
A SPATIO-TEMPORALLY RESOLVED HEPATIC PHARMACOKINETICS MODEL

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VLN Retreat

Hünfeld, 2012-11-28



Outline

1. Perfusion Model

2. Metabolization Model

3. Outlook

1. Perfusion Model

Contents

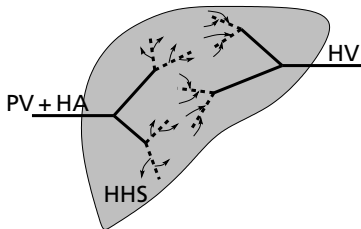
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2. Metabolization Model

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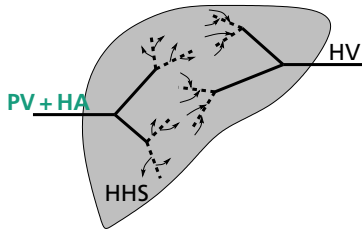
1. Perfusion Model

Model Overview



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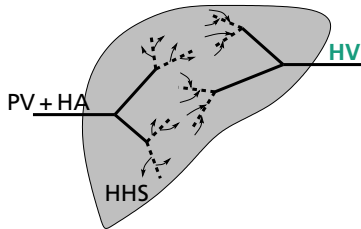
Model Overview



- supplying vascular system **PV + HA**

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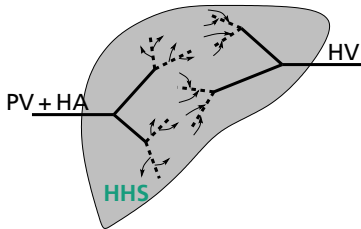
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- supplying vascular system PV + HA
- draining vascular system HV

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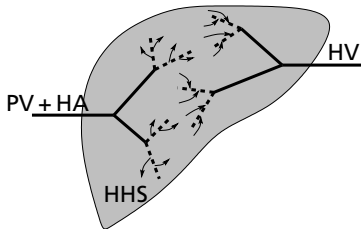
Model Overview



- supplying vascular system PV + HA
- draining vascular system HV
- homogenized hepatic space $HHS = HHS_{sin} + HHS_{cell} + HHS_{rest}$
 - sinusoidal volume fraction (blood flow)
 - cellular volume fraction (metabolization)
 - remaining volume

1. Perfusion Model

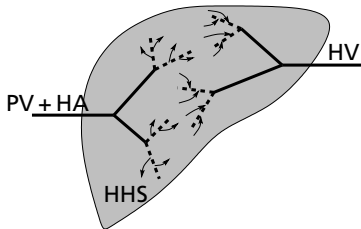
Blood Flow



- transport through PV + HA

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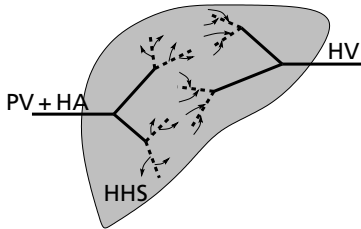
Blood Flow



- transport through **PV + HA**
- outflow from terminal edges **PV + HA** → **HHS_{sin}**

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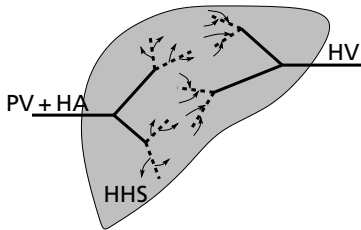
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- transport through **PV + HA**
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- **HHS** viewed as porous medium

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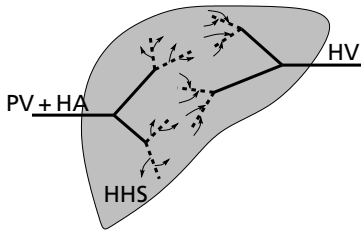
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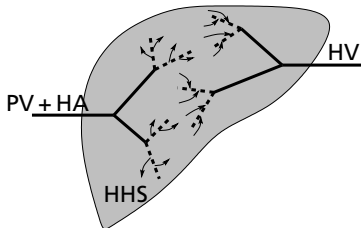
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1. Perfusion Model

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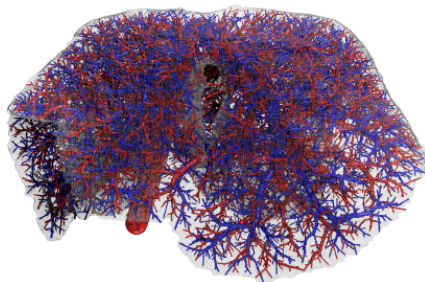
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- transport through **HV**

Transport described by velocities $v(x)$, constant in time.

