

Background

For many research questions, model complexity needs to be adapted during the modelling process, e.g. by refining empirical models or coarsening mechanistic models.

Established software tools mostly support either an empirical PK/PD approach (e.g. NONMEM, Monolix) or a mechanistic PBPK / Systems Pharmacology approach (e.g., GastroPlus, PK-Sim, SimCYP) and **lack the flexibility** to switch between these two paradigms.

Building on a MATLAB toolbox developed over the years in research and teaching as part of the PharMetrX PhD program [1-5], we developed a **new MATLAB-based pharmacometric modelling framework** specifically designed to

- adapt model complexity to the research question under investigation
- support integration of databases
- promote modelling transparency

Scope of toolboxes

	Databases (physiology / drug properties)	Virtual populations and scaling methods	Fully flexible model design (empirical / mechanistic)	Check for unit consistency / tracking of assumptions
PBPK toolboxes (PK-Sim, SimCyp, GastroPlus)	✓	✓		
Plain Matlab / R			✓	
This toolbox	✓	✓	✓	✓

Computation with units

- Extension of contributed MATLAB toolbox [6]
- Unit consistency check during any computation

Solving ODEs with units

class-based design, operator overloading

same ODE syntax with/without units

unit check frequency is flexible

Runtime comparison

	Frequency of unit check		
Model	Never	Once	Always
1 cmt PK	1.0 ms	1.3 ms	18 ms
13 cmt PBPK	35 ms	41 ms	1.2 s

