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COMPLEX HIERARCHICAL MODELING OF THE DYNAMIC PERFUSION TEST: APPLICATION TO LIVER

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Abstract. We propose a multicompartment model of hepatic blood perfusion that serves as a form of feedback for numerical simulations of dynamic CT investigation. The blood flow in the human liver can be characterized at several scales, using different models for each of them. In this paper, we focus on two levels: The flow in branching vessels with lumen diameters above 2 mm is described by a simple 1D model based on the Bernoulli equation completed with correction terms representing the local friction loss. This flow model is coupled through point sources/sinks with a 3D model describing multicompartment flows in tissue parenchyma. The compartments in the tissue parenchyma are associated with segments and hierarchies that confine the flow to a certain subdomain within the organ and respect the complexity of flow distribution according to the branching vascular trees of the portal and hepatic veins. Because the present research is motivated by the modeling of liver perfusion with the purpose to enable an improved analysis of CT scans, the model of contrast fluid propagation in each compartment is introduced as well. In this way, the time-space distribution of the so-called tissue density can be computed and compared with the measured data obtained form the CT scans.

1 INTRODUCTION

Modeling of tissue perfusion by blood belongs to quite challenging problems in biomechanical and biomedical research. In clinical practice, it is often necessary to identify tissue with an insufficient blood supply, to localize anomalies in blood micro-circulation and to quantify locally the perfusion efficiency. In the context of hepatic blood perfusion, the model proposed in this paper forms a basis for the reconstruction of liver segments, anatomical parts with autonomous perfusion related to a terminal branch of the hepatic

portal vein. Our effort is to improve the existing modeling techniques for processing the standard dynamic CT (computed tomography) investigations. For this purpose, we developed a multicompartment hierarchical model of tissue parenchyma [1], cf. [2], coupled with a 1D model describing the blood flow through the upper level of the portal (P) and hepatic (H) veins. The perfusion velocities in all the compartments are involved in the transport equations governing the distribution of the contrast fluid in the hepatic tissue.

The paper is organized as follows: In Section 2, we explain the concept of the hierarchical flow model in relation to the liver. For the modeling at the organ level, we use a lumped model with multiple sectors and hierarchies. In the present version of the model, permeabilities and perfusion parameters are defined ad hoc, as discussed in Section 2.2. In Section 3, we describe the model for contrast fluid propagation in parenchyma and branching networks of the portal and hepatic veins. For illustration, Section 4 contains numerical examples computed using the model implemented in the SfePy software [3].

2 HIERARCHICAL MODEL OF PERFUSION

The simulation of tissue perfusion by blood in organs such as liver or brain belongs to problems that necessitate the use of multiscale modeling of some sort, cf. [4]; the term "multiscale" is employed in a slightly different manner than in [5], where the "geometrical multiscale" modeling was introduced in the context of the cardiovascular system. Obviously, the difficulty of the problem consists in the nature of the flow on branching structures incorporating blood vessels of very different diameters. For instance, the blood is conveyed to the liver by the hepatic portal vein with lumen diameter of $D = 1.3\,\mathrm{cm}$. At the tissue parenchyma level, the blood channels are formed in the lobular hexagonal structures with the characteristic size of $1.5\,\mathrm{mm}$, so that the sinus, through which the blood flows from the portal to the hepatic compartments, is formed by microvessels with lumen diameters about $d = 10\,\mu\mathrm{m}$. Moreover, the scale change characterized by the ratio $d/D = 0.001$ is continuous. In general, the perfusion trees have several hierarchies distinguished by the number of "new" branches and reduced vessel diameters.

Besides the simulation of blood perfusion, the model that we develop should also enable the simulation of the contrast fluid (tracer) propagation during a dynamic perfusion test. In this way, a computational feedback can be provided, which would make it possible to perform a detailed analysis of patient-specific CT scans acquired by means of standard perfusion scanning, cf. [6]. Nowadays the methods based on the deconvolution, or maximum slope techniques give some characteristics such as the blood flow, blood volume and transition times for each voxel of the tissue, cf. [7]. Our approach should provide an alternative and more detailed interpretation of the perfusion CT scans. The proposed strategy is based on the following tasks:

- to describe all involved hierarchies of the perfusion trees including that of the parenchyma by suitable models involving a few undetermined parameters;
- to reconstruct the organ (liver) shape and the blood vessels geometries up to a

certain hierarchy using image segmentation techniques (based on "static" CT data);
- to tune (by solving some optimization problems) selected parameters of the parenchyma model such as permeability), so that the simulated dynamic CT test is as close as possible to the measured data.