1. Perfusion Model

Target Resolution

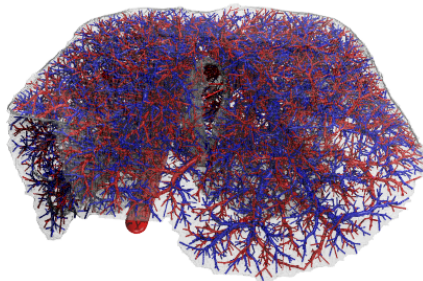
Mouse liver vascular systems down to lobular scale



1. Perfusion Model

Target Resolution

Mouse liver vascular systems down to lobular scale

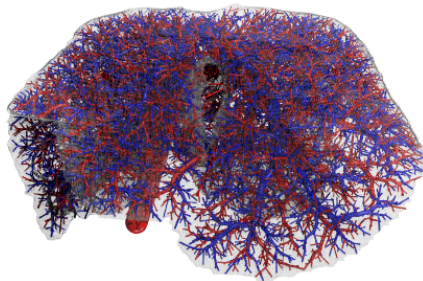


we can't see anything here

1. Perfusion Model

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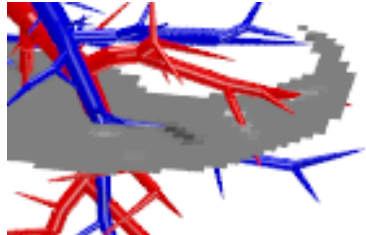
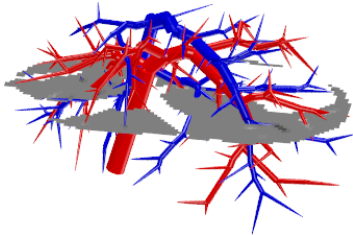
Mouse liver vascular systems down to lobular scale



we can't see anything here
...so let's consider a coarser tree

1. Perfusion Model

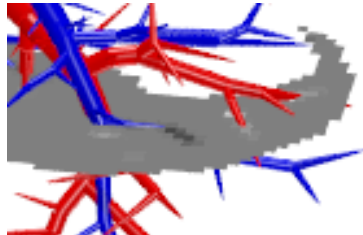
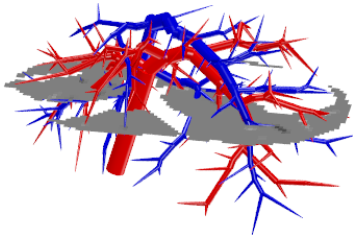
Velocity Computation I – Flow Sources



- vascular structures are cylinders 1D + radius

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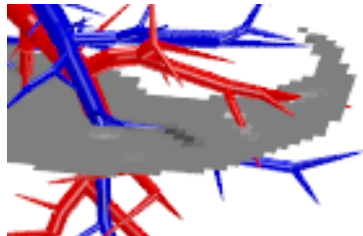
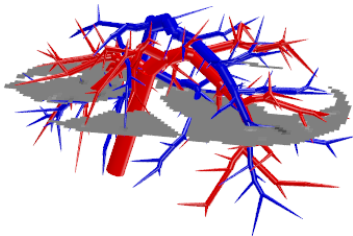
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1. Perfusion Model

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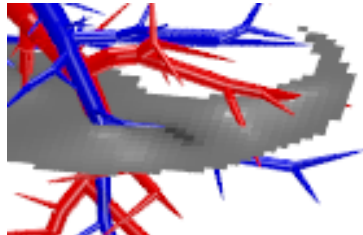
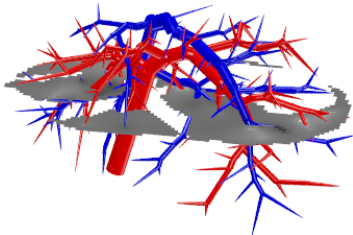
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this translates to a PDE

$$- \operatorname{div}(\alpha(x)\nabla p(x)) = \text{1D flow sources at terminal edges}$$

