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Multiscale 1D-3D models for tissue perfusion and applications.

C. D'Angelo

MOX labs
Politecnico di Milano
Piazza Leonardo da Vinci, 32
20133 Milano - Italy
carlo.dangelo@polimi.it

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ABSTRACT

Mass transport in tissues is led by blood *perfusion*, that is the blood volume flow exchange through a given volume of tissue. This includes oxygen transport, waste removal and drug release among the most clinically interesting phenomena. Moreover, blood perfusion levels are valuable indicators of the physiological condition of a given tissue; in general, the evaluation of the microcirculation in a variety of tissues is a relevant information to the clinicians in a number of cases, from surgical intervention to the design of biomedical devices.

From this picture, it is clear that mathematical models of blood perfusion and transport of chemicals in tissues are important tools for diagnosis and research in medicine. However, the description of blood flow from large vessels down to the network of hundreds of thousands of capillaries per square centimeter supplying a tissue, is a very complex matter. The more precise the models, the more expensive the corresponding computations: thus, a complete three-dimensional simulation of blood flow and transport in a tissue resolving all levels of vessel branching is unaffordable, and reduced multiscale models have to be employed.

In this talk we present a multiscale approach that aims to accurately describe tissue perfusion and transport phenomena in biological tissues without resolving all the vascular hierarchies. Indeed, we look at perfusion as flow in a porous three-dimensional medium with one-dimensional fractures, where the capillary network is represented by the porous matrix, and the major blood vessels are described by the fractures embedded in the porous medium. In this sense we aim to create a link between the well known multiscale analysis of blood flow in vessels (for 3D/1D/0D models and their coupling we refer for instance to [1]) and the perfusion models based on porous media theory [2], introducing a novel aspect: the influence of the geometry of the network of medium and large vessels on the perfusion pattern in a tissue.

From the mathematical point of view, the kind of problems that we address are coupled diffusion-reaction equations, one taking place in a three-dimensional domain Ω, the other in a one-dimensional subdomain $\Lambda \subset \Omega$. The 3D equation features a measure term to account for mass conservation, which

makes the considered problem non-standard. After presenting the analytic tools [3] that can be used to establish the well-posedness of the problem, we introduce a finite element scheme for the numerical approximation of the coupled problem. Then, we discuss the issues of treating the 1D geometry and of adopting suitable time advancing schemes for the unsteady case. We also consider more advanced strategies (for instance using hyperbolic 1D models) for modeling flow in larger vessels.

Finally, we discuss some applications in biomedicine: in particular, we show how our techniques can be used to study quite different phenomena, from brain perfusion and blood flow in the Circle of Willis (see figure 1) to the complex drug release by coated stents into the vessel wall.

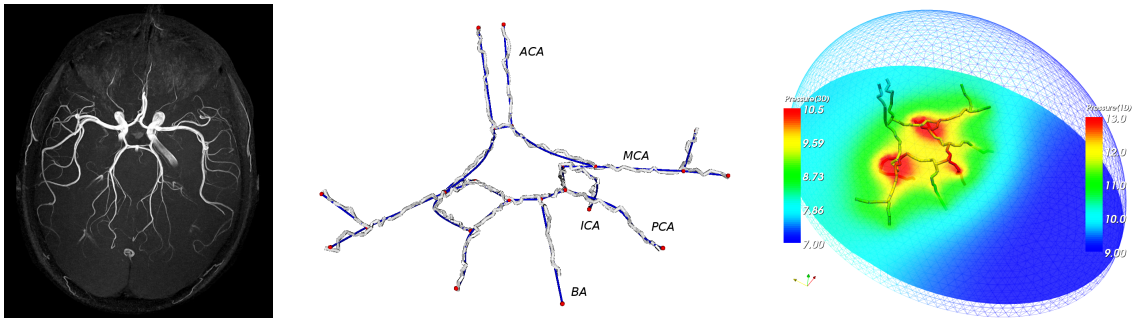

Figure 1: 1D-3D simulation of blood flow in the Circle of Willis and of brain perfusion. From the left to the right: brain angiography showing the geometry of the Circle of Willis, 1D reconstruction of the Circle of Willis, and blood pressures in the Circle of Willis and in the surrounding cerebral tissue.

REFERENCES

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