

Steps Towards a Robust Generic Method for Deconvolution Directly on Pharmacokinetic Profiles

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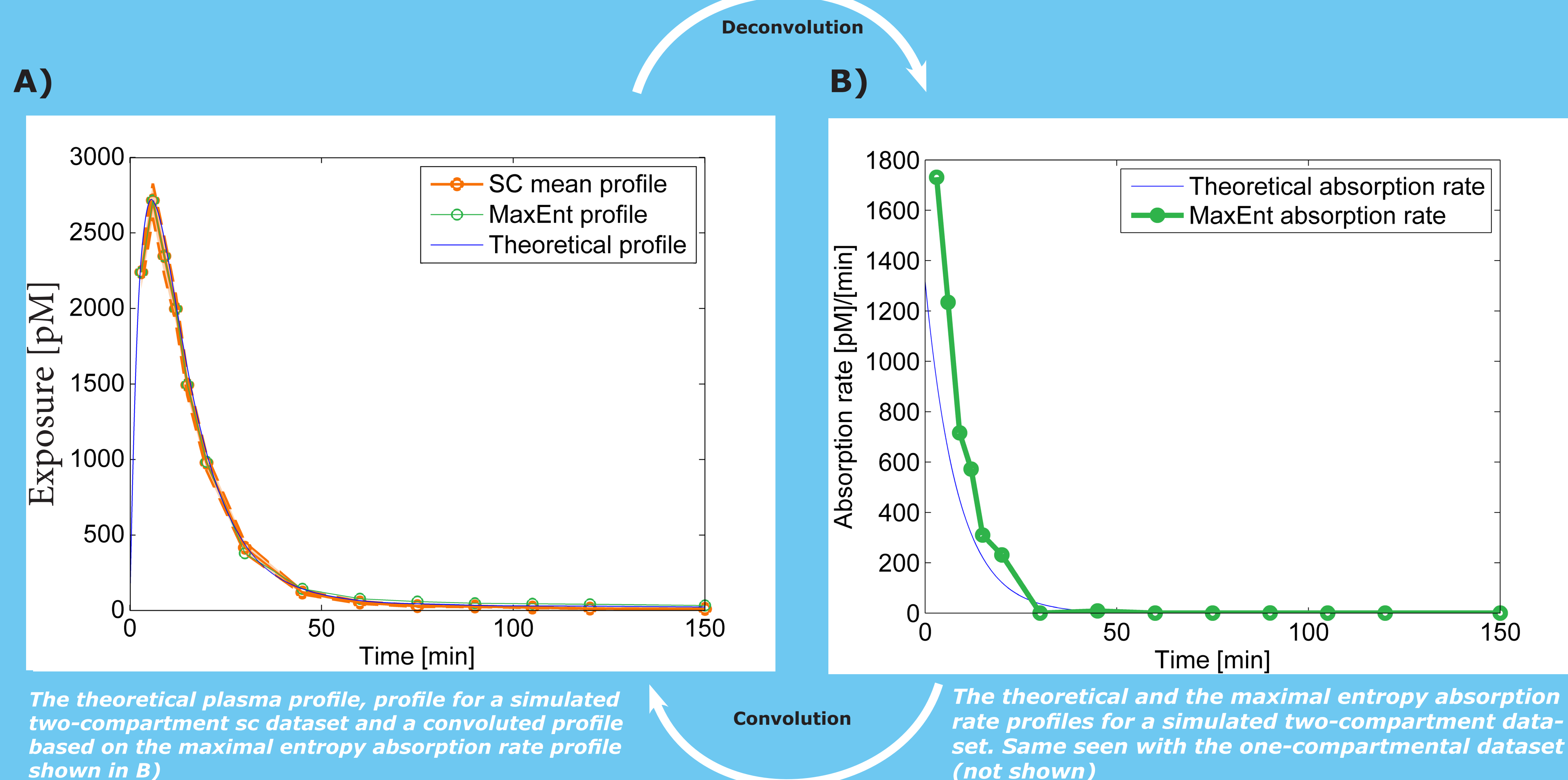
Why ?

- At early *in vivo* screening a high number of drug candidates is evaluated - a fast deconvolution method is beneficial
- Data driven - equivalent to non compartment analysis & without compartmental model assumptions

How ?

- One and two compartment models were fitted to intravenous (iv) and subcutaneous (sc) data from pig
- Simulation of datasets (iv and sc) with 20 individuals
- Applying a maximal entropy deconvolution method to estimate absorption rate from data^{1,2}
- Assessing how the calculated mean absorption rate fits the population mean absorption rate

Results



A generic method for deconvolution directly on PK profiles profiles was developed and tested on simulated datasets. The method resulted in similar absorption rate profiles as expected from the theoretical absorption rate, except for the initial timepoint(s)

Next

Investigate influence of variability - Monte Carlo simulations

Will differences between the theoretical and the maximal entropy absorption rate profiles be larger at fast absorption rates?

[1] Skilling J. Bryan R.K. Monthly Notices Roy. Astronom. Soc. 211:111-124, 1984

[2] Madden F.N. et al. Journal of Pharmacokinetics and Biopharmaceutics 24, 3:283-299, 1996