1. Perfusion Model

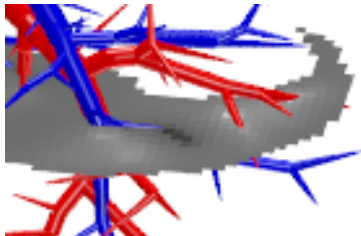
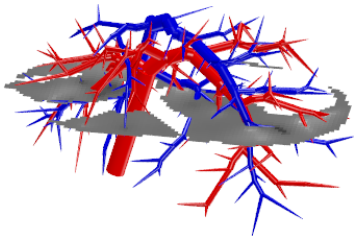
Velocity Computation II – Relative Pressures



- relative pressure profile $p(x)$ is solution of PDE

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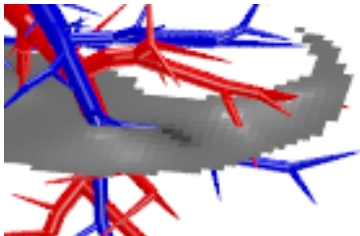
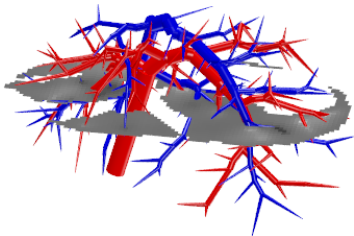


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- velocity along pressure gradient (Darcy)

$$v(x) = \frac{\alpha(x)}{n(x)} \nabla p(x)$$

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- velocity is directed PV + HA outflows \rightarrow HV inflows

2. Metabolization Model

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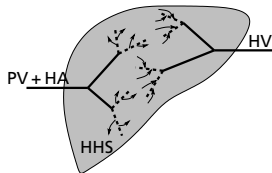
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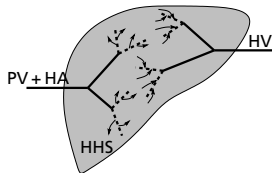


consider **concentration** of substances (drug, metabolite, ...) in the blood

- transport through PV + HA, HHS_{sin} , HV with velocities as before

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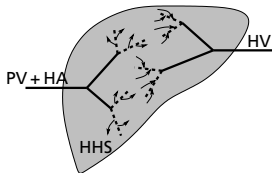


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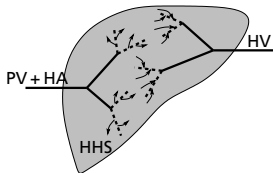


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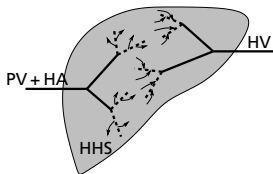
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- metabolization described as reaction (ordinary differential equation)
- one ODE per discretization point in HHS

2. Metabolization Model

Simplest Example: Macromolecular Contrast Agent (Bolus)

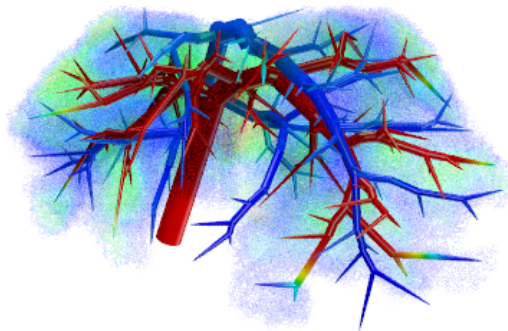
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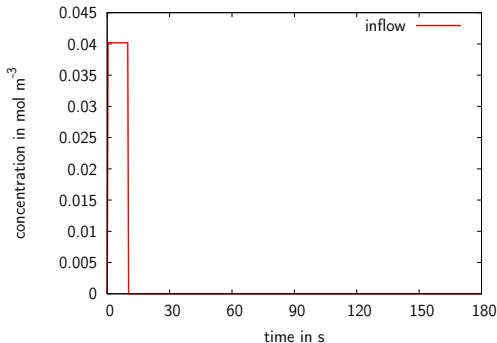
→ Video