Thus "tuned" model would enable blood flow analysis in particular compartments and be able to predict the effects of potential medical treatments such as surgical resection of pathological tissue. Unfortunately, the proposed strategy contains several hurdles. On one hand, the model should reflect the microstructure and fit the complex geometry of the perfusion trees, on the other hand, it should be parameterized just using not too many parameters to prevent ill conditioning of the "tuning" step involving simulations of the steady blood flow and dynamic tracer transport. For this purpose, the tuning parameters must reflect some important features of the whole perfusion system.

In this paper, we describe a simplified model on which we test the modeling of the perfusion and tracer transport. It consists of the two following parts:

1. The "inlet" and "outlet" trees, which in the case of the liver, describe the portal and hepatic veins, respectively. These trees are formed by pipes and junctions representing the vessel branching. For simplicity, we consider the blood flow to be a 1D flow of an incompressible Newtonian fluid, see Section 2.3.
2. The parenchyma model is constituted by equations governing a multicompartment Darcy flow in a 3D porous medium involving a pressure field associated with each compartment. Thus, at any point of the organ domain $\Omega \subset \mathbb{R}^3$, several (at least two) different pressure values are defined, each corresponding to a different compartment, see Section 2.2. The parenchyma model is connected to the 1D trees via point sources and sinks defined in Ω, Fig. 1.

We intend to describe the blood flow in the parenchyma using a more accurate model based on homogenization of the tissue microstructure, cf. [8].

2.1 Structure of compartments in parenchyma

The compartments are established as connected parts of the vasculature with a given range of characteristic vessel cross-sections, Fig. 1. The range is indicated by a hierarchy labeled by index $j = 0, 1, \ldots, N$. Each compartment is associated with a segment $\Omega_e \subset \Omega$, $e \in \mathcal{S}^G$, where $G = P, H$ indicates the group of the vascular system; the segments are introduced w.r.t. a partitioning that takes into account the branching of the portal or hepatic vascular trees, respectively. Therefore, any compartment belongs either to the portal or hepatic group, see Fig. 1. By $\mathcal{C}(e, j)$ we denote the compartment belonging to the e-th segment and j-th hierarchy. By $\mathcal{C}$ we denote the index set of all compartments. Thus, the compartment $k = \mathcal{C}(e, j)$ is presented by a multi-index consisting of two indices referring to a segment (i.e., the spatial localization) and to a hierarchy (i.e., the substructural type). These multi-indices are used below to label model parameters. Further $\mathcal{S}(\mathcal{C}(e, j)) = e$ and $\mathcal{H}(\mathcal{C}(e, j)) = j$, thus, $\mathcal{S}$ and $\mathcal{H}$ are the index operators pointing any

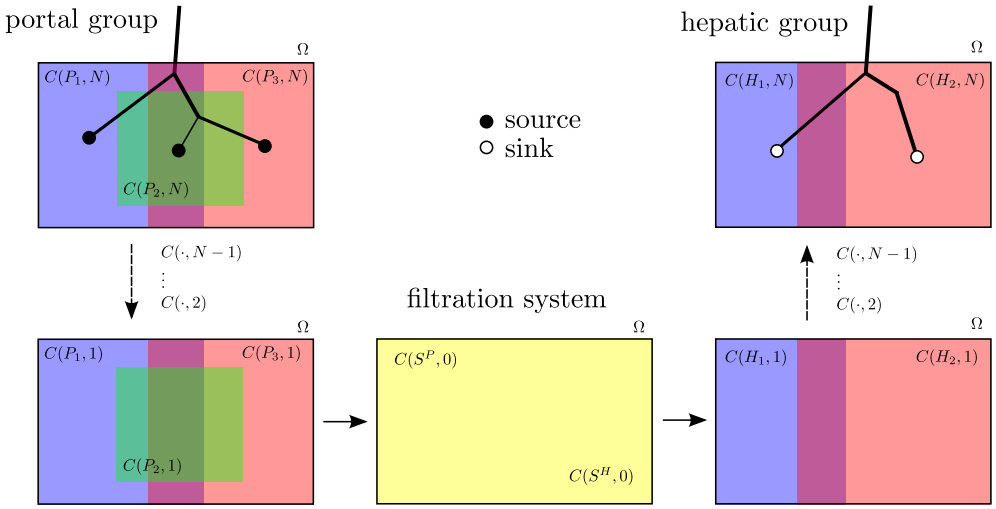

Figure 1: Schematic drawing of parenchyma compartments (each one associated with segment and hierarchy) and its connection with the portal and hepatic venous trees via sources and sinks. Here, the portal group consists of 3 overlapping segments and the hepatic group consists of 2 overlapping segments.

compartment to its segment and hierarchy, respectively.

