

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

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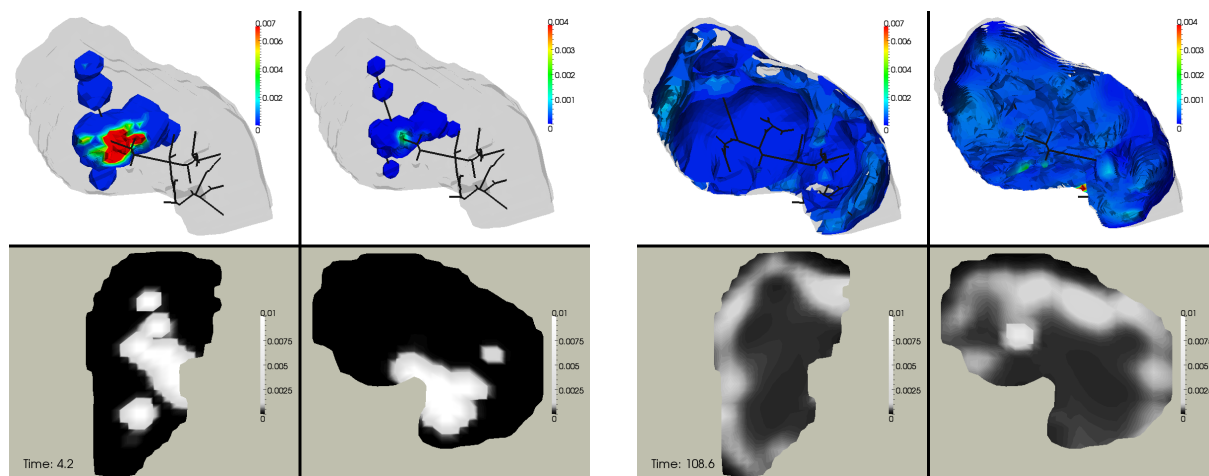
Simulations of tissue perfusion is aimed to find accurately parts of the tissue with an insufficient blood supply, to localize anomalies in the blood micro-circulation and to quantify locally the perfusion efficiency.

In the context of liver tissue, the model proposed in this paper forms a basis for reconstruction of the liver segments, the anatomical parts of the autonomous perfusion related to a terminal branch of the portal vein tree. Our effort is to improve modeling techniques for processing the standard dynamic CT (computed tomography) investigations. For this we developed a multicompartment hierarchical model [1], cf. [2], of the tissue parenchyma which is coupled with a 1D model describing blood flow through the upper level of portal (P) and hepatic (H) veins. The perfusion velocities in all compartments are involved in the transport equations governing the contrast fluid distribution.

The multicompartment perfusion model describes Darcy flows in a 3D volume. The compartments are associated with distinguished branches of the lower levels of the P and H trees. They can overlap in the space, however the fluid flow between any two overlapping compartments with different pressure is controlled independently by the transmission coefficients. The lowermost level corresponds to the precapillary networks constituting the lobular structure. The permeability and transmission coefficients are determined for a defined locally periodic structure by the homogenization method [3].

The upper level “1D” trees, being connected with the upper level Darcy flow compartments by point sources and sinks, describe the portal and hepatic veins of the liver, respectively. They are formed by pipes and junctions representing the branching structures. 1D flows are described by the Bernoulli model extended by the dissipation terms accounting for the fluid viscosity and pressure losses associated with the bifurcations.

The third part of the model describes distribution of the tracer in time with the aim of simulating the dynamic CT perfusion test which provides scans of the tissue density. This quantity is proportional to the local concentration of the contrast fluid (the tracer). We assume that the tracer is dissolved in the blood; its content in the solution is expressed by the saturation defined for each of the individual compartments of the Darcy flow model. Using the pre-computed perfusion velocities, the mass conservation law, and taking into account fluid exchange between the compartments we derive transport equations for all the compartments. Thus, we obtain a system of hyperbolic equations for resolving the saturations. Then the tissue contrast is defined locally as the weighted sum of all the saturations; 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 arterial branching tree (the portal vein in the liver) and a given output pressure at the outlet of the venous tree.



Simulation of the liver perfusion: saturation in the portal and hepatic compartments (top), computed density of the tissue (bottom); two time instants.

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