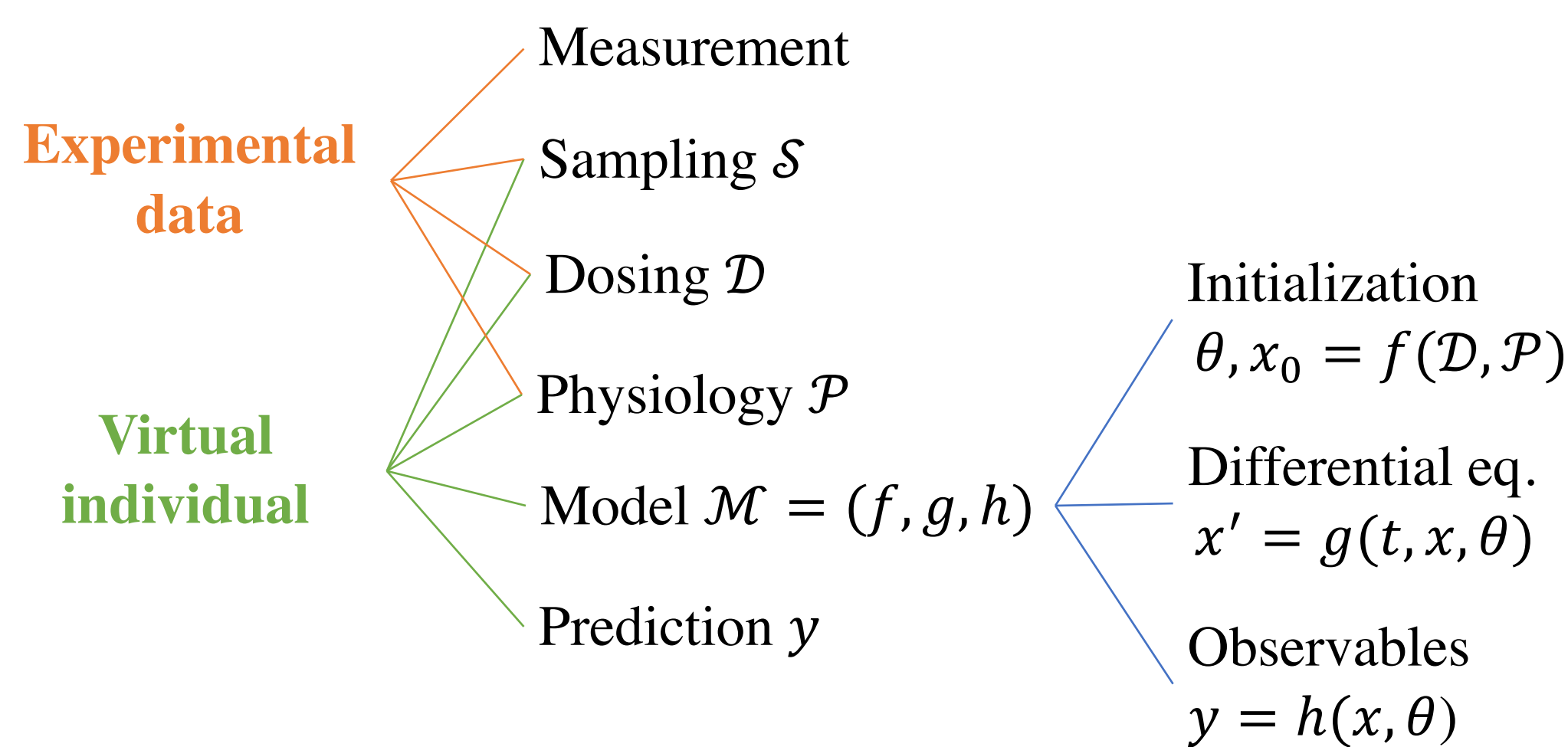
Example: units

How many drug molecules per E. coli cell?

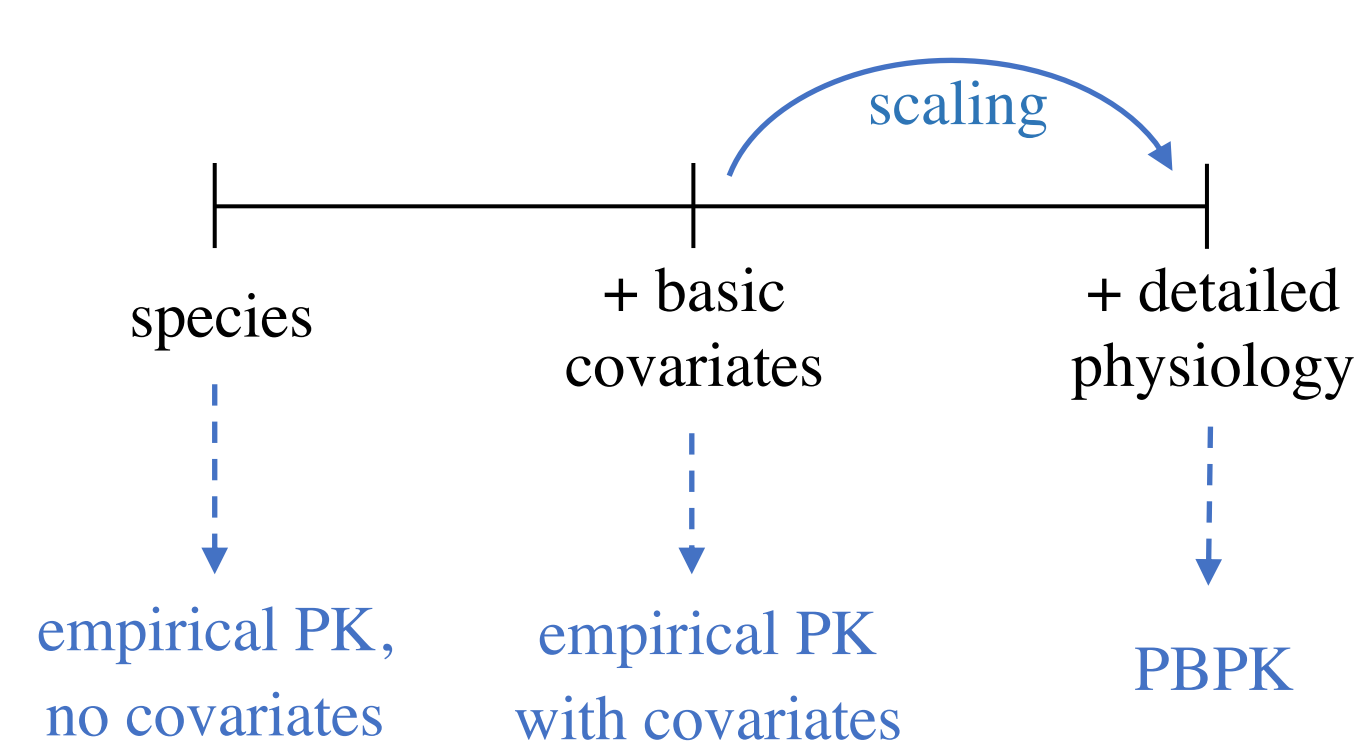
```
>> V = 2e-15*u.L; % E. coli volume
>> C = 1*u.nM; % drug concentration
>> n = V*C*u.NA
n = 1.2
```

