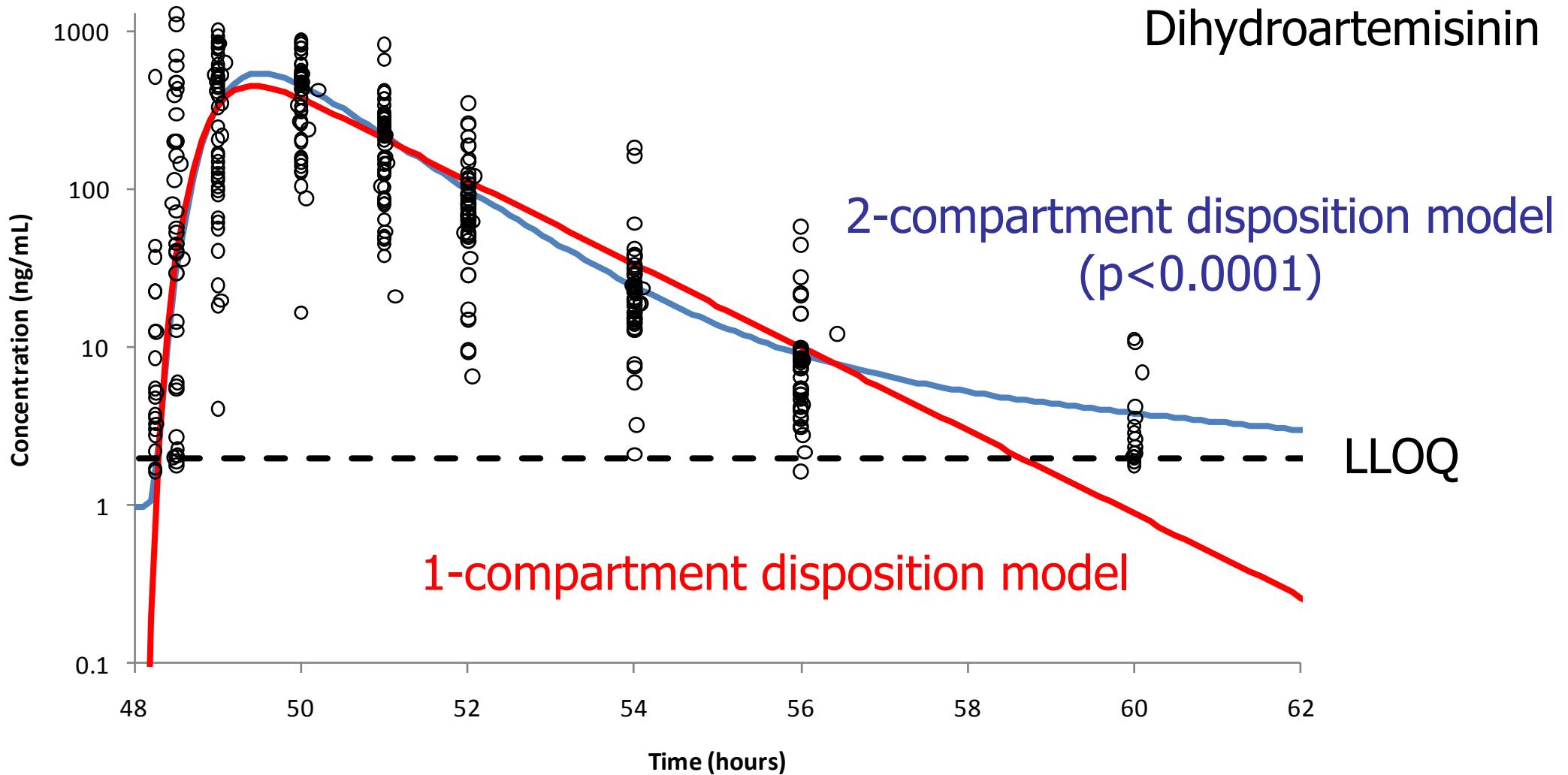
Population pharmacokinetics of dihydroartemisinin and piperaquine in pregnant and non-pregnant women with uncomplicated malaria

Joel Tarning^{1,2*}, Marcus J. Rijken³, Rose McGready^{1,2,3}, Aung Phae Phyoe³, Warunee Hanpitakpong¹, Nicholas P. J. Day^{1,2}, Nicholas J. White^{1,2}, Francois Nosten^{1,2,3}, Niklas Lindegardh^{1,2}

- 48 (24+24) Karen patients
- Standard DHA-PQ (3×40-320 mg) for 3 days
- Dense venous blood sampling (9 weeks)
- PQ and DHA analysed with LC-MS/MS
- NCA (traditional statistics)
- Nonlinear mixed-effects modelling
 - Covariate models

