

Integration of Representative Sinusoids into a Physiologically Based Whole-Body Model for a Detailed Description of Biliary Transport

Lars Ole Schwen¹, Lars Kuepfer², Raymond Reif³, Ahmed Ghallab³, Jan G. Hengstler³, Tobias Preusser¹

¹Fraunhofer MEVIS, Bremen ²Bayer, Leverkusen ³IfADO, Dortmund

Introduction

- Enterohepatic circulation (EHC) important for distribution and clearance of drugs
- Transport mechanisms involve biliary transport
- Cholyl-lysyl-fluorescein (CLF), an analogon of natural bile acids, is used as probe molecule

Goals

- Quantify kinetics of transport processes
- Include them in physiologically based pharmacokinetics (PBPK) models
- Obtain parameters via fluorescence imaging [2]

Approach

- Combine well-stirred organism-scale model and detailed liver model
- Multi-scale, spatially resolved “representative sinusoid model” extended from [3, 4]

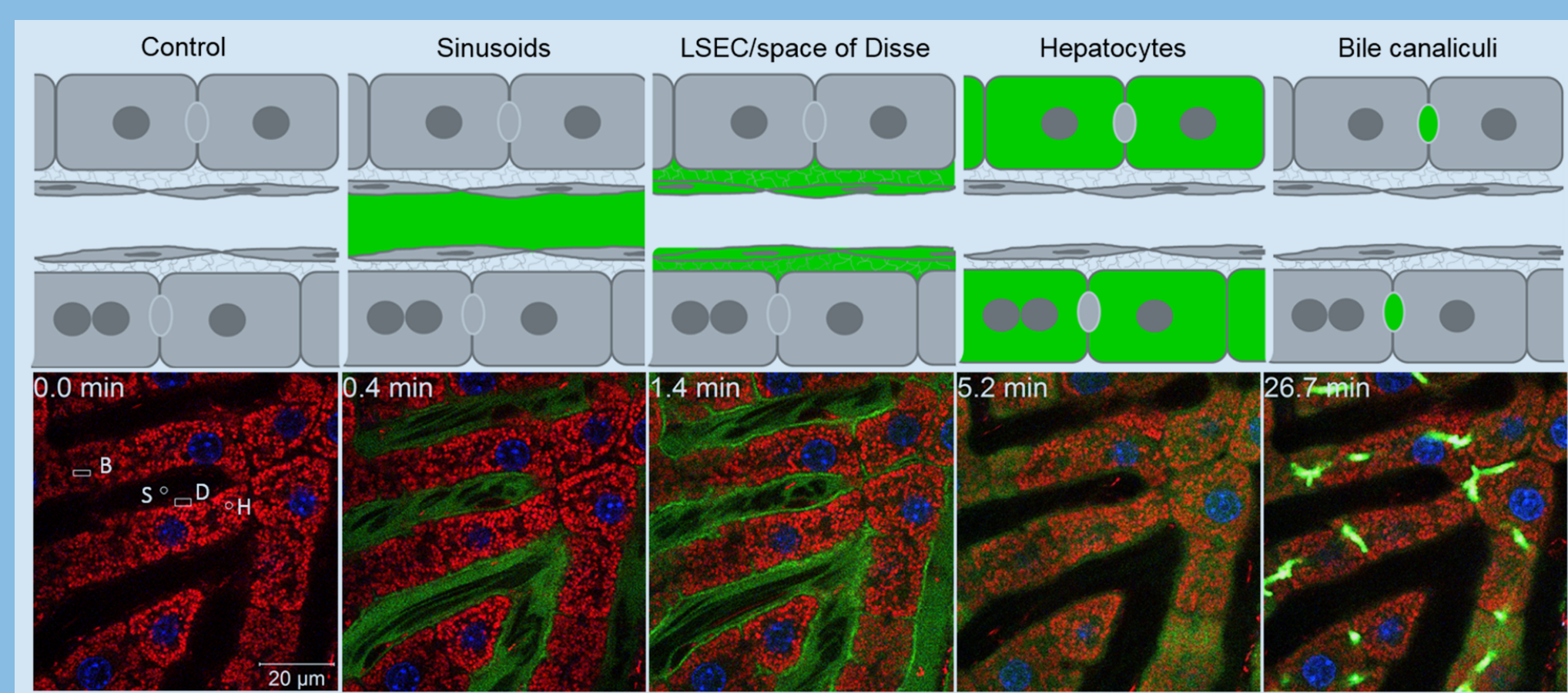


Fig. 1. CLF concentration measurements by intravital two-photon imaging [2] (CC-BY)