Toolbox overview

Infrastructure



Physiology: levels of detailedness



Simple workflow

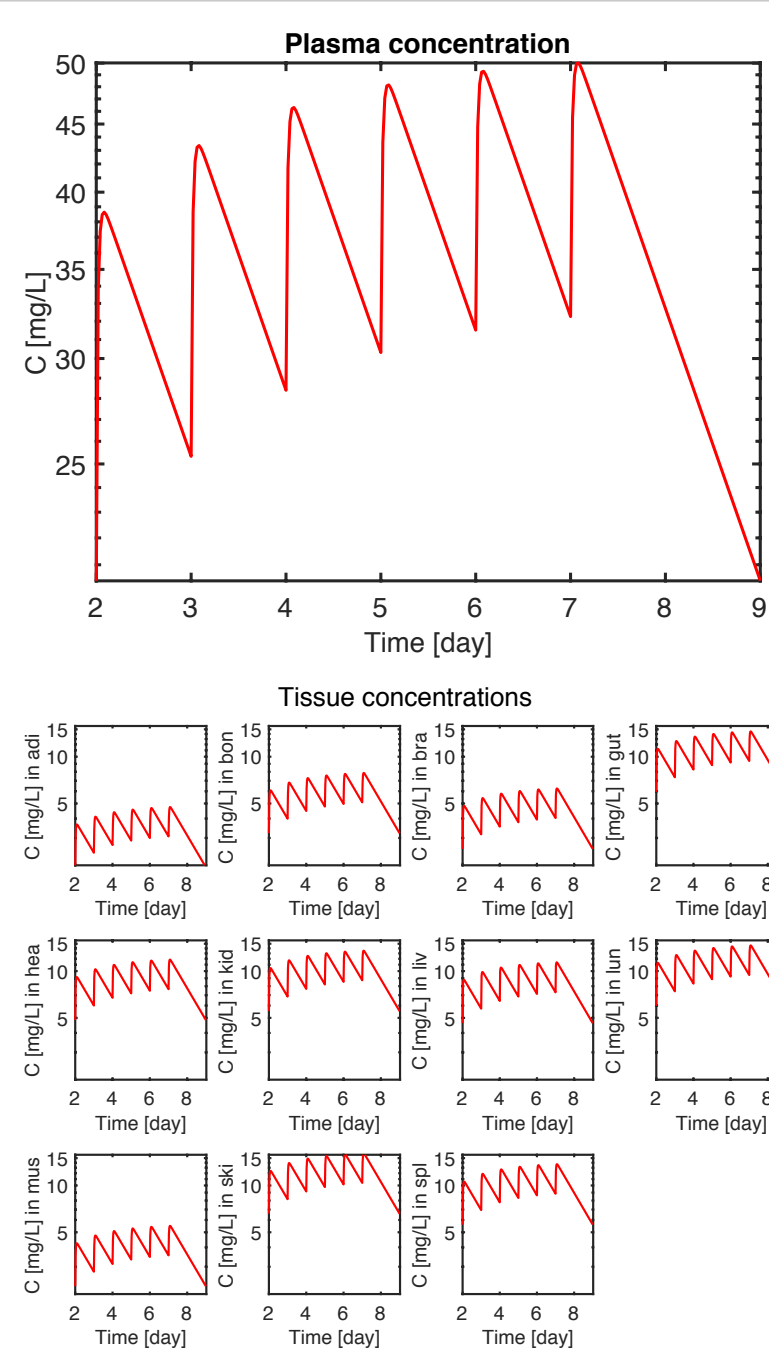
1. define $\mathcal{S}, \mathcal{D}, \mathcal{P}, \mathcal{M}$
2. initialize: $\mathcal{D}, \mathcal{P} \xrightarrow{f} x_0, \theta$
3. simulate: $x_0, \theta, \mathcal{S} \xrightarrow{g} x$
4. plot: $x, \theta \xrightarrow{h}$