The segments of the portal and hepatic groups overlap, Fig. 1; it holds that $\Omega = \bigcup_{i\in\mathcal{S}^P} \Omega_i$ and also $\Omega = \bigcup_{j\in\mathcal{S}^H} \Omega_j$. Moreover, in general, overlaps of segments belonging to the same group are possible $\Omega_i \cap \Omega_k \neq \emptyset$ for $k, i \in \mathcal{S}^P$ (and in analogy for the group H, thus segments $\mathcal{S}^H$). Hierarchies with the index $j = 0$ correspond to precapillary vessels of the lobular structure. In particular, the compartment $\mathcal{C}(\mathcal{S}^P, 0)$ is the precapillary network of the portal vein system, whereas $\mathcal{C}(\mathcal{S}^H, 0)$ is the similar network of the hepatic vein system. In these special cases, we unify the compartmental indices, thus $k = \mathcal{C}(\mathcal{S}^P, 0)$ is one compartment associated with the entire body Ω. In analogy, $l = \mathcal{C}(\mathcal{S}^H, 0)$ is treated as one compartment as well (although $\mathcal{S}(k) \neq \mathcal{S}(l)$).

The fluid flow between any two compartments is controlled by the so-called perfusion coefficient $G_i^j = G_j^i$; obviously $G_i^i = 0$. In general,

$$\text{if } \mathcal{H}(i) + \mathcal{H}(j) > 0, \text{ then } G_i^j = 0 \text{ whenever } \mathcal{S}(i) \neq \mathcal{S}(j) \text{ or } |\mathcal{H}(i) - \mathcal{H}(j)| > 1\,. \qquad (1)$$

Note that the case $\mathcal{H}(i) + \mathcal{H}(j) = 0$ and $i \neq j$ implies $i = \mathcal{C}(\mathcal{S}^P, 0)$ and $j = \mathcal{C}(\mathcal{S}^H, 0)$ (or vice versa) so that G_i^j controls the blood filtration in the capillary sinus of the liver lobule.

Groups, segments, hierarchies and volume fractions. The concept of volume fractions is a very natural basis on how to correlate model parameters with structural features. In the context of the present model, we need to relate the volume fractions ϕ_i to compartments i. Vessels of a given group G and associated with hierarchy h are distributed with volume fractions φ_h^G. Obviously $\sum_{h=0,\dots,N} \sum_{G=H,P} \varphi_h^G(x) + \varphi_m(x) = 1$ (all volume fractions must be nonnegative) and at any point $x \in \Omega$, where φ_m is the volume fraction

of all parts of the parenchyma that are not included in any compartment. Because of our assumption that segments belonging to the same group can overlap, a condition preserving portion of φ_h^G must be prescribed. For this, let $\chi_s(x)$ be the characteristic function of a segment s, and $\chi^G(x)$ be the characteristic function of overlaps, for any hierarchy h and for any $x \in \Omega$ the condition reads as follows:

$$\sum_{i\in\mathcal{C}(\mathcal{S}^G,h)} \phi_i(x)\chi^G(x) = \varphi_h^G(x)\ , \quad \text{where } \chi^G(x) = \prod_{s\in\mathcal{S}^G} \chi_s(x). \tag{2}$$

2.2 Macroscopic modeling of Darcy flow in parenchyma

The perfusion at the level of tissue parenchyma is approximated using a macroscopic model describing parallel flows in multiple compartments, cf. [1]. The model involves pressures $\{p^i\}_i$ associated to each compartment $i = 1, \ldots, \bar{i}$. Any i-th compartment occupying domain Ω_i can be saturated from an external source (or drained by a sink); in general one may define the local source/sink flux f^i. Alternatively, the pressure can be prescribed in a given subdomain $\Sigma_i \subset \Omega_i$ that can represent junctions with upper hierarchies of the perfusion system treated by the 1D flow model on branching networks, see Section 2.3; in practice, Σ_i can be formed by "small" balls, $|\Sigma_i| << |\Omega_i|$. The mass conservation for compartment i is expressed by the following condition (to be satisfied in $\Omega_i \setminus \Sigma_i$):

$$\begin{aligned} \nabla\cdot\boldsymbol{w}^i + \sum_j \mathcal{J}_j^i = f^i\ , \quad i = 1,\ldots,\bar{i} \quad \text{in } \Omega_i\setminus\Sigma_i,\\ \boldsymbol{w}^i = -\boldsymbol{K}^i\nabla p^i\ ,\\ \mathcal{J}_j^i = G_j^i(p^i - p^j)\ , \end{aligned} \tag{3}$$

