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# Upscaling mass transfer in brain capillary networks

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Various imaging techniques are now capable measuring spatio-temporal concentration fields of various endogenous or exogenous tracers in the brain. For example, the concentration of radio-labeled water injected transiently in the vascular system can be measured by Positron Emission Tomography (PET), while the presence of paramagnetic deoxy-hemoglobin induces contrast in functional Magnetic Resonance Imaging (fMRI). The resolution of PET is about  $(10 \text{ mm})^3$  while fMRI can achieve resolutions down to  $1 \text{ mm}^3$ . This is much coarser than the diameters of most arterioles and venules, which are typically below  $100 \text{ }\mu\text{m}$ , and, of course, of capillaries, whose diameters are tenfold smaller.

This implies that methods to deduce the regional blood flow rate out of these large-scale concentration fields must rely on upscaled models which take into account the micro-structure of the vascular system. Consequently, capturing the strong link between micro-vascular structure and mass transfer at mesoscopic scales is a major hurdle in the challenge to better understand and exploit the information obtained by these imaging techniques, as discussed in [1].

It has been shown in [3] that at the capillary level, the vessels exhibit a space filling mesh-like structure, for which a Representative Elementary Volume (REV) can be extracted. This property allows for the use of the Volume Averaging Technique on the advection-diffusion equations at this particular scale. This method has been developed for upscaling mass transfer in heterogeneous porous media [2]. It requires solving closure equations on a REV to deduce effective coefficients representative of the micro-structure. The REV is a 3D network of capillaries with diameters ranging from  $1$  to  $10 \text{ }\mu\text{m}$  embedded in tissue. Its typical volume is about  $(150 \text{ to } 300 \text{ }\mu\text{m})^3$ . Being able to solve closure equations on several geometries taking into account the presence of individual vessels is a computational challenge.

We developed a numerical framework to solve partial differential equations on anatomically accurate vascular networks using the high performance finite element library Feel++ [4].

This framework is used to solve the closure equations on a VER needed to get the effective coefficients from the homogenization method as well as to perform direct simulations of mass transfers to check the homogenization procedure. In the first part of the presentation we will present this framework, with focus on, the way to obtain a mesh adapted to vascular networks. Then, we will detail the procedure to obtain effective coefficients in the capillary network. Finally, we will show that the homogenized and the direct approach are in good agreement.

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## References

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