Example: main script

```
% Prepare scaling
refhuman = Physiology('human_male_35y_73kg_176cm');
tallhuman = Covariates('species', 'human', ...
    'sex', 'male', 'age', 35*u.year, 'BW', 90*u.kg, ...
    'BH', 1.90*u.m);

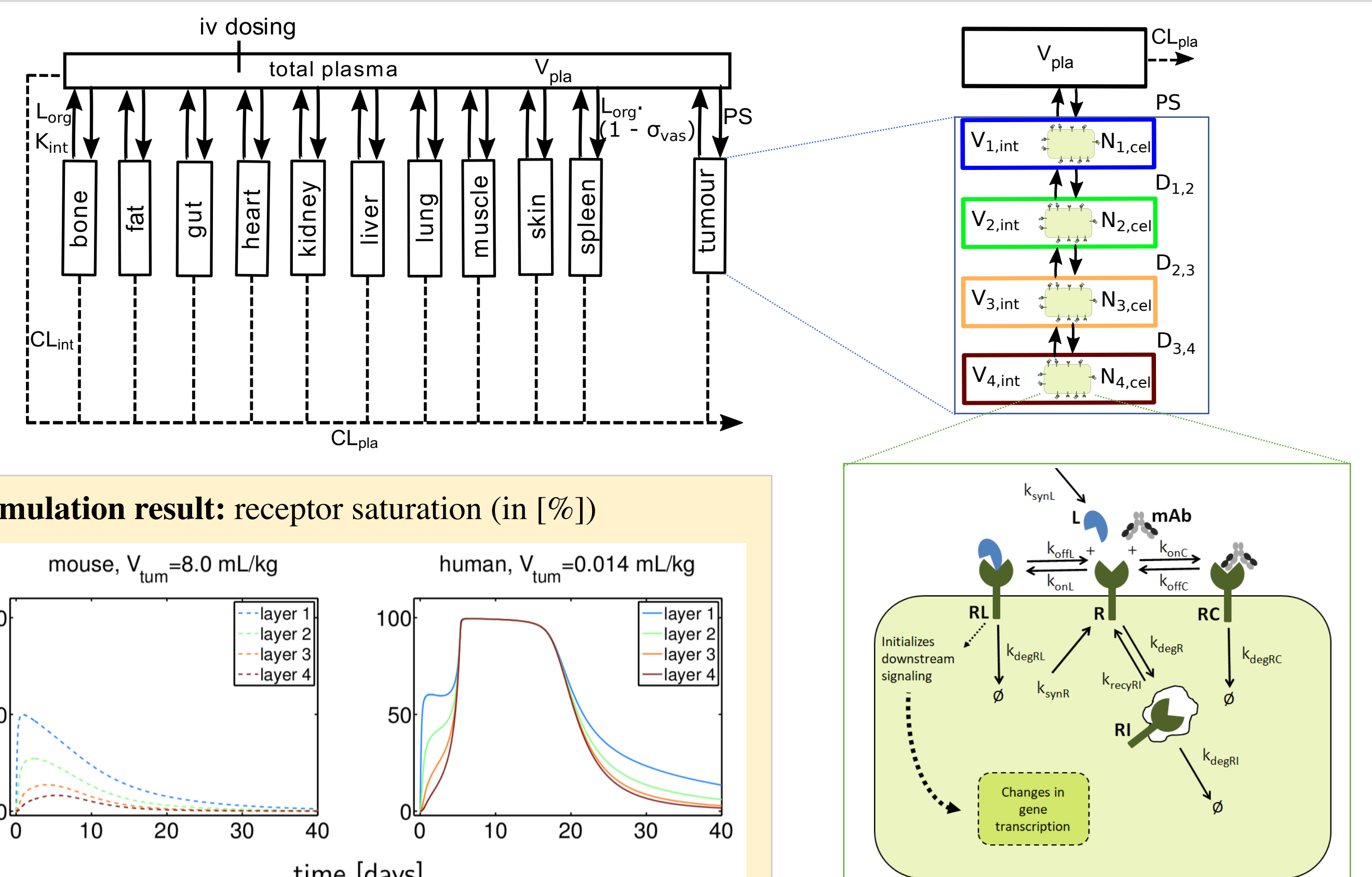
% define sampling (S), dosing (D), physiology (P), model (M)
indv = Individual;
indv.physiology = scaling_LBW(refhuman, tallhuman);
indv.dosing = oral('Warfarin', (0:1:7)*u.day, 250*u.mg);
indv.sampling = Sampling(2*u.day:30*u.min:8*u.day);
indv.modelfun = @SMD_PBPK_13CMT_wellstirred;
indv.options.tissuePartitioning = @rogersrowland;

% initialize, simulate, plot
indv.model = initialize(indv);
indv.output = simulate(indv);
plot(indv)
```