where $\boldsymbol{K}^i$ is the local permeability of the i-th compartment network and G_j^i is the perfusion coefficient related to compartments i, j, so that $\mathcal{J}_j^i$ describes the amount of fluid, which flows from i to j (drainage flux; obviously $\mathcal{J}_i^j = -\mathcal{J}_j^i$). Eq. (3) is supplemented by the non-penetration condition, and by the Dirichlet condition:

$$\begin{aligned} \boldsymbol{n}\cdot\boldsymbol{w}^i = -\boldsymbol{n}\cdot\boldsymbol{K}^i\nabla p^i = 0 \quad \text{on } \partial\Omega_i\ ,\\ p^i = \bar{p}^i \quad \text{on } \partial\Sigma_i,\ i = 1,\ldots,\bar{i}\ . \end{aligned} \tag{4}$$

For the weak formulation of the problem (3)-(4), we shall need the following admissibility sets:

$$\begin{aligned} \mathcal{V}^i = \{q \in H^1(\Omega_i)|\ q = \bar{p}_i \text{ on } \partial\Sigma_i\}\ ,\\ \mathcal{V}_0^i = \{q \in H^1(\Omega_i)|\ q = 0 \text{ on } \partial\Sigma_i\}\ . \end{aligned} \tag{5}$$

In our numerical tests, we consider $\bar{p}_i$ being given by point values in vertices of the finite element mesh. For some compartments, Σ_i can vanish, so that $\mathcal{V}^i = \mathcal{V}_0^i = H^1(\Omega_i)$.

The numerical model is based on the weak formulation of the problem: Find $\boldsymbol{p} = (p^1, p^2, \ldots, p^{\bar{i}})$ such that $p^j \in \mathcal{V}^j$, $j = 1, \ldots, \bar{i}$ and

$$\int_{\Omega_i \setminus \Sigma_i} \boldsymbol{K}^i \nabla p^i \cdot \nabla q^i + \int_{\Omega_i \setminus \Sigma_i} \sum_j G^i_j (p^i - p^j) q^i = \int_{\Omega_i \setminus \Sigma_i} f^i q^i \ , \quad \forall q^i \in \mathcal{V}^i_0 \ ,$$

for all compartments $i = 1, \ldots, \bar{i}$. The summation in the second term takes only over nonvanishing G^i_j, recalling (1). All the parameters $\boldsymbol{K}^i(x)$ and $G^i_j(x)$ depend on the local volume fractions $\phi_i(x)$.

2.3 Flow on upper-level vascular trees

Let $\mathcal{T}(\{J^j\}_j \{\ell_e\}_e)$ be a branching tree formed by pipes ℓ_e and junctions J^j. By J^0 we denote the input junction, whereas the terminal branches end by junctions $\hat{J}^k$ through which they are connected with the parenchyma. Any junction $J^j = \{e\}$ of $\mathcal{T}$ joins several vessels (pipes) ℓ_e, although the input and terminal junctions are just one-element sets. Further by $\hat{n}$ we denote the number of all terminal junctions contained in the tree.

The model describing the flow on $\mathcal{T}$ can be given by the following $(\hat{n} + 1)$ equations:

$$\begin{aligned} A_0 w_0 &= \sum_k^{\hat{n}} A_k w_k \ , \\ \frac{1}{2}\rho w_0^2 + p_0 &= \frac{1}{2}\rho w_k^2 + p_k + e_k^{\text{loss}} \ , \quad k = 1, 2, \ldots, \hat{n}, \end{aligned} \tag{6}$$

where $(6)_1$ is the mass conservation and $(6)_2$ are the Bernoulli equations completed with the terms e_k^{loss} representing the friction loss in inelastic tubes and defined as

$$e_k^{\text{loss}} = \frac{1}{2}\varrho w_k^2 \frac{L}{D} \frac{64}{\text{Re}_k} \ , \tag{7}$$

where ϱ is the fluid density, L and D are the length and diameter of the pipes, respectively, and Re_k is the local Reynolds number. By A_k we denote the cross-sections of terminal and input branches, i.e., of the associated vessels. The unknown input pressure p_0 and terminal velocities $\{w_k\}_k$, $k = 1, \ldots, \hat{n}$ are computed on the basis of a given input velocity w_0 and terminal pressures $\{p_k\}_k$. In this paper, the system of non-linear algebraic equations (6) is numerically solved using the Newton method.