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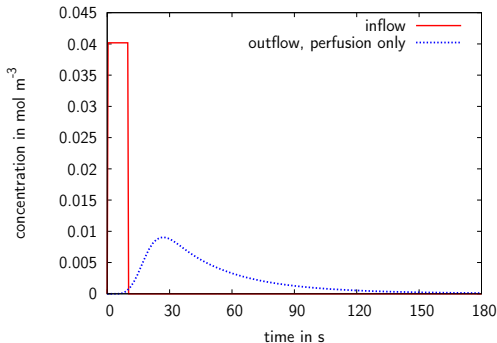
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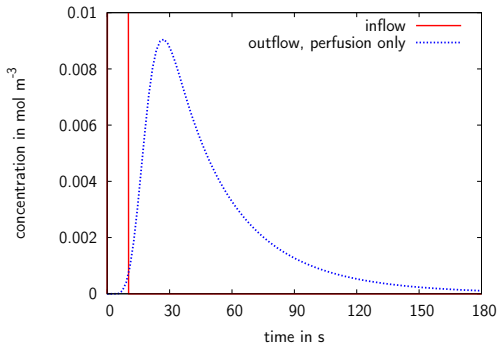
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2. Metabolization Model

Simple Examples: Linear Decay

- passive transport $HHS_{\text{sin}} \leftrightarrow HHS_{\text{cell}}$

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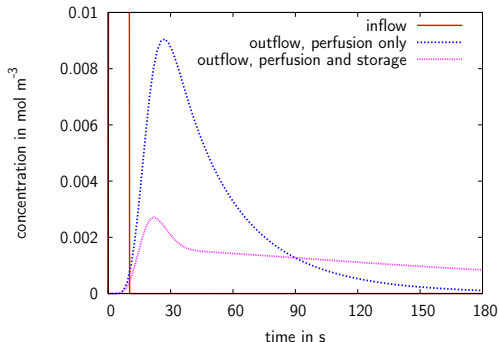
Simple Examples: Linear Decay

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- metabolization of torasemide by linear decay

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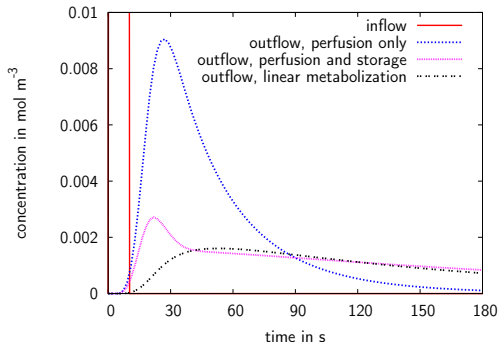
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2. Metabolization Model

Complicated Example: "Glycolysis" Model

[BioModels Database # 42]

- 15 substances, nonlinear ODE

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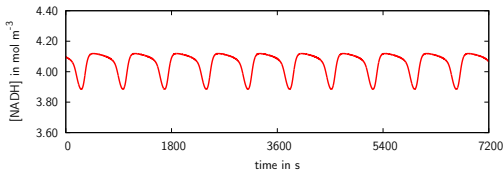
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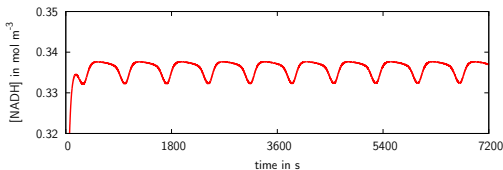
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outflow from
bioreactor model



PV outflow
our model

3. Outlook

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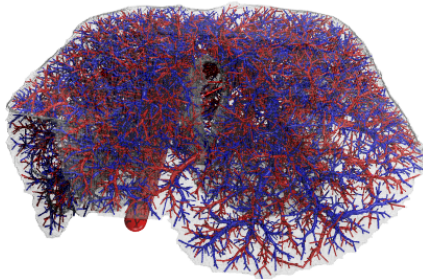
2. Metabolization Model

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Required Input

- vascular geometry



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Required Input

- vascular geometry
- total perfusion
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- inflow concentrations of considered substances
- ODE (form and parameters) describing metabolization

3. Outlook

Challenges

- proper implementation

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- proper implementation
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but that is your (the experimentalist's) job 😊

3. Outlook

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After we've finished a first implementation and publication ...

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- better geometric model of vascular structures

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- better geometric model of vascular structures
- other metabolization reactions

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After we've finished a first implementation and publication ...

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- other metabolization reactions
- validation

3. Outlook

References

-  Z. E. Heinemann, *Fluid flow in porous media*, 2005.
-  N. Le Novère, C. Flamm, and L. Endler, *Nielsen1998_glycolysis*, Model 42 in BioModels Database, 2012.
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