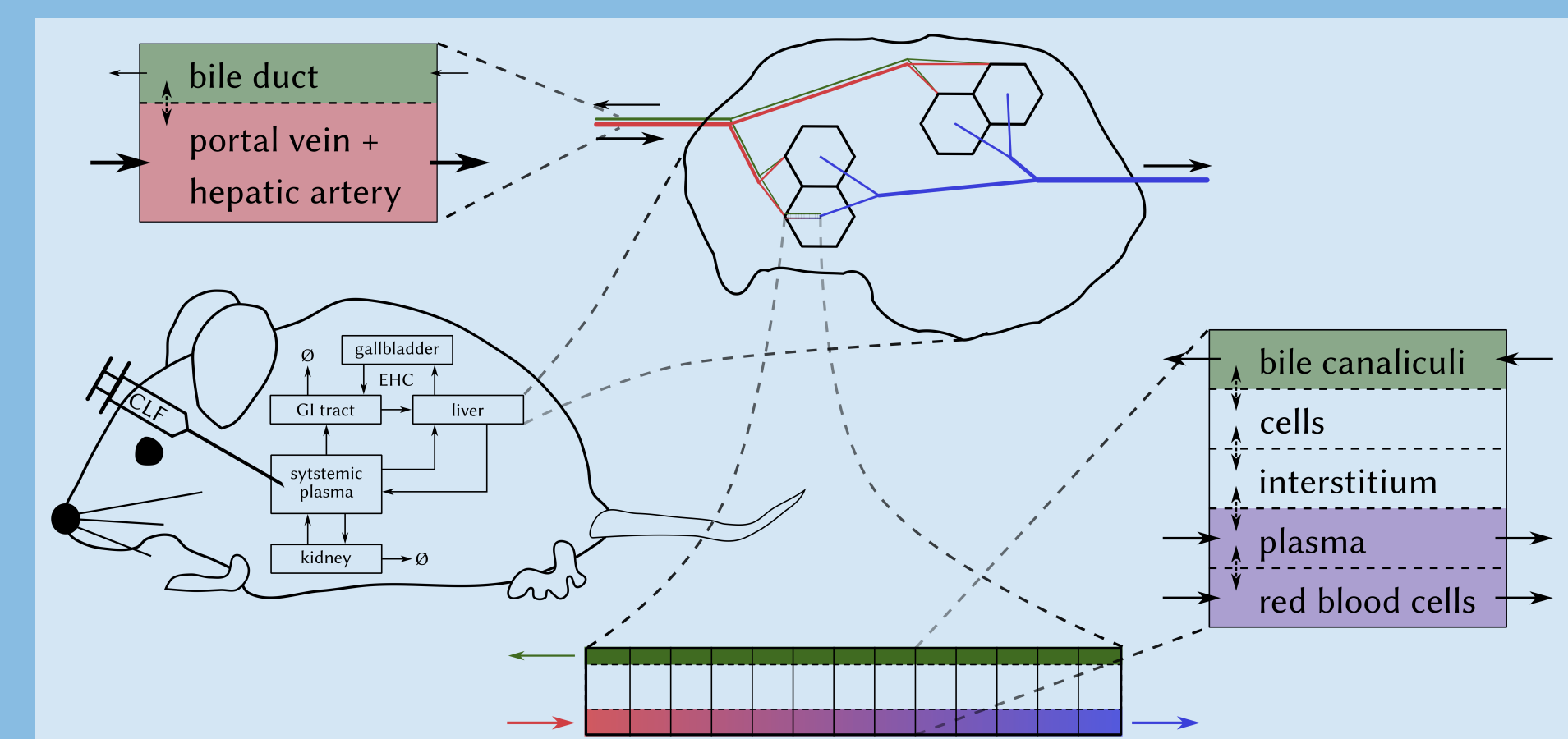


Fig. 2. Conceptual sketch of the multiscale CLF model including biliary transport

First Step: Isolated Perfused Liver

$$\partial_t \begin{bmatrix} c^{rbc} \\ c^{pls} \\ c^{int} \\ c^{cell} \\ c^{bile} \end{bmatrix} = \underbrace{\begin{bmatrix} -\frac{P_{rbc,pls}}{\kappa_{rbc,pls}\varphi^{rbc}} & \frac{+P_{rbc,pls}}{\varphi^{rbc}} & 0 & 0 & 0 \\ \frac{+P_{rbc,pls}}{\kappa_{rbc,pls}\varphi^{pls}} & -\frac{P_{rbc,pls}}{\varphi^{pls}} + \frac{-P_{pls,int}}{\varphi^{pls}} & \frac{+P_{pls,int}}{\kappa_{pls,int}\varphi^{pls}} & 0 & 0 \\ 0 & \frac{+P_{pls,int}}{\varphi^{int}} & -\frac{P_{pls,int}}{\kappa_{pls,int}\varphi^{int}} + \frac{-P_{int,cell}\kappa^{int}}{\varphi^{int}} & \frac{+P_{int,cell}\kappa^{cell}}{\varphi^{int}} & 0 \\ 0 & 0 & \frac{+P_{int,cell}\kappa^{int}}{\varphi^{cell}} & -\frac{P_{int,cell}\kappa^{cell}}{\varphi^{cell}} & 0 \\ 0 & 0 & 0 & 0 & 0 \end{bmatrix}}_{\text{passive diffusion}} \begin{bmatrix} c^{rbc} \\ c^{pls} \\ c^{int} \\ c^{cell} \\ c^{bile} \end{bmatrix} + \underbrace{\begin{bmatrix} 0 \\ 0 \\ -\frac{V_{max}^{int,cell}\kappa^{int}c^{int}}{\varphi^{int}(K_m^{int,cell} + \kappa^{int}c^{int})} + \frac{V_{max}^{int,cell}\kappa^{int}c^{int}}{\varphi^{cell}(K_m^{int,cell} + \kappa^{int}c^{int})} \\ 0 \end{bmatrix}}_{\text{active transport}} + \underbrace{\begin{bmatrix} 0 \\ 0 \\ 0 \\ -\frac{V_{max}^{cell,bile}\kappa^{cell}c^{cell}}{\varphi^{cell}(K_m^{cell,bile} + \kappa^{cell}c^{cell})} + \frac{V_{max}^{cell,bile}\kappa^{cell}c^{cell}}{\varphi^{bile}(K_m^{cell,bile} + \kappa^{cell}c^{cell})} \end{bmatrix}}_{\text{blood/bile flow}} + \begin{bmatrix} +V_{blood}\nabla_x c^{rbc} \\ +V_{blood}\nabla_x c^{pls} \\ 0 \\ 0 \\ -V_{bile}\nabla_x c^{bile} \end{bmatrix}$$