At this point, it should be noted that the substitution of the "3D" flow model by the simple "1D" model, as presented in this paper, is naturally associated with some loss of accuracy. On the other hand, this loss is not too serious and is clearly outweighed by the many advantages of the "1D" model application (minimal computational demand, results obtained in a matter of seconds etc.). For a detailed analysis of "3D" and "1D" blood flows in two realistic portal vein networks with either 9 or 39 terminal branches, see [9].

2.4 Coupled "1D" – "0D" model

The "1D" model described above is coupled with the "0D" model through the terminal junctions, which specify the sources and sinks f^i for all the considered compartments. For the i-th compartment saturated by the tree $\mathcal{T}$, we define

$$f^i(x) = \sum_{k=1}^{\hat{n}} \delta(x - \hat{x}^k) A_k w_k \ , \qquad p^i(\hat{x}^k) = p_k \ , \tag{8}$$

where $\delta(x - \hat{x}^k)$ is the Dirac distribution at point $\hat{x}^k \in \Omega$ associated with the terminal junction k. The condition $(8)_2$ couples the pressures at the terminal junctions of the "1D" model with the pressure fields in Ω. In practice, we use an approximation of $\delta(x - \hat{x}^k)$, which is based upon the finite element discretization that in this paper is also used for the numerical solution of the "0D" model.

Taking into consideration the presence of two trees $\mathcal{T}$, Fig. 1, let us denote the quantities associated with the portal and hepatic veins with the indices P and H, respectively. The computation of the perfusion pressure and velocity fields is carried out by a simple iterative algorithm: For the given values $\bar{w}_0^P$ and $\bar{p}_0^H$, i.e., the velocity in the portal vein (inlet) and the pressure in the hepatic vein (outlet), the computation proceeds by repeating the following steps:

1. Set all interface velocities and pressures to zero: $\{p_k^P\} = 0$ and $\{w_k^H\} = 0$. Set $i = 0$ and $\tau = 1/N$ for a given $N \in \mathbb{N}$.
2. For the new iteration $i := i+1$, update $w_0^P := \min\{i\tau, 1\}\bar{w}_0^P$ and $p_0^H := \min\{i\tau, 1\}\bar{p}_0^H$.
3. Solve (6) on trees $\mathcal{T}^P$ and $\mathcal{T}^H$, so that $\big(w_0^P, \{p_k^P\}\big) \mapsto \big(p_0^P, \{w_k^P\}\big)$ for the portal vein, and $\big(p_0^H, \{w_k^H\}\big) \mapsto \big(w_0^H, \{p_k^H\}\big)$ for the hepatic vein.
4. Solve (3)-(4) in Ω, so that $\big(\{w_k^P\}, \{p_k^H\}\big) \mapsto \big(\{p_k^P\}, \{w_k^H\}\big)$ and $(p^i(x), \boldsymbol{w}^i(x))$ is computed for a.a. $x \in \Omega$.
5. Use the conditions (8) to update the interface variables for the next iteration $i + 1$.
6. Go to step 2, unless a steady state is obtained.

3 CONVECTED CONTRAST FLUID IN POROUS MATERIALS

In clinical practice, the dynamic CT perfusion imaging is one of the possible ways how to observe and quantify the blood flow in the hepatic tissue. This type of perfusion scanning is based on CT scans with different levels of tissue density, a quantity proportional to the local concentration of the contrast fluid (tracer) dissolved in the blood. In order to simulate the tissue perfusion using data computed with the hierarchical model described in Section 2, we adopt the assumption that the content of the tracer in the blood is expressed by the saturation S defined for each of the individual compartments of the Darcy flow model used in the parenchyma, or for any branch of the upper level portal and hepatic perfusion trees. Then, considering possible fluid exchange between the

compartments, transport equations for the contrast fluid can be derived using the pre-computed perfusion velocities and the mass conservation law. This derivation yields a system of hyperbolic equations for the saturation in all the compartments. Based on this, the tissue contrast is defined locally as the weighted sum of all the saturations, where the weights are given by the volume fractions. The coupled system of equations constituting the hierarchical perfusion model is solved iteratively for a given flow rate at the input part of the portal vein and a given pressure at the output part of the hepatic veins.

