

# Comparison of different tools for the optimization of a pediatric clinical trial

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Raffaele, living with epilepsy



2009

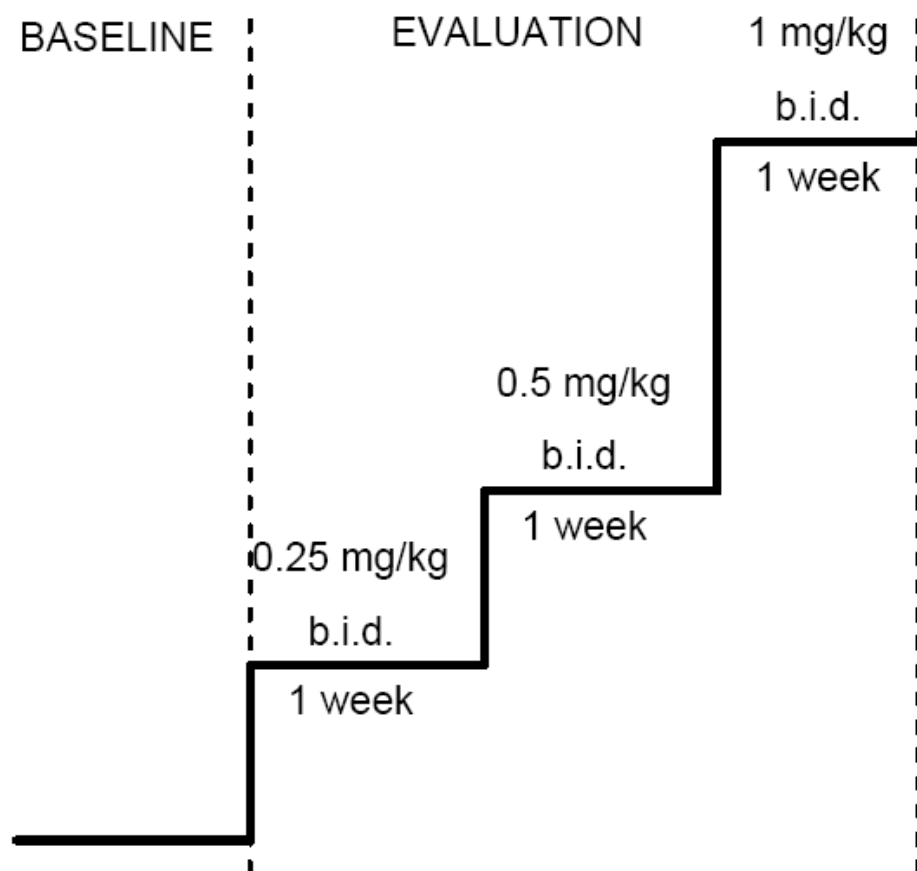
# The pediatric clinical trial

## Objective of the trial:

Characterize the steady-state pharmacokinetics (PK) of a drug under development in children aged 1 month to 16 years old

## Design

- a fixed 3-step dose up-titration study
- B.i.d. doses
- 48 patients:
  - 1 month-2 years: 12
  - 2 – 4 years: 12
  - 4 – 8 years: 6
  - 8 – 12 years: 6
  - 12 – 16 years: 6



# The pediatric clinical trial

- ▶ Initial dose dependent on weight category
- ▶ PK samples constraints:
  - One visit per dose at the end of the treatment week;
  - No more than 2 PK samples per visit



# Optimisation of the pediatric clinical trial

- Objective: optimise the times of the limited number of samples to reduce the compromise for the pediatric parameter estimation
  
- Optimal design tools employed:
  - PFIM version 3.0
  - POPT version 3.0
  - PopED version 2.08



# Rapid overview of the optimisation tools

	PFIM3.0	POPT3.0	PopED2.08
Optimisation	<ul style="list-style-type: none"> <li>➤ D-optimal</li> </ul>	<ul style="list-style-type: none"> <li>➤ D-optimal</li> <li>➤ ED-optimal</li> </ul>	<ul style="list-style-type: none"> <li>➤ D-optimal</li> <li>➤ ED-optimal</li> </ul>
Algorithm	<ul style="list-style-type: none"> <li>➤ Simplex (continuous time)</li> <li>➤ Federov-Wynn (discrete time)</li> </ul>	<ul style="list-style-type: none"> <li>Exchange &amp; Simulated annealing (continuous &amp; discrete times)</li> </ul>	<ul style="list-style-type: none"> <li>➤ Random search &amp; Stochastic gradient &amp; Line search (continuous)</li> <li>➤ Modified Fedorov Exchange Algorithm (discrete)</li> </ul>
Interface	Yes	Yes (limited)	Yes (limited)
Language	R (freeware)	Matlab or Stand-Alone version (limited)	Matlab
Developers	INSERM, University Paris 7 (S.Retout & F.Mentré)	University of Otago, University of Queensland, J&J (S.Duffull)	Uppsala University (A. Hooker, J. Nyberg)