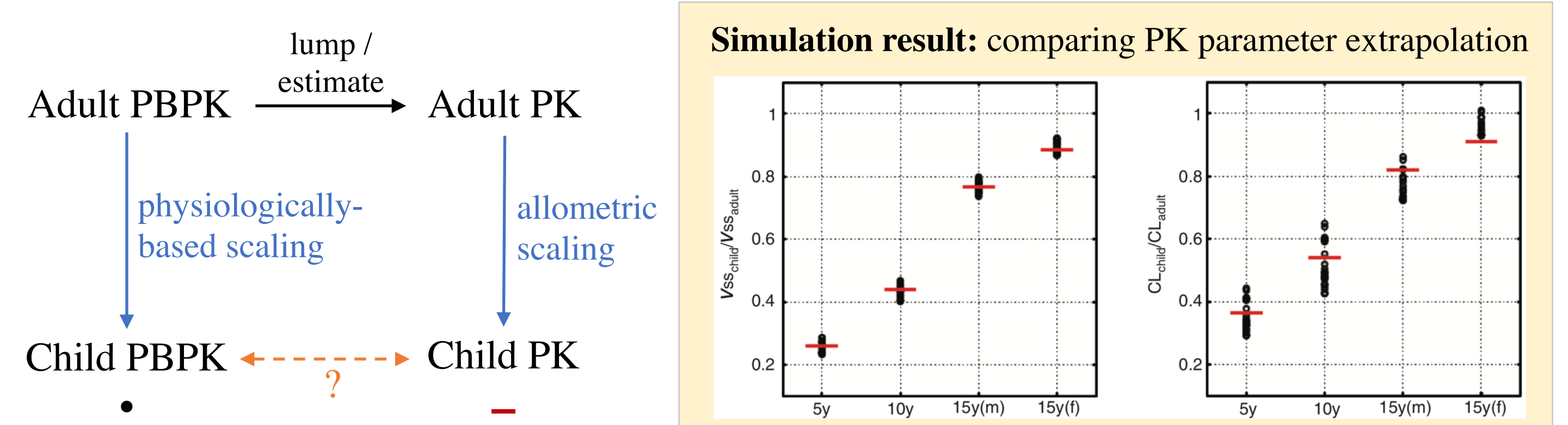


Examples shown in live demo

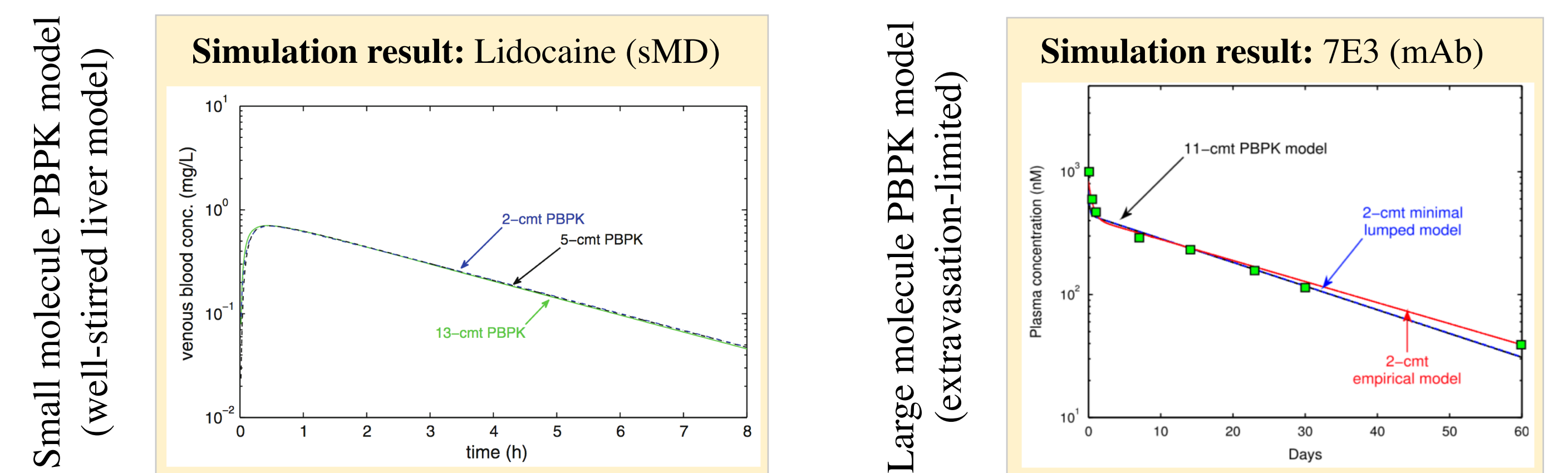
Kinetics of monoclonal antibodies in tumour [4]



