A NEW OPEN-SOURCE WORKFLOW FOR MULTISCALE MODELING OF HEPATIC PERFUSION

Mohamed A CHETOUI (1), Mathilde MORVAN (1), Pierre BEAUREPAIRE (1), Antoine VACAVANT(1)

1. Université Clermont Auvergne, Clermont Auvergne INP, CNRS, Institut Pascal, France

Introduction

A failure of the blood micro-circulation in the liver is generally linked to the loss of cell functions and the development of hepatic diseases such as fibrosis. Therefore, studying liver perfusion allows us to better understand its degenerative and pathological behavior. The mechanism of hepatic perfusion is particular and involves several phenomena. The liver receives about 70% of the blood from the portal vein (PV) and 30% from the hepatic artery (HA) and drains it toward the hepatic vein (HV). These vessels bifurcate within the liver to form three vascular trees covering the entire organ tissue. Vessel bifurcation is accompanied by a size reduction resulting in a variation of diameter from 10^{-2}m at the principal vessels to 10^{-5}m at the final capillaries. The exchange between these vascular trees occurs at the final capillaries level. Given the strong dependency between macro- and micro-circulations, a multiscale model is essential to a better understanding of hepatic perfusion. The two main obstacles to a such model are the range of variation of the vessel diameters and the inability of current imaging techniques to capture small vessels. Recent studies have introduced a multi-compartment model that overcomes these locks in modeling highly perfused tissue [1] and it was applied to cervical, cardiac, and hepatic perfusion. This model uses optimization methods such as the CCO algorithm to generate low-level vessels in a way to mimic the anatomical vascular tree properties [2]. The current paper presents a patient-specific application of the multi-compartment model to liver perfusion using a fully open-source workflow that will be published in open access after its validation.

Methods

In this study, the HA supply is neglected, only the flows in PV and HV are considered. The geometry of the liver and the principal vessels of PV and HV are constructed based on CT-Scan sequences of a 62-years old male without a tumor (IRCAD database [3]). The flow in the vessels captured by CT is supposed unidirectional and is computed using mass conservation and Bernoulli equations. The results of the 1D flow at the terminal segments of the principal trees will be defined as boundary conditions for the flow in the parenchyma.

The smaller vessel trees, non-captured by CT are generated artificially using CCO. The artificial, but anatomically veracious, network is used to define a 3D flow in the parenchyma assimilated to a porous media. The main idea of the multi-compartment model is to divide each artificial vascular tree into N hierarchies based on vessel diameter. Let $C_{T,I}$ be a compartment defined by the hierarchy I (1 .. N) and the tree T (PV or HV). The blood exchange between HV and PV is only possible at the smallest capillary level defined by the compartment $C_0 = C_{PV,0} \cup C_{HV,0}$. The flow in parenchyma is computed at each compartment $C_{T,I}$ according to the following Darcy system:

$$-k_{T,I}\, div(p_{T,I}) + \sum_{J=0}^{N} \chi_{T,IJ}(p_{T,I} - p_{T,J}) = 0$$

where $k_{T,I}$ is the permeability of $C_{T,I}$, $p_{T,I}$ its pressure, and $\chi_{T,IJ}$ is a coupling coefficient between $C_{T,I}$ and $C_{T,J}$. The permeability and the coupling coefficients are obtained by a parametrization process based on the architecture of the artificial tree [1]. Three compartments are defined in the current model. The parameterization process is carried out using a Python script and the FE simulations are performed using FreeFem++.

Results

The pressure distribution in the lower level is in the physiological range (Fig.1). The pressure value is maximal near to PV source points and minimal near to HV sink points. As expected, the velocity magnitude drops from higher to lower compartments since the pressure variation range decreases in the small vessels.

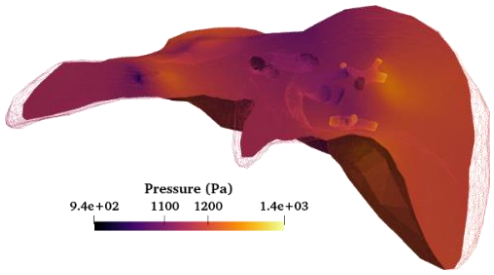

Figure 1: Pressure in compartment C_0

Discussion

The multi-compartment model permits to study the multiscale mechanism of liver perfusion. For lack of experimental data, the model can be validated by comparing the obtained results with a Poiseuille flow computed in the whole vascular tree. After validation, the presented workflow can be used to study the effect of pathological alterations on liver micro-circulation.

References

1. Rohan et al, J Math. Biol., 77:421-454, 2018.
2. Talou et al, Sci Rep, 11, 6180, 2021.
3. 3D Image Reconstruction for Comparison of Algorithm Database. https://www.ircad.fr/research/data-sets/