3.1 Tracer redistribution in parenchyma

Let S^i be the tracer saturation of the i-the compartment, so that $c^i = \phi^i S^i$ (no summation) is the tracer partial concentration associated with i. Clearly, $S^i \in [0,1]$; this boundedness must be guaranteed by the transport equations (the conservation law). Then, the total apparent concentration C corresponding to the gray level in CT scans is defined as

$$C = \sum_i c^i = \sum_i \phi^i S^i \ . \tag{9}$$

The local conservation in a domain $\omega \subset \Omega$ for the i-th compartment is expressed as

$$\int_\omega \phi^i \frac{\partial S^i}{\partial t} + \int_{\partial\omega} \boldsymbol{w}^i \cdot \boldsymbol{n} S^i \mathrm{d}\Gamma + \sum_j \int_\omega Z^i_j(S) \mathcal{J}^i_j = \int_\omega S_{\mathrm{in}} f^i_+ + \int_\omega S^i f^i_- \ , \tag{10}$$

where S_{in} is the external source saturation, $f^i_+ > 0$ is the positive part (flow-in) of f^i, whereas f^i_- is the out-flow, and the Z switches:

$$Z^i_j(S) = \left\{ \begin{array}{ll} S^i & \text{if } \mathcal{J}^i_j > 0 \ , \\ S^j & \text{if } \mathcal{J}^i_j \leq 0 \ . \end{array} \right. \tag{11}$$

From Eq. (10), the following problem can be deduced: For the known velocity fields $\{\boldsymbol{w}^i\}_i$, perfusion pressure $\{p^i\}_i$ and initial conditions $\{S^i(t=0,x)\}_i = \{S^i_0(x)\}_i$ given in Ω, find $\{S^i(t,x)\}_i$ such that

$$\begin{gathered} \phi^i \frac{\partial S^i}{\partial t} + \nabla \cdot (S^i \boldsymbol{w}^i) + \sum_j Z^i_j(S) \mathcal{J}^i_j = S_{\mathrm{in}} f^i_+ + S^i f^i_- \quad x \in \Omega, \quad t > 0 \ , \quad i = 1, \ldots \bar{i} \ , \\ S^j \text{ given on } \partial_{j-}\Omega(\boldsymbol{w}^j) \ , \end{gathered} \tag{12}$$

where $\partial_{j-}\Omega(\boldsymbol{w}^j) = \{x \in \partial\Omega |\ \boldsymbol{w}^j \cdot \boldsymbol{n} < 0\}$.

In the present paper, the numerical solution of Eq. (12) is based on the upwind cell-centered finite volume scheme formulated for unstructured hexahedral grids in combination with the two-stage Runge-Kutta method of second order accuracy in time.

3.2 Transport on branching network

With reference to Section 2.3, we consider a branching network consisting of pipes and junctions. For this structure, we can derive the transport (advection) equations. Let $\ell =]x_0, x_1[$, $x_0, x_1 \in \mathbb{R}$ be a pipe. Thus, by x we refer to the axial coordinate along the oriented(!) pipe with the end-points x_0, x_1, while by $X \in \mathbb{R}^3$ we mean the spatial positions associated with x. We consider a velocity $w(x)$ and cross-section $A(x)$ given at any $x \in \ell$, which satisfy the mass conservation

$$\frac{\partial}{\partial x}(wA) = \frac{\partial Q}{\partial x} = 0 \ , \quad x \in \ell, \tag{13}$$

where Q is the flux in the pipe. With this in mind, the equation for the transport of the contrast fluid can be easily derived

$$\frac{\partial}{\partial t}S(x,t) + w(x)\frac{\partial}{\partial x}S(x,t) = 0 \ , \quad x \in \ell, \tag{14}$$

where $S(x,t)$ is the local instantaneous saturation. At the pipe ends, we consider the boundary conditions:

$$\begin{aligned} S(x_0,t) &= S_0(t) \quad \text{given for } Q > 0 \ , \\ S(x_1,t) &= S_1(t) \quad \text{given for } Q \leq 0 \ . \end{aligned} \tag{15}$$

For more details on the transport of the contrast fluid in the branching network, we refer the reader to [10]. As for the effect of network simplification on the tracer transport, the only drawback that can be clearly noted when "1D" networks are used instead of realistic "3D" ones is the absence of gradual tracer wash-out at the ends of the terminal branches, which in the case of the "3D" network is a result of tracer accumulation near the walls [9].

4 NUMERICAL EXAMPLES

The multiscale modeling approach described in this paper is tested for steady blood flow and tissue perfusion in two different models of liver. The first one is an artificially generated model consisting of 7 compartments (portal group: 3 overlapping segments, hepatic group: 2 overlapping segments) and the second one is a simplified patient-specific model consisting of only 2 compartments. Assuming the porosity of the hepatic tissue ϕ^i to be constant in both liver models and set equal to 0.8, the propagation of the contrast fluid is simulated by prescribing an external source saturation in the form of a time bolus at the inlet of the portal vein network [10].