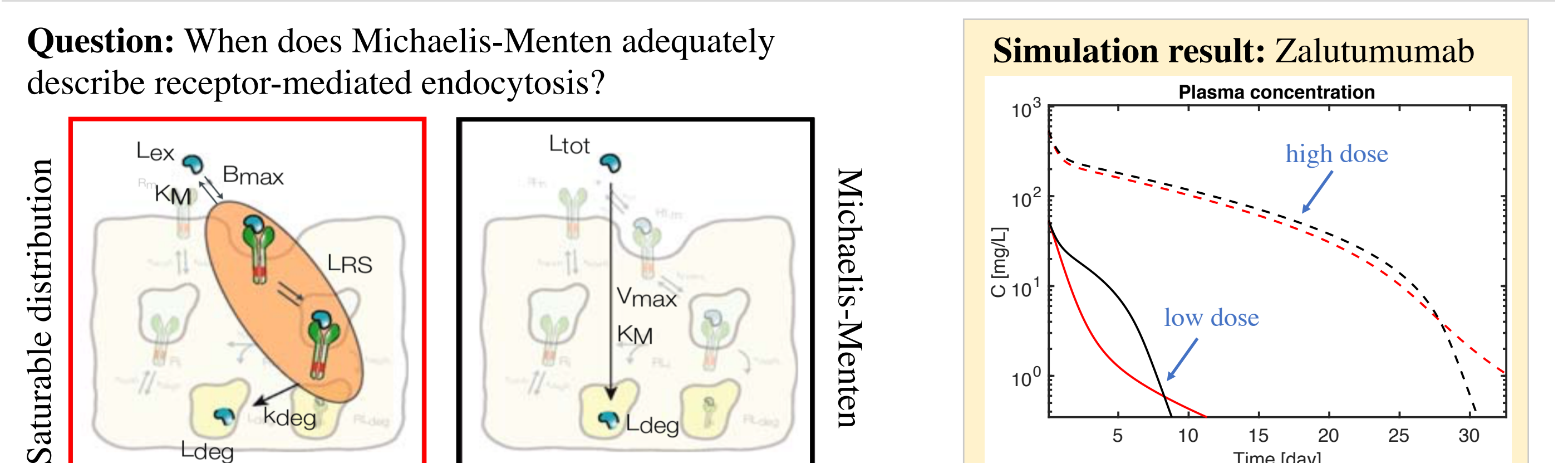
Comparison of scaling methods to children [1]



Interpretation of compartmental models via lumping [7]



Receptor-mediated endocytosis of therapeutic proteins [8]



References

- [1] Huisinga W et al. CPT:PSP (2012) 1:e4
- [2] Fronton L et al. J PKPD (2014) 41(2):87–107
- [3] Huisinga W et al. (2016) “Target-driven pharmacokinetics of biotherapeutics” in: Zhou, Theil (Eds.), Wiley
- [4] Fuhrmann S et al. J PKPD (2017) 44(4):351–374
- [5] <https://www.pharmetrx.de/>

- [6] Physical Units toolbox, version 4.1.0.0
<https://de.mathworks.com/matlabcentral/fileexchange/38977-physical-units-toolbox>
- [7] Pilari S, Huisinga W. J PKPD (2010) 37:365–405
- [8] Krippendorff BF et al. J PKPD (2009) 36:239–260

Contact

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