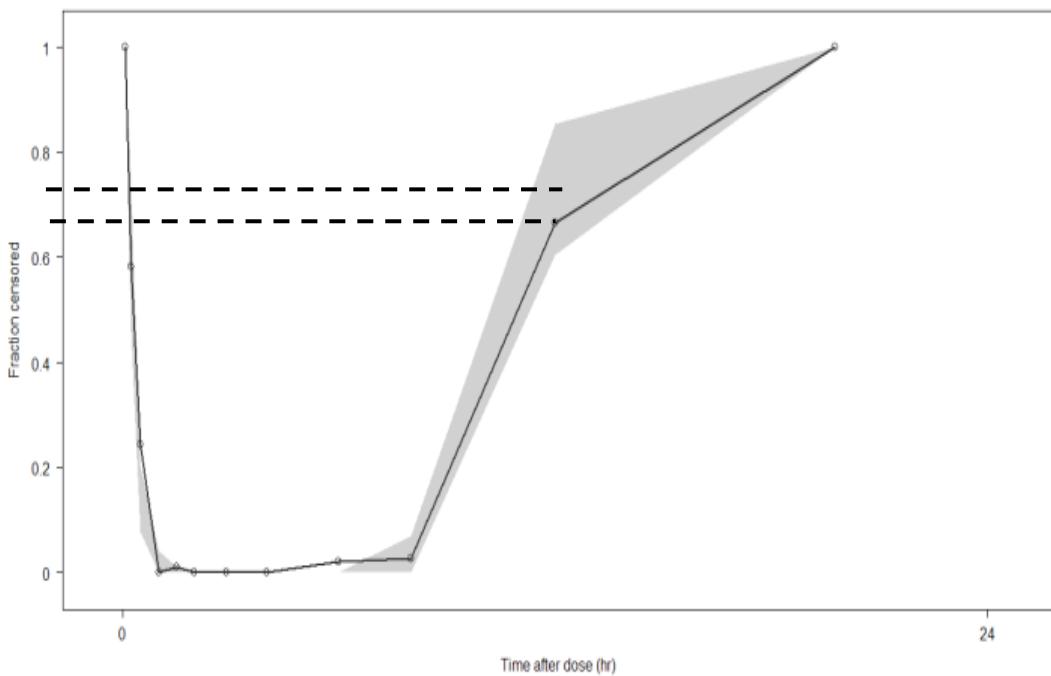


Antimalarial examples



Antimalarial examples

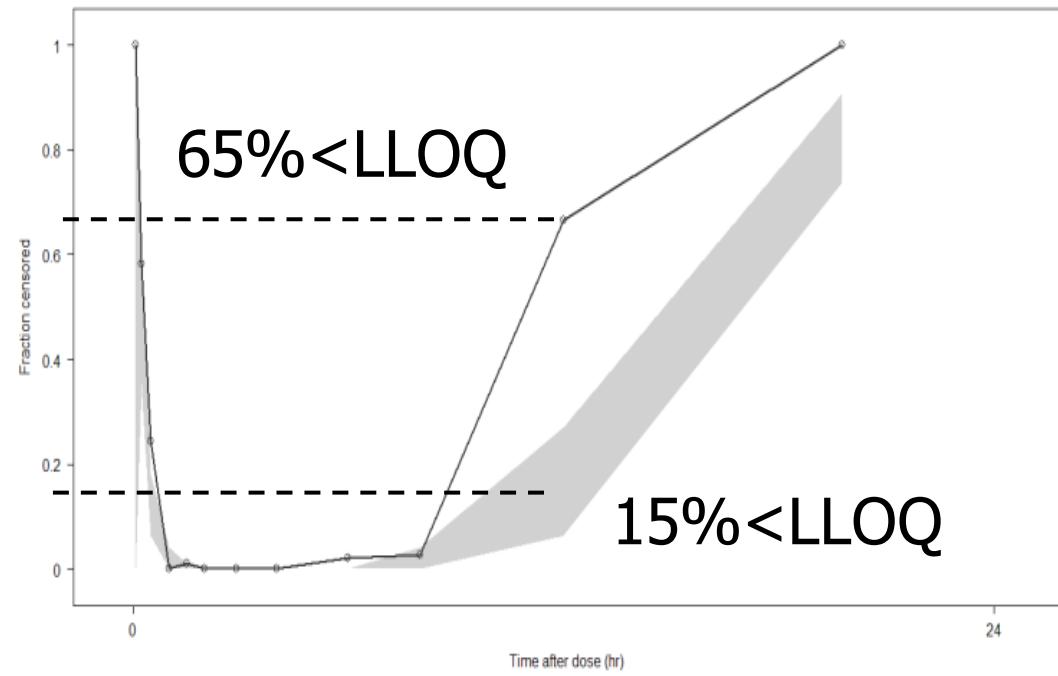
1-compartment disposition model



— Observed

■ Predicted

2-compartment disposition model



— Observed

■ Predicted

Inaccurate structural model if only using the OFV and not simulation-based diagnostics

Thank you

Department of Pharmacology - MORU



*Joel Tarning
Consensus meeting
South Africa 2011-10-18*



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