# Common major assumption

- The PK is assumed to follow a population PK model built with **adult** data, in particular:

$$K_a [h^{-1}] = \theta_{K_a} \times \exp(\eta_{K_a}) \quad \text{where } \theta_{K_a} = 0.902$$

$$CL/F [L/h] = \theta_{CL} \left( \frac{\text{WT}}{69} \right)^{0.75} \times \exp(\eta_{CL}) \quad \text{where } \theta_{CL} = 3.63$$

$$V/F [L] = \theta_V \left( \frac{\text{WT}}{69} \right) \times \exp(\eta_V) \quad \text{where } \theta_V = 35.9$$

Variances of  $\eta_{K_a, CL, V} = 0.611; 0.0575$  and  $0.0150$

Proportional error with variance  $0.0402$

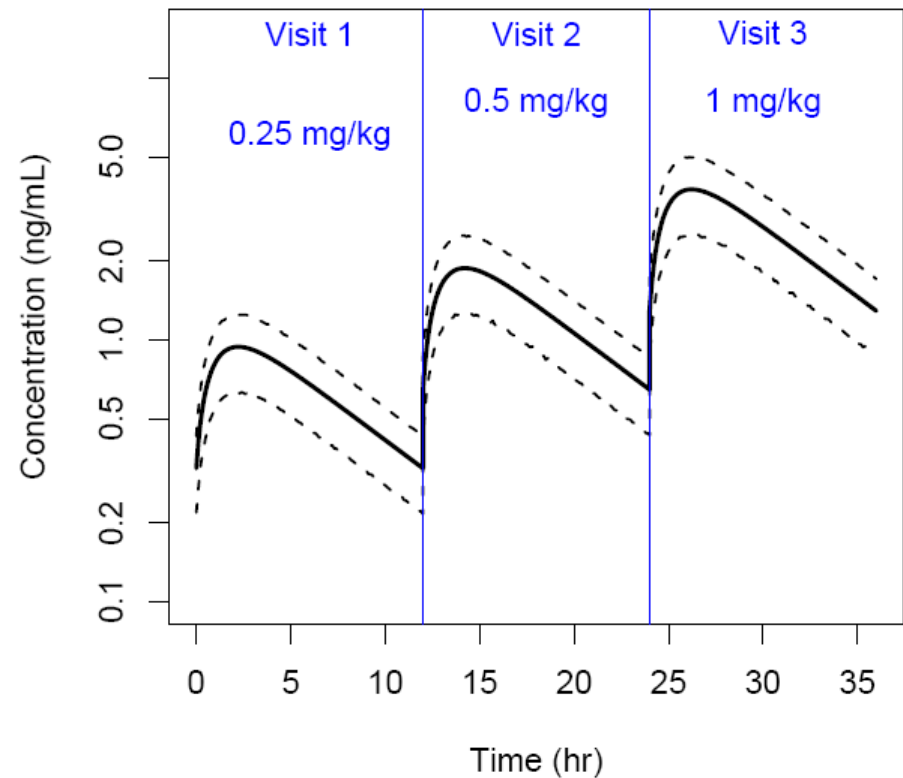
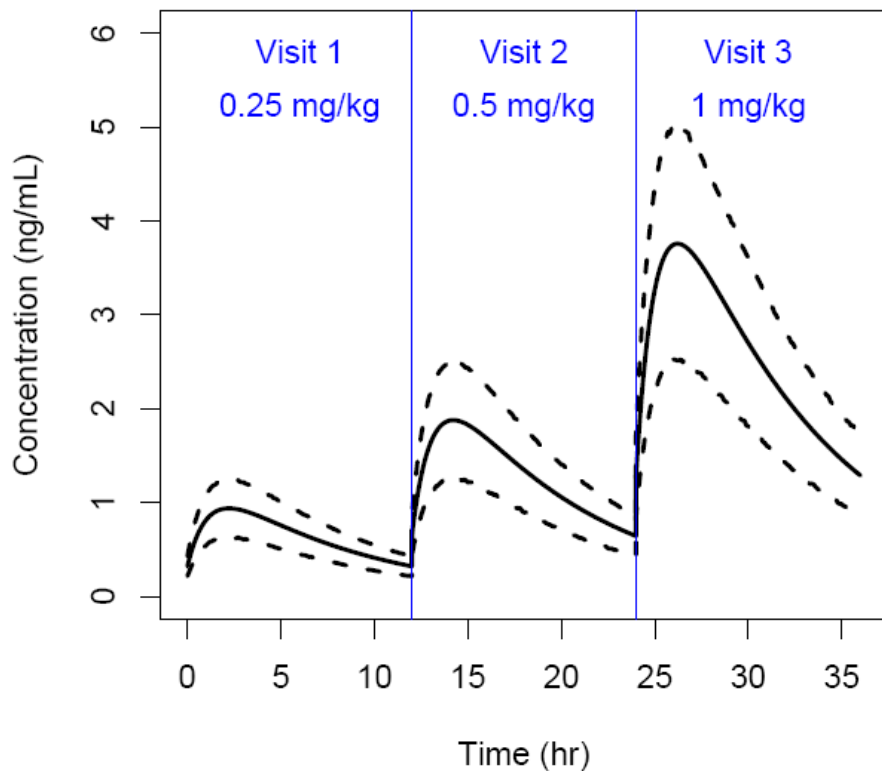
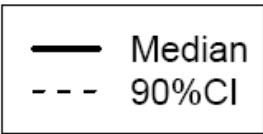


# Time-Concentration equations

Linear scale

Logarithmic scale  
(proportional error becomes additive)

Profile of a 30 kg individual including residual error



# Comparison of problem implementation and output

	PFIM	POPT	POPED
Up-titration	Log-transformation	Fix dose for each sampling time	Log-transformation
Weight-dependent PK	Optimise individual sampling times	5 age groups with 3 competing models – each corresponding to 5 <sup>th</sup> , 50 <sup>th</sup> and 95 <sup>th</sup> quantile weights	5 age groups with a uniform weight distribution between minimum and maximum weights
Outcome	Intervals of optimised times over a large population	<ul style="list-style-type: none"> <li>• Optimised times;</li> <li>• Expected parameter precision for the « median » and extreme populations</li> </ul>	<ul style="list-style-type: none"> <li>• Optimised times;</li> <li>• Expected parameter precision of the clinical trial</li> </ul>

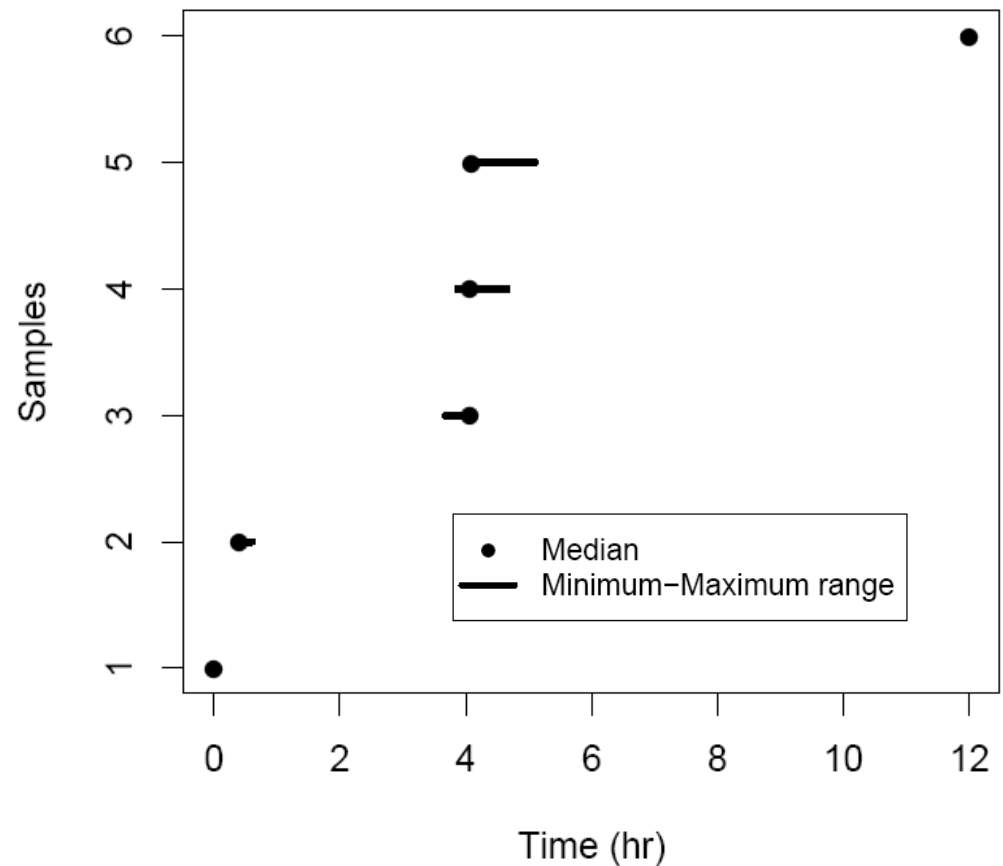
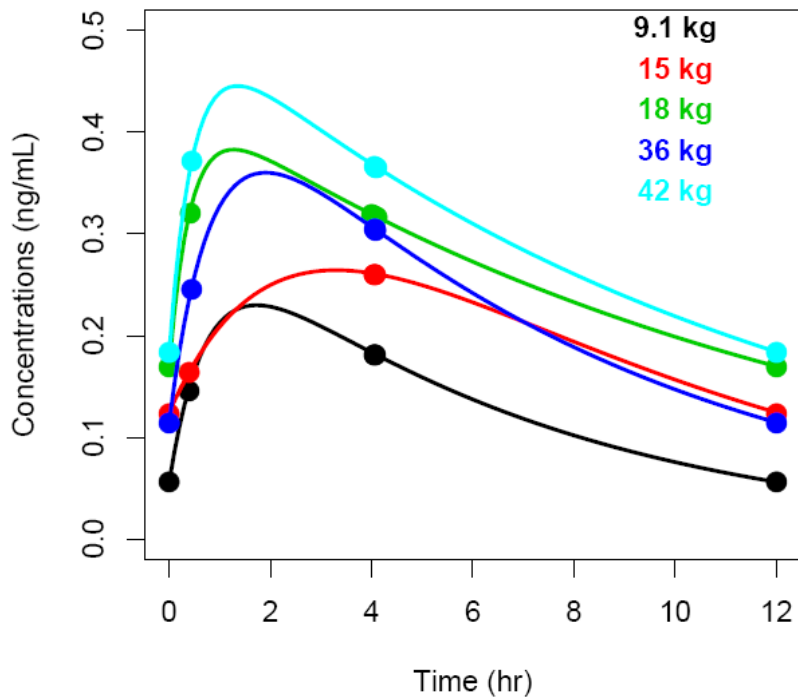


# Outcome in PFIM

## Outcome

- Intervals of optimised sampling times over a large population... but no information on expected parameter precision

A few individual profiles and optimised times

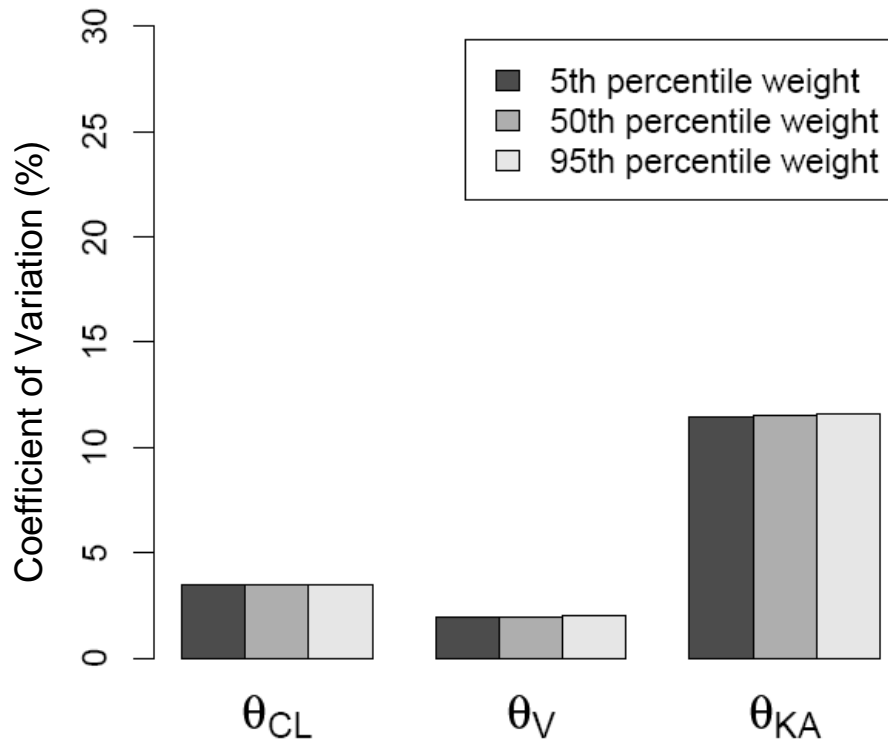


# Outcome in POPT

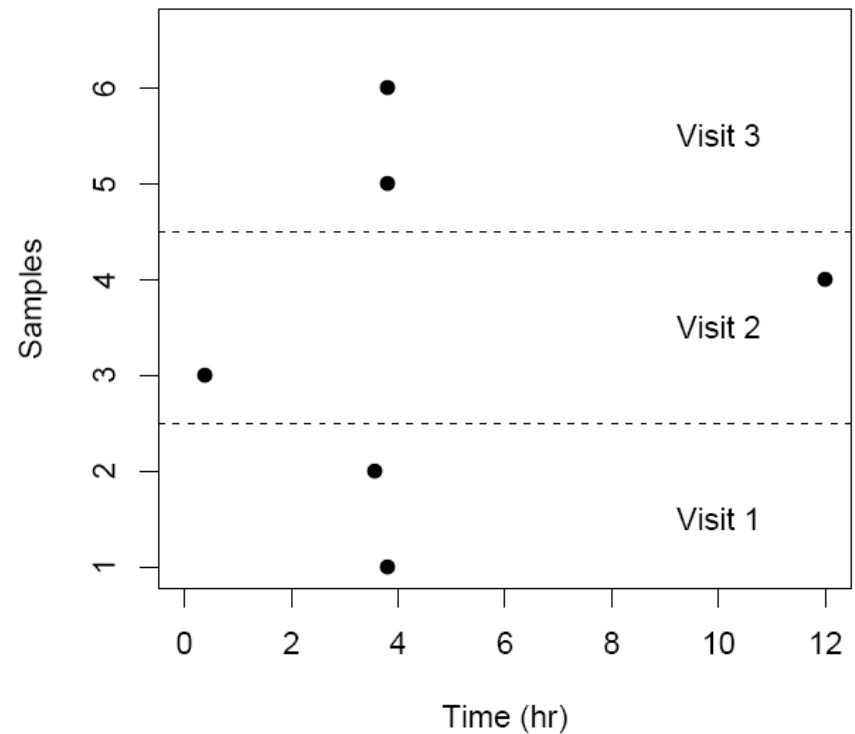
## Outcome

- Overall 6 sampling times;
- Expected precision of the parameters for each model

**Expected precision of the main parameters**



**Optimised sampling times**

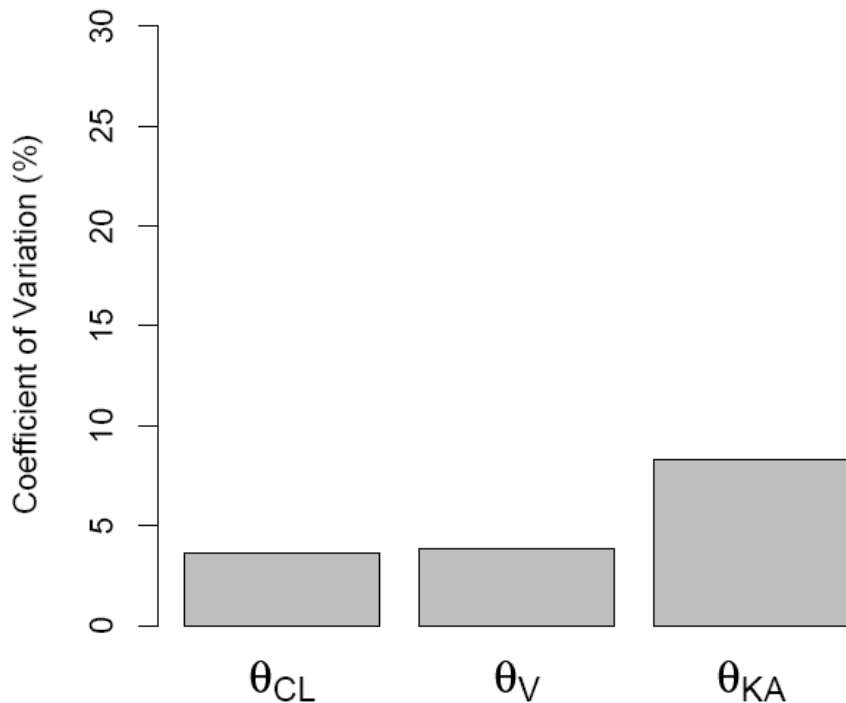


# Outcome in POPED

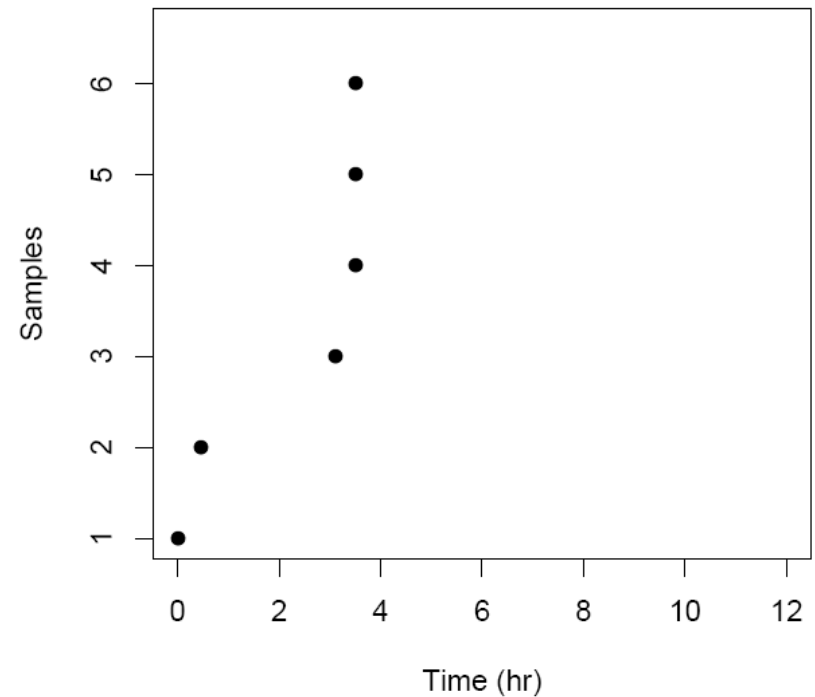
## ➤ Outcome

- Overall 6 sampling times;
- Expected precision of the parameters of the trial

**Expected precision of the main parameters**

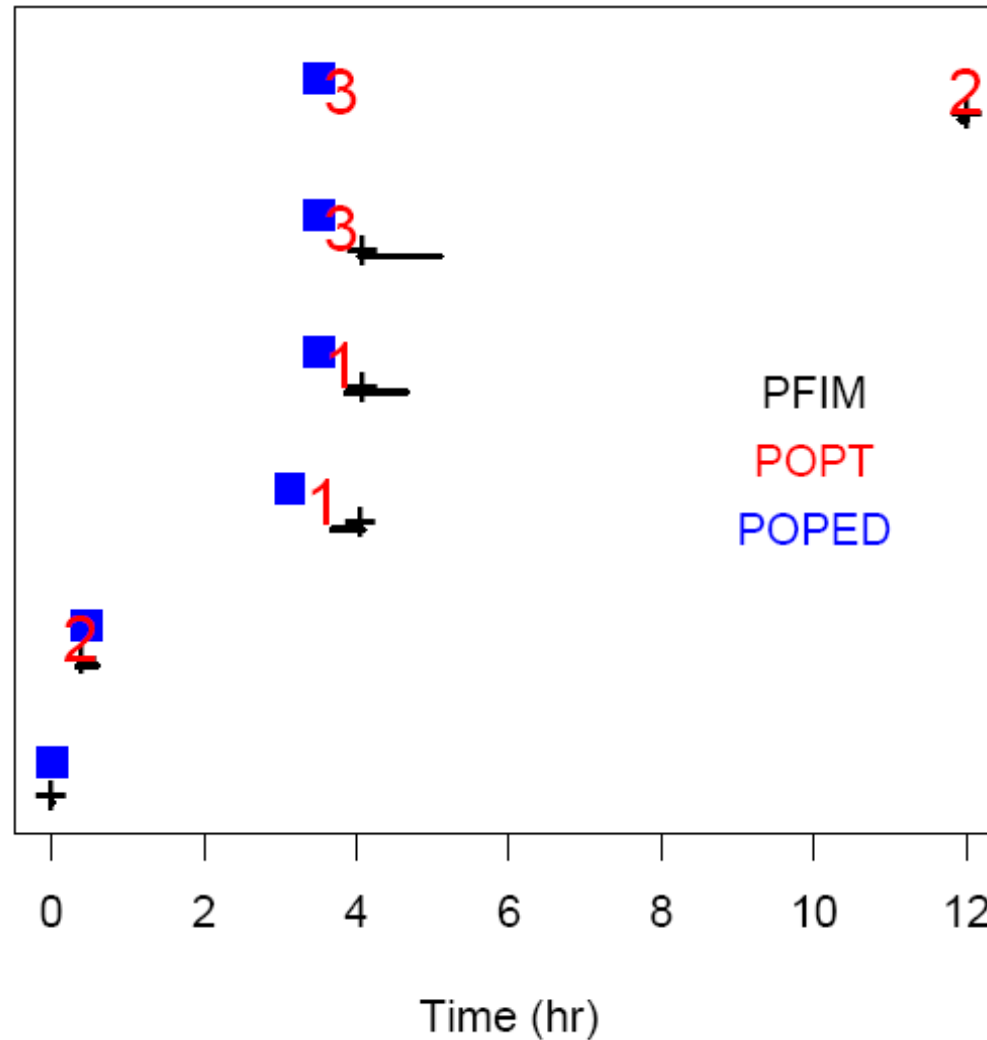


**Optimised sampling times**

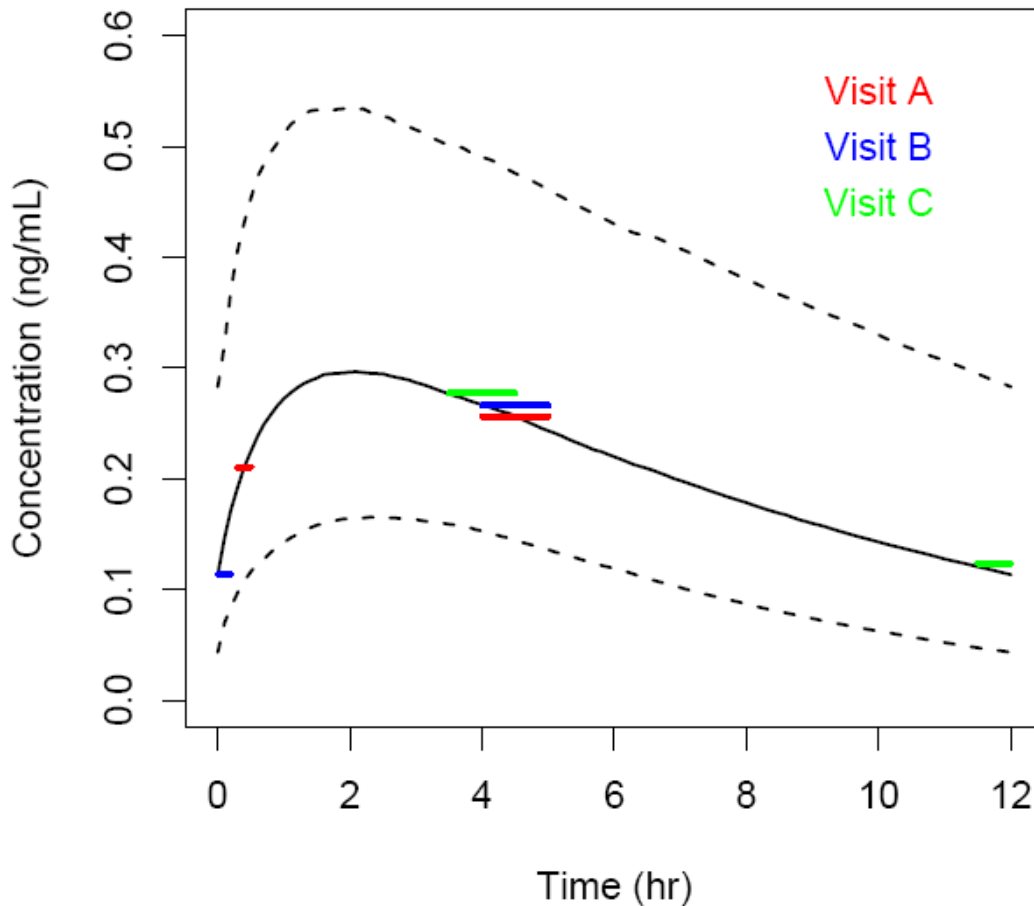


# Comparison of the results

## Optimised sampling times



# Design retained



Visit	Sampling times
A	0.3-0.5hr 4-5 hr
B	Postdose (0-0.2 hr) 4-5 hr
C	Predose (11.5-12hr) 3.5-4.5 hr

Times for visits 1, 2, 3:

- A-B-C for 1/6th of the patients
- A-C-B for another 1/6th patients
- B-A-C for another 1/6th patients
- B-C-A for another 1/6th patients
- C-A-B for another 1/6th patients
- C-B-A for another 1/6th patients



# Evaluation of the design

## ➤ Methodology

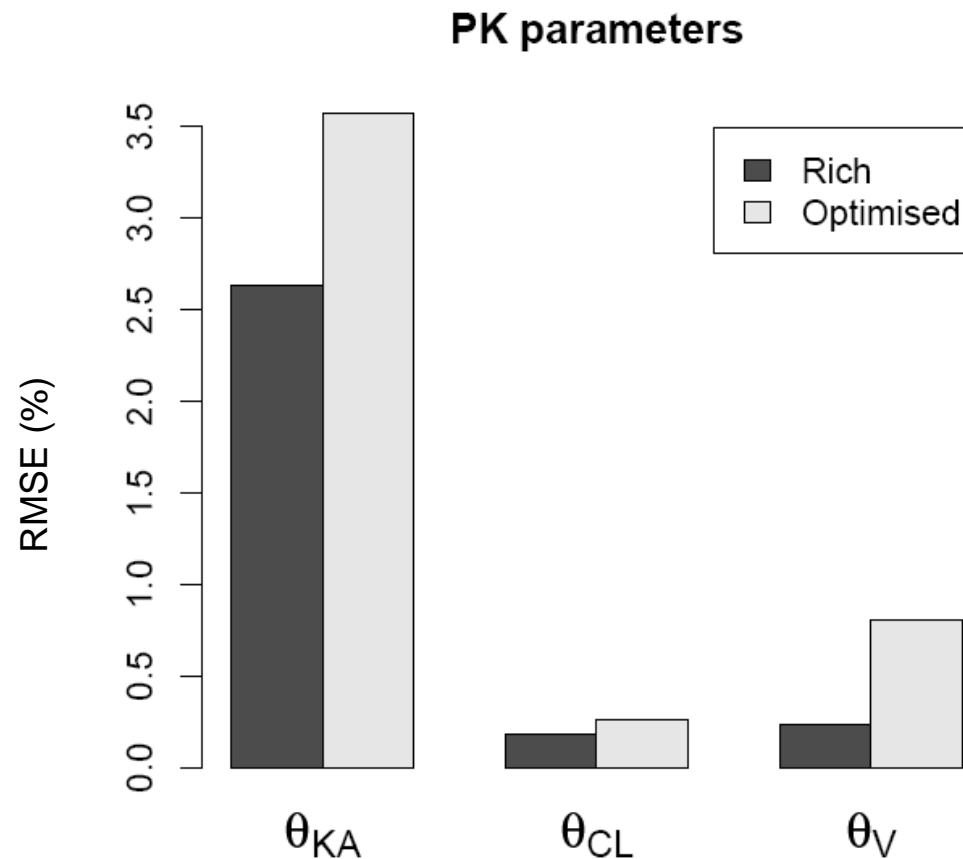
- Simulated a large number of trials;
- Evaluated the parameters with NONMEM;
- Compared the estimated parameters with the « true » parameters used for the simulation;
- Calculated RMSE values (see Hooker et al, 2003)

$$\text{RMSE} = \frac{1}{\theta_k^{\text{TRUE}}} \sqrt{\left[ \frac{1}{N} \sum_{i=1}^N (\theta_{k,i} - \theta_k^{\text{TRUE}})^2 \right]} \times 100 (\%)$$



# Evaluation of the design

- Rich sampling profile: 7 samples per visit  
(0,0.25,0.5,1,3,6,12), i.e. 21 samples per subject



# Conclusions

- ▶ The main differences between the 3 optimising tools are:
  - the implementation of the problem
  - the outputs
- ▶ The sampling times optimised by the 3 different tools were similar for this case;
- ▶ However, the optimised design is very much dependent on the assumed PK profile....





# Acknowledgement

- ▶ Steve Duffull
- ▶ Andrew Hooker
- ▶ Joakim Nyberg