The numerical simulations of tracer transport in the two considered liver models are documented in Figs. 2 and 3. Fig. 2 shows the time development of the saturation in three selected compartments of the idealized liver model, while Fig. 3 presents the time-dependent distribution of the saturation in the two considered compartments of the simplified patient-specific liver model. For illustration, Fig. 3 also includes the transverse section of the patient-specific model with the computed total concentration.

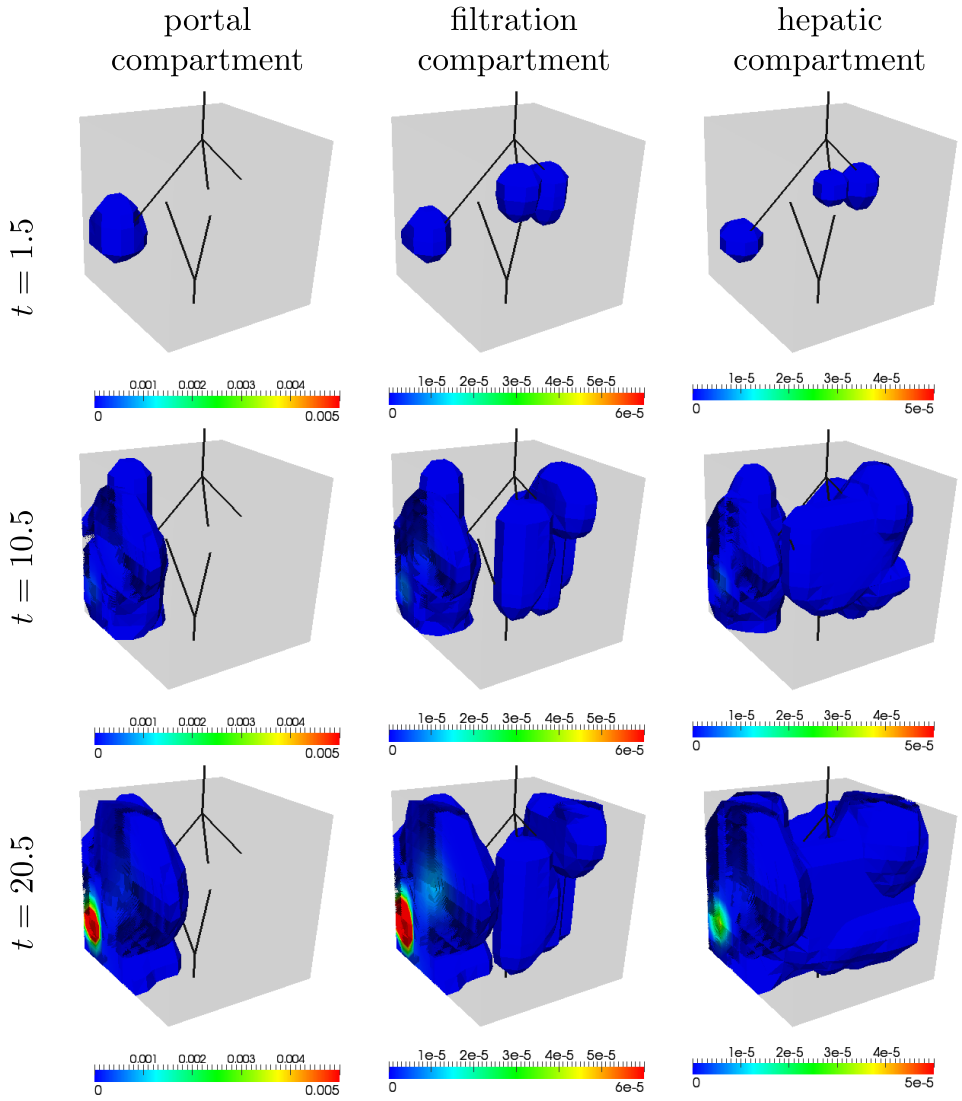

Figure 2: Time development of the saturation in selected compartments of the idealized liver model. The "1D" branching networks of the portal and hepatic veins are represented by black lines.