rbc: red blood cells, pls: plasma, int: interstitium, cell: hepatocytes, bile: bile canaliculi

P : permeabilities, κ : partition coefficients, φ : volume fractions, v : flow velocities, parameters partially from [1]

First Results

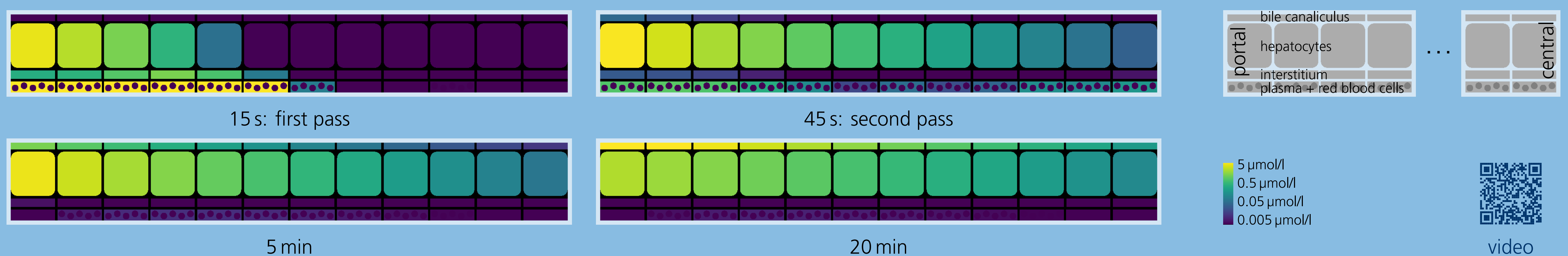


Fig. 3. Simulation of CLF distribution after bolus injection, representing the liver by a single sinusoid and the organism only by a blood pool.

Next Steps

- refine physiology and physicochemistry in model structure and parameters
 - at sinusoidal scale
 - at organ-scale, including vascular systems and heterogeneity
 - at organism-scale, including excretion
- calibrate model parameters
- validate by comparison to experiments

Literature

- [1] K. Meyer, O. Ostrenko, G. Bourantas, H. Morales-Navarrete, N. Porat-Shliom, F. Segovia-Miranda, H. Nonaka, A. Ghaemi, J.-M. Verbavatz, L. Bruschi, I. Szalzarini, Y. Kalaidzidis, R. Weigert, and M. Zerial, *A predictive 3D multi-scale model of biliary fluid dynamics in the liver lobule*, Cell Systems 4 (2017), no. 3, 277–290. DOI 10.1016/j.cels.2017.02.008
- [2] R. Reif, A. Ghallab, L. Beattie, G. Günther, L. Kuepfer, P. M. Kaye, and J. G. Hengstler, *In vivo imaging of systemic transport and elimination of xenobiotics and endogenous molecules in mice*, Archives of Toxicology 91 (2017), no. 3, 1335–1352. DOI 10.1007/s00204-016-1906-5
- [3] L. O. Schwen, M. Krauss, C. Niederalt, F. Gremse, F. Kiessling, A. Schenk, T. Preusser, and L. Kuepfer, *Spatio-temporal simulation of first pass drug perfusion in the liver*, PLoS Computational Biology 10 (2014), no. 3, 1–18, e1003499. DOI 10.1371/journal.pcbi.1003499
- [4] L. O. Schwen, A. Schenk, C. Kreutz, J. Timmer, M. M. Bartolomé Rodríguez, L. Kuepfer, and T. Preusser, *Representative sinusoids for hepatic four-scale pharmacokinetics simulations*, PLoS ONE 10 (2015), no. 7, e0133653. DOI 10.1371/journal.pone.0133653