Modeling momentum and mass transport in brain microvascular networks

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1. Introduction

The cerebral microvascular system is key to a large variety of cerebral processes, including oxygen and nutrient delivery to brain cells as well as blood flow regulation as a function of neural activity. It plays a central role in numerous pathologies ranging from strokes to neurodegenerative diseases. In spite of these important implications, most of the brain microvascular system still remains unexplored. However, recent anatomical functional *in vivo* imaging techniques, such as two photon laser scanning microscopy together with optical manipulation of blood flow, have permitted significant breakthroughs [1]. These methods generate massive amounts of data that are difficult to interpret without proper theoretical and numerical frameworks. Our goal is, therefore, to develop models for both momentum and mass transport in the brain microcirculation.

2. Methods and models

2.1. Blood flow

We consider the blood as a monophasic, non-Newtonian fluid which rheology strongly depends on the vessel diameter and discharge hematocrit. Blood flow splitting at bifurcations is also non-linear because of the inequal repartition of red blood cells between branches [5]. In this context, a simple linear pore network model does not provide an accurate representation of momentum transport. To overcome this issue, we use an algorithm based on a non-linear iterative solver, which was previously developed by our group [3], [4] and tested for large anatomical networks as shown in figure 1.

2.2. Mass transfers

The complexity of anatomical networks, which can include thousands of vessels, makes it difficult to use classic direct numerical simulation methods such as finite elements (FEM) or finite differences. Here, we develop mesh reduction methods to model mass transport and transfer phenomena. Homogenization methods [6, 7] are first used to reduce the 3D transport equation inside the vessel to a 1D axial equation with exchange terms with the surrounding tissues. As for the transport in tissues surrounding the vessel, taking advantage of the linearity of the diffusion equation, we use a boundary element method (BEM) inspired by Hsu et Secomb [2]. This approach significantly reduces the number of unknowns from hundred of thousands to barely a thousand for a single vessel geometry. Initially developed for the stationary diffusion equation the model has been extended to the instationary domain for simple geometries.

3. Results and perspectives

First simulations of mass transfer have been performed for a single vessel and show very good agreement with classic direct numerical simulation using finite element methods as shown in figures 2 and 3. The results of our model suggest, for stationary simulation, an improvement when compared to those obtained with the original model of Hsu and Secomb, as shown in figure 2. The equations solved

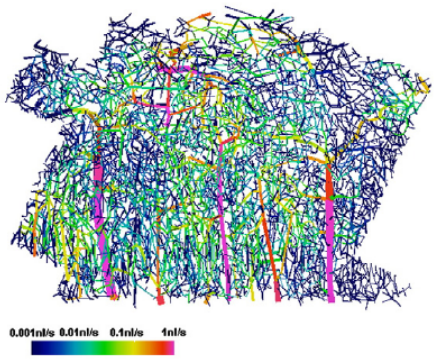

Figure 1: Stationnary flow rate distribution (logarithmic scale) in a human brain microvascular network (10 000 segments), from Ref [1].

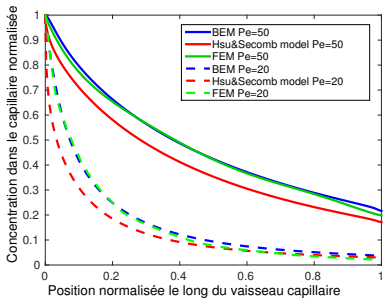

Figure 2: Comparison of normalized tracer concentration field along the vessel axis between stationary BEM (blue curves), FEM (green curves) and the original model of Hsu and Secomb (red curves) for a Péclet number of 50 (plain cruves) and 20 (dashed curves).

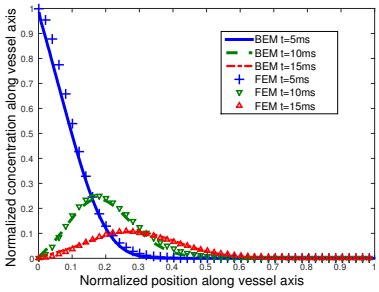

Figure 3: Comparison of normalized tracer concentration field along the vessel axis between time dependent BEM (lines) and FEM (symbols) methods with a unit concentration square function of 5ms as the inlet boundary condition

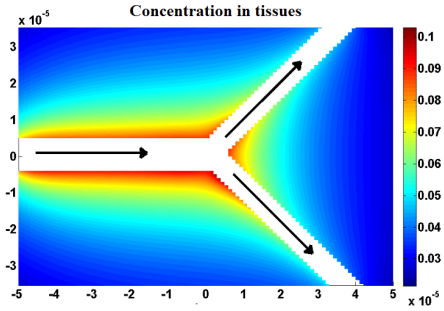

Figure 4: Plane cut concentration field in the tissue for a bifurcation geometry using the stationary BEM model with imposed concentration at the inlet and zero concentration at infinity. The white parts symbolize the vessel in which blood flow carries the concentration function from left to right.

in figure 2 correspond to the stationary transport of a passive tracer convected by a flat velocity profile in a single vessel embeds in an infinite volume of tissue for different Péclet numbers, while figure 3 refers to the time dependant version of the equation. Since these preliminary results were encouraging, we started to extend our stationary model to bifurcations, as shown in figure 4. In future work we plan to adapt the mass transport model to deal with pressure driven velocity profiles and transport of reactive molecule such as oxygen, using the homogenization methods. In addition, we will extend the mass transport model to larger networks and couple it with the non linear flow solver described above and study the impact of targeted occlusions of particular vessels on both mass transfer and blood flow.

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