5 CONCLUSION

Considering the complexity of organ perfusion, the multicompartment hierarchical model proposed in this paper is designed to describe the blood flow at several scales, i.e., from large- and middle-sized vessels to parenchyma. One of the model advantages is the fact that it takes into consideration the actual blood distribution within the organ by connecting the parenchyma with the supply and drainage vascular trees via a system of point sources and sinks. With this approach, we are confident that the developed model can provide a more accurate way on how to observe and quantify hepatic tissue perfusion than it would be the case with the classical conventional compartment models, cf. [6]. In

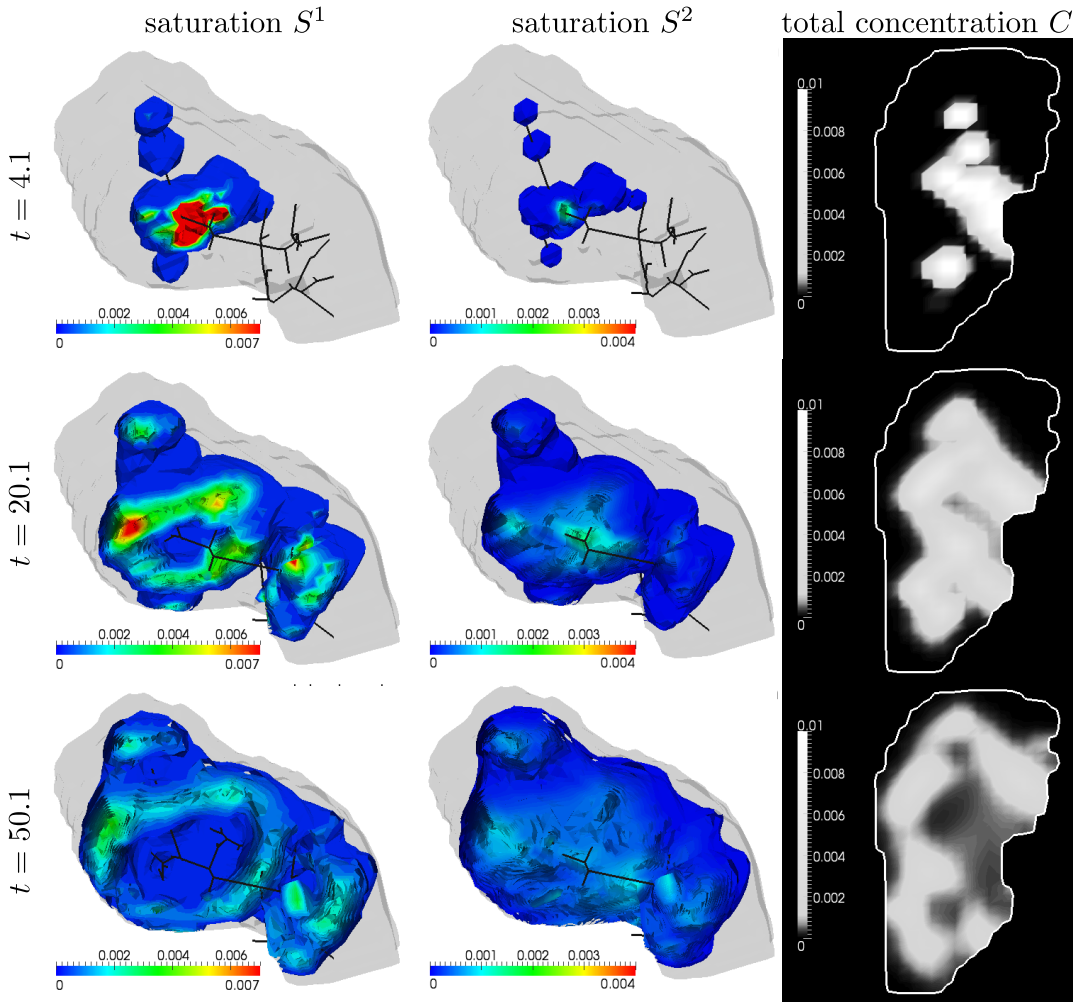

Figure 3: Time development of the saturation S^i, $i = 1, 2$ in the simplified patient-specific liver model and the corresponding distribution of the total concentration C in the transverse section. The "1D" branching networks of the portal and hepatic veins are represented by black lines.

order to get some feedback regarding the perfusion simulations and to provide a way how to possibly "tune" the parenchyma model based on real CT scans, the perfusion velocities computed by the proposed model can be further utilized in the simulation of contrast fluid propagation. In this paper, the modeling of tissue perfusion and tracer transport was illustrated for idealized and patient-specific liver geometries, both with supply and drainage "1D" vascular trees.

At this point, it should be noted that besides the necessary simplifications, the most serious drawback of the present multiscale modeling lies in the identification of model parameters. In order to address this issue, we intend to formulate and solve an inverse problem. Namely, perfusion CT scans should serve as a means to compute an optimal set of parameters that would be able to provide the best fit in terms of tissue densities.

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