

Monolix benefits from external modules to manage complex ODE

Illustration with a population analysis of Irinotecan and its metabolites

B. Ribba¹, K. Chatel², M. Tod¹, P. Girard¹, G. Freyer^{1,3}, B. Tranchand^{1,4}

¹Université de Lyon, Lyon, F-69003, France; ²Université Lyon 1, Ciblage Thérapeutique en Oncologie (EA3738), Faculté de Médecine Lyon-Sud, Oullins, F-69921, France; ³INRIA Saclay - Île de France, Equipe projet SELECT; ⁴Service d'Oncologie Médicale, Centre Hospitalier Lyon-Sud, Oullins, F-69921, France; ⁵Centre Léon Bérard, F-69373 Lyon Cedex 08, France

Background

The development of molecular targeting therapies may require the use of “systems biology” approaches in PK/PD modelling.

As a consequence, structural models may be complex, composed by stiff ordinary differential equations (ODE) and characterized by multiscale dynamics.

Their evaluation in the context of parameter estimation requires sophisticated ODE solvers.

Monolix proposes, in its last version 2.3.1, two ODE C++ solvers.

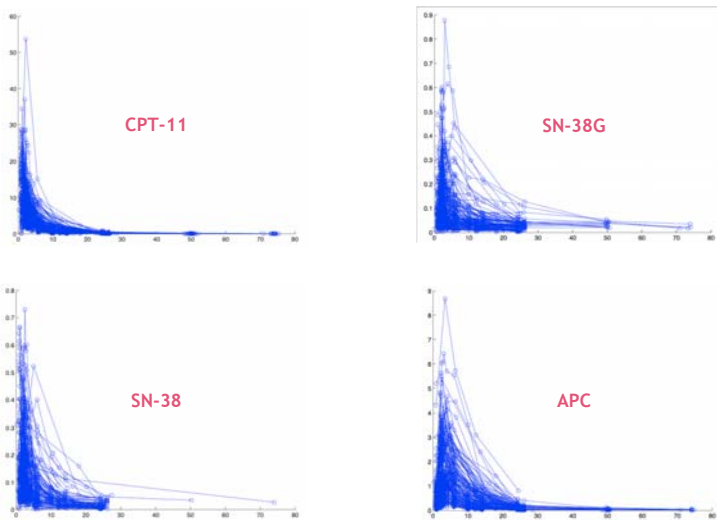
Objectives

- To test the efficiency of the coupling Monolix/ODE C++ solvers to characterize complex PK models of Irinotecan and its metabolites.

Material and Methods

- Data -

- Irinotecan (CPT-11) and three of main metabolites (SN-38, SN-38G, APC) plasma concentrations:
 - CPT-11 infusion over 90 minutes
 - 162 patients, phase I and II pediatric clinical trials
 - 5345 observations (33 on average per patients: 9.3 for CPT-11, 7.1 for SN38, 7.7 for SN38G, and 8.9 for APC)



Plasma concentrations of CPT-11 (top left), SN-38 (bottom left), SN-38G (top right) and APC (bottom right) in micromolar over time in hours

- Monolix software -

- Monolix 2.3.1 / package C++ CVODE (SUNDIALS)
 - ADAMS/Moulton method (recommended for non-stiff systems)
 - can be switched to BDF (Backward Differentiation Formulas)

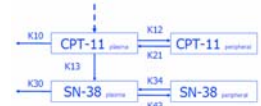
- Methodological approach -

- Step-by-step approach
- Initial values of parameters set to 1

Results

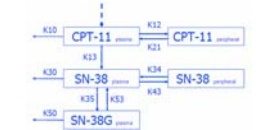
STEP I : CPT-11 and SN-38 data

- Linear 4 compartments model (residual error: additive)
- Run duration: 13.5 minutes (PC, 2 GHz Intel Core 2 Duo)



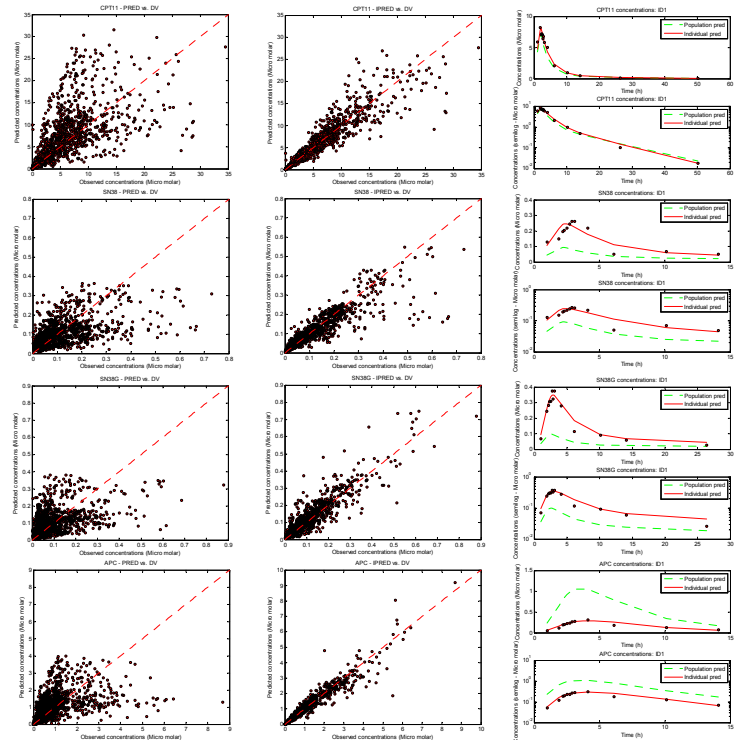
STEP II : CPT-11, SN-38 and SN-38G data

- Linear 5 compartments model (residual error: additive)
- Run duration: 20 minutes



STEP III : CPT-11, SN-38, SN-38G and APC data

- Linear 7 compartments model (residual error: additive)
- Run duration: 33.3 minutes



Goodness of fit plots for STEP III: IPRED vs DV (left column), PRED vs DV (centre) and individual/population fits of ID1 (right) for CPT-11 (top line), SN-38 (second), SN-38G (third), APC (bottom) plasma concentrations

- Comparison with NONMEM VI-

- STEP I: CPT-11 and SN38 data
 - ADVAN7 and FO (analytic resolution): Successful run in 19 minutes
 - ADVAN8 and FO (BDF method) : Successful run in 45 minutes
 - Difficulties with ADVAN6 (Runge-Kutta-Verner order 5 and 6) and ADVAN9 (LSODA)

Conclusions

- Monolix 2.3.1 using external modules may constitute a very relevant tool to develop physiologically